

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3229:

Met	Ala	Arg	Ser	Pro	Ala	Ala	Ser	Ser	Ser	Ser	Tyr	Thr	Asp	Ser	Thr
1				5						10				15	
Gly	Ser	Ser	Ser	Asp	Ser	Gly	Ser	Thr	Ser	Ser	Gly	Ile	Asp	Arg	Arg
				20				25					30		
Arg	His	Glu	Arg	Glu	Arg	Arg	Ser	Ala	Ser	Asp	Asp	Asp	Ser	Tyr	
				35				40				45			
Ser	Thr	Ser	Ser	Tyr	Asp	Ser	Asp	Arg	Glu	Val	Ser	Gly	Arg	Ser	Arg
				50			55				60				
Lys	His	Lys	Lys	Ser	Ser	Arg	Ser	Arg	Lys	Ser	Arg	Glu	Arg	Glu	Arg
65				70				75						80	
Ser	Lys	Asp	Arg	His	His	Lys	Arg	Asp	Lys	Ser	Lys	His	Lys	Glu	Lys
				85				90					95		
Lys	Glu	Ser	Glu	His	Ala	Asp	Gly	Pro	Val	Gln	Leu	Ser	Lys	Phe	Leu
				100				105					110		
Gly	Arg	Asp	Lys	Glu	Lys	Glu	Glu	Gly	Thr	Gln	Arg	Ser	Ala	Ile	Ser
				115				120				125			
Gly	Lys	Lys	Ile	Met	Met	Lys	Leu	Glu	Lys	Thr	Lys	Glu	Asp	Lys	Ala
				130			135				140				
Ala	Glu	Ser	Lys	Arg	Asn	Glu	Leu	Leu	Lys	Phe	Leu	Asn	Ala	Ser	Tyr
				145		150				155				160	
Asp															

(2) INFORMATION FOR SEQ ID NO:3230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..921
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3230:

atatttagac	gacaccccta	cccgacccga	tcggcgggag	agcacgagac	gccagcgcca	60
tccatcgggg	caaaagccga	gacgacccag	gaatctcgcc	accgtcgccc	ccctttctct	120
ctcgctcaaa	agttgctgct	ggagccctct	ccctctctct	cgaccacca	ccatggatga	180
ggcgcaagct	gtggagtcac	aggatggaac	catctcggtt	gcttctgcat	ttgctgggta	240
tcaggaaagt	gtgcaagaca	gggatccaca	attcttgaca	maagcagtg	aagaagcata	300
tcgaggagtc	gattgcggtg	acggaggtcc	attcggagca	gttgctgctc	gtaatgacga	360
agTagtatgc	agctggccata	acatggttct	gaagcacact	gaccctactg	cgcattgctga	420
agtaactgca	attagagagg	cttgcaaaaa	gcttggggaa	attgagctct	cagactgcga	480
aatttacgcg	tcctcgagcg	catgcccaat	gtgccttagt	gcagttcatc	ttcccgaagt	540
caagaggctg	gtttatgggg	ccaaggcaga	ggctgcccat	gccattggat	ttgatgactt	600
cattgcagat	gctctgagag	gcactggggt	ctaccagaag	gccaaacttg	agatcaagaa	660
agctgacggc	aatgggtgat	tgatcgctga	gcaagtcctt	gaaaaagacta	aagagaaggtt	720
ccagatgtac	tgatgctgag	cagaagagag	atctcagatt	tgtacaatgc	ttactcataa	780
ggacaagaaa	taatacagtg	cccaaatgtc	caattgtttc	ggaaaaaaat	ctcaattcca	840
ctgttcaaca	ttttgatgat	gcctgaattt	cttgtaacca	gacacaagat	tgttatttgc	900
tgtaaaatgt	gcagttgatg	g				

(2) INFORMATION FOR SEQ ID NO:3231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3231:

Phe Leu Asp Asp Thr Pro Thr Arg Pro Asp Arg Arg Glu Ser Thr Arg
1 5 10 15
Arg Gln Arg His Pro Ser Arg Gln Lys Pro Arg Arg Pro Arg Asn Leu
20 25 30
Gly Thr Val Ala Pro Leu Ser Leu Ser Leu Lys Ser Cys Cys Trp Ser
35 40 45
Pro Leu Pro Ser Leu Arg Pro Pro Thr Met Asp Glu Ala Gln Val Val
50 55 60
Glu Ser Lys Asp Gly Thr Ile Ser Val Ala Ser Ala Phe Ala Gly Tyr
65 70 75 80
Gln Glu Ala Val Gln Asp Arg Asp His Lys Phe Leu Thr Xaa Ala Val
85 90 95
Glu Glu Ala Tyr Arg Gly Val Asp Cys Gly Asp Gly Gly Pro Phe Gly
100 105 110
Ala Val Val Val Cys Asn Asp Glu Val Val Val Ser Cys His Asn Met
115 120 125
Val Leu Lys His Thr Asp Pro Thr Ala His Ala Glu Val Thr Ala Ile
130 135 140
Arg Glu Ala Cys Lys Lys Leu Gly Lys Ile Glu Leu Ser Asp Cys Glu
145 150 155 160
Ile Tyr Ala Ser Cys Glu Pro Cys Pro Met Cys Phe Ser Ala Val His
165 170 175
Leu Ser Arg Ile Lys Arg Leu Val Tyr Gly Ala Lys Ala Glu Ala Ala
180 185 190
Ile Ala Ile Gly Phe Asp Asp Phe Ile Ala Asp Ala Leu Arg Gly Thr
195 200 205
Gly Phe Tyr Gln Lys Ala Asn Leu Glu Ile Lys Lys Ala Asp Gly Asn
210 215 220
Gly Ala Leu Ile Ala Glu Gln Val Phe Glu Lys Thr Lys Glu Lys Phe
225 230 235 240
Gln Met Tyr

(2) INFORMATION FOR SEQ ID NO:3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3232:

Met Asp Glu Ala Gln Val Val Glu Ser Lys Asp Gly Thr Ile Ser Val
1 5 10 15
Ala Ser Ala Phe Ala Gly Tyr Gln Glu Ala Val Gln Asp Arg Asp His
20 25 30
Lys Phe Leu Thr Xaa Ala Val Glu Glu Ala Tyr Arg Gly Val Asp Cys

	35		40		45														
Gly Asp	Gly Gly	Pro Phe	Gly Ala	Val Val	Val Val	Cys Asn	Asp Glu	Val											
50			55			60													
Val Val	Ser Cys	His Asn	Met Val	Leu Lys	His Thr	Asp Pro	Thr Ala												
65		70			75		80												
His Ala	Glu Val	Thr Ala	Ile Arg	Glu Ala	Cys Lys	Lys Leu	Gly Lys												
		85			90		95												
Ile Glu	Leu Ser	Asp Cys	Glu Ile	Tyr Ala	Ser Cys	Glu Pro	Cys Pro												
		100			105		110												
Met Cys	Phe Ser	Ala Val	His Leu	Ser Arg	Ile Lys	Arg Leu	Val Tyr												
		115			120		125												
Gly Ala	Lys Ala	Glu Ala	Ile Ala	Ile Gly	Phe Asp	Asp Phe	Ile												
130			135		140														
Ala Asp	Ala Leu	Arg Gly	Thr Gly	Phe Tyr	Gln Lys	Ala Asn	Leu Glu												
145			150		155		160												
Ile Lys	Lys Ala	Asp Gly	Asn Gly	Ala Leu	Ile Ala	Glu Gln	Val Phe												
		165			170		175												
Glu Lys	Thr Lys	Glu Lys	Phe Gln	Met Tyr															
		180			185														

(2) INFORMATION FOR SEQ ID NO:3233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455

(D) OTHER INFORMATION: / Ceres Seq. ID 1576134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3233:

aaatggatgg	cattatgaac	acggcctccg	caagcatgtc	catgtacgct	taccttgctc	60
tctctcaagcc	ccaggggcaag	atgatcctgc	tggcgctgcc	tgagaagcct	ctgcagatct	120
ccgcctttctc	tttggttact	gggggcaaga	ctctggccgg	gagctgcattg	ggagcatca	180
gggacacgca	ggagatgatg	gacttcgcag	ccaagcacgg	gttgacacgg	gacatcgaa	240
tgatcggcac	cgaagaagtt	aatgaggcca	tggaacngyc	tcgccaaggg	cgaggNtcag	300
gtaccgcttc	gtcatcgaca	tcggcaacac	catcagcgcg	gcatactag	ggagctgcc	360
gggtccagct	ctgtagctgc	gacacttggt	cctgcttgga	tatatcgctc	gataagcaag	420
tatatctgga	ataaaaaagga	actcaattta	aacgc			

(2) INFORMATION FOR SEQ ID NO:3234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1576135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3234:

Met Asp	Gly Ile	Met Asn	Thr Ala	Ser Ala	Ser Met	Tyr Ala	
1		5		10		15	
Tyr Leu	Ala Leu	Leu Lys	Pro Gln	Gly Lys	Met Ile	Leu Leu	Gly Leu
	20		25		30		
Pro Glu	Lys Pro	Leu Gln	Ile Ser	Ala Phe	Ser Leu	Val Thr	Gly Gly
	35		40		45		
Lys Thr	Leu Ala	Gly Ser	Cys Met	Gly Ser	Ile Arg	Asp Thr	Gln Glu
50		55		60			
Met Met	Asp Phe	Ala Ala	Lys His	Gly Leu	Thr Ala	Ser Ile	Glu Leu
65		70		75		80	

Ile Gly Thr Glu Glu Val Asn Glu Ala Met Glu Xaa Xaa Arg Gln Gly
85 90 95
Arg Xaa Ser Gly Thr Ala Ser Ser Ser Thr Ser Ala Thr Pro Ser Ala
100 105 110
Arg His His
115

(2) INFORMATION FOR SEQ ID NO:3235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3235:

Met	Asn	Thr	Ala	Ser	Ala	Ser	Met	Ser	Met	Tyr	Ala	Tyr	Leu	Ala	Leu
1			5						10				15		
Leu	Lys	Pro	Gln	Gly	Lys	Met	Ile	Leu	Leu	Gly	Leu	Pro	Glu	Lys	Pro
			20					25				30			
Leu	Gln	Ile	Ser	Ala	Phe	Ser	Leu	Val	Thr	Gly	Gly	Lys	Thr	Leu	Ala
			35				40					45			
Gly	Ser	Cys	Met	Gly	Ser	Ile	Arg	Asp	Thr	Gln	Glu	Met	Met	Asp	Phe
			50			55					60				
Ala	Ala	Lys	His	Gly	Leu	Thr	Ala	Asp	Ile	Glu	Leu	Ile	Gly	Thr	Glu
65					70				75					80	
Glu	Val	Asn	Glu	Ala	Met	Glu	Xaa	Xaa	Arg	Gln	Gly	Arg	Xaa	Ser	Gly
			85					90						95	
Thr	Ala	Ser	Ser	Ser	Thr	Ser	Ala	Thr	Pro	Ser	Ala	Arg	His	His	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:3236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3236:

aaacgcacac	tccatatacc	gccgccatcg	tctcgggctc	tccatctctaa	tcttcggggtt	60
cgcgctgcag	tgtctttccg	ccgggctacc	accatgccga	agcagatcca	cgagatcaag	120
gacttctctgc	tgactgcgcg	gcggaaggac	gcacggtcgg	tgcggatcaa	gcggggccaag	180
gacgcgcgtca	agttcaaggt	gcgctgctcc	aggtacctct	acacctctcg	cgtccacgac	240
gcgcacaagg	ccaacaagct	caagcagtcg	ctcccgccag	gtctgactgt	ccaggagagt	300
taaggtatca	agccacaaac	tgtgcttttt	ttgcgggtgc	agggacgttt	gctccagttg	360
tacttttagtt	tgtaggtggg	ctccattgct	gtgtttgaat	gaattatgaa	gtttgagttt	420
agagatgcgaa	tgatgtgtcg	aacctatgag	Gcctgtgttg	taatggttac	cccagaccgg	480
aaaagatggc	aattctatcat	aaagtaaaact	gatttccg			

(2) INFORMATION FOR SEQ ID NO:3237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1576139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3237:

Lys	Arg	Thr	Leu	Leu	Tyr	Pro	Pro	Pro	Ser	Arg	Ala	Leu	Ile	Ser
1				5					10				15	
Asn	Leu	Arg	Val	Arg	Val	Ala	Val	Ser	Ser	Ala	Arg	Ala	Thr	Met
			20					25					30	
Pro	Lys	Gln	Ile	His	Glu	Ile	Lys	Asp	Phe	Leu	Leu	Thr	Ala	Arg
		35					40					45		
Lys	Asp	Ala	Arg	Ser	Val	Arg	Ile	Lys	Arg	Ala	Lys	Asp	Ala	Val
	50					55					60			
Phe	Lys	Val	Arg	Cys	Ser	Arg	Tyr	Leu	Tyr	Thr	Leu	Cys	Val	His
	65				70				75				80	
Ala	Asp	Lys	Ala	Asn	Lys	Leu	Lys	Gln	Ser	Leu	Pro	Pro	Gly	Leu
				85					90				95	
Val	Gln	Glu	Ile											
			100											

(2) INFORMATION FOR SEQ ID NO:3238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1576140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3238:

Met	Pro	Lys	Gln	Ile	His	Glu	Ile	Lys	Asp	Phe	Leu	Leu	Thr	Ala	Arg
1			5						10					15	
Arg	Lys	Asp	Ala	Arg	Ser	Val	Arg	Ile	Lys	Arg	Ala	Lys	Asp	Ala	Val
			20					25					30		
Lys	Phe	Lys	Val	Arg	Cys	Ser	Arg	Tyr	Leu	Tyr	Thr	Leu	Cys	Val	His
		35					40					45			
Asp	Ala	Asp	Lys	Ala	Asn	Lys	Leu	Lys	Gln	Ser	Leu	Pro	Pro	Gly	Leu
	50				55						60				
Thr	Val	Gln	Glu	Ile											
			65												

(2) INFORMATION FOR SEQ ID NO:3239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1034 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1034
(D) OTHER INFORMATION: / Ceres Seq. ID 1576144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3239:

accaaagatg	ttgcctgggc	ctgcgccgac	aagaaaaatca	cagcagtaca	gcaccagaaa	60
cagaaaagta	gtagatcaag	gaacgccagt	gcggcgacaa	tgaccggcag	tggaagcacg	120
ggcgcaaatg	gcaagagcca	gagatccagg	gccaaggcaa	tgctgttcgc	cttgggcaag	180
agctttccctg	accaagtctc	gcctcaggag	aaggttgtgg	agagctacct	ccaagaaagc	240
agctgcgacg	atcccgccac	caggggccaag	cttcagcgcc	tttgacgac	tacaacagtg	300
aagacaagggt	acactgttat	gtccaaggag	ctattggata	agcaccacga	gctgaagatg	360
gaGggtactc	cgacactgac	acctcgccct	gacatctgca	atgccgcggt	gatcgacctt	420
ggtgctgcgc	cagCtcgcgc	tgcccttgac	gaatggggtc	gccctgcagc	tgatattacc	480
caectcatct	acatctcatc	cagtgacctt	cgctctccag	ggggcgacct	tcaactgggt	540

gctgcgcttg gccttagacc aaacacccgtg cgcacttccc ttcttctctt tggctgctcc 600
gggtggtgctg ctgcctctcg cactgccaaag gacattgctg agaacaatcc agggagccgt 660
gtcctagtaa cagctgctga gaccactgtg ctaggcttcc ggccaccaag ttatgacctg 720
ccttatgacc ttgttgggtst gcgctgtttg gtgatgggtc atcagccgtg attataggag 780
cagggtccat gacaccagca gaaaaatcctt tcttggagct tgagttctcc acgcaggagt 840
tcttacctgg gactgataag gtaattgatg gcaaaatctc agaggaagga attaatatta 900
aactagggcg tgatttgcct gagaagattg aaagccgcct agaaggttcc tgcaggactc 960
tcattgaacca ggtagggata aaggatttca acgatataatt ttgggtgctg catctcggtg 1020
gaccagcaat attg

(2) INFORMATION FOR SEQ ID NO:3240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3240:

Thr	Lys	Asp	Val	Ala	Val	Ala	Ser	Pro	His	Lys	Lys	Ile	Thr	Ala	Val
1			5						10					15	
Gln	His	Gln	Lys	Gln	Lys	Gly	Ser	Arg	Ser	Arg	Asn	Ala	Ser	Ala	Ala
			20					25						30	
Thr	Met	Thr	Gly	Ser	Gly	Ser	Thr	Gly	Ala	Asn	Gly	Lys	Ser	Gln	Arg
			35				40					45			
Ser	Arg	Ala	Lys	Ala	Met	Leu	Phe	Ala	Leu	Gly	Lys	Ser	Phe	Pro	Asp
			50				55				60				
Gln	Val	Leu	Pro	Gln	Glu	Lys	Val	Val	Glu	Ser	Tyr	Leu	Gln	Glu	Ser
					70				75					80	
Ser	Cys	Asp	Asp	Pro	Ala	Thr	Arg	Ala	Lys	Leu	Gln	Arg	Leu	Cys	Thr
				85					90					95	
Thr	Thr	Thr	Val	Lys	Thr	Arg	Tyr	Thr	Val	Met	Ser	Lys	Glu	Leu	Thr
			100					105					110		
Asp	Lys	His	Pro	Glu	Leu	Lys	Met	Glu	Gly	Thr	Pro	Thr	Leu	Thr	Pro
			115				120						125		
Arg	Leu	Asp	Ile	Cys	Asn	Ala	Ala	Val	Ile	Asp	Leu	Gly	Ala	Ala	Ala
			130				135					140			
Ala	Arg	Ala	Ala	Leu	Asp	Glu	Trp	Gly	Arg	Pro	Ala	Ala	Asp	Ile	Thr
			145			150			155					160	
His	Leu	Ile	Tyr	Ile	Ser	Ser	Ser	Asp	Leu	Arg	Leu	Pro	Gly	Gly	Asp
				165					170					175	
Leu	His	Leu	Ala	Ala	Arg	Leu	Gly	Leu	Ser	Pro	Asn	Thr	Val	Arg	Thr
			180					185					190		
Ser	Leu	Leu	Phe	Leu	Gly	Cys	Ser	Gly	Gly	Ala	Ala	Ala	Leu	Arg	Thr
			195				200						205		
Ala	Lys	Asp	Ile	Ala	Glu	Asn	Asn	Pro	Gly	Ser	Arg	Val	Leu	Val	Thr
			210				215					220			
Ala	Ala	Glu	Thr	Thr	Val	Leu	Gly	Phe	Arg	Pro	Pro	Ser	Tyr	Asp	Arg
			225			230			235					240	
Pro	Tyr	Asp	Leu	Val	Gly	Xaa	Arg	Cys	Leu	Val	Met	Val	His	Gln	Pro
			245						250					255	

(2) INFORMATION FOR SEQ ID NO:3241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1576146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3241:

```
Met Thr Gly Ser Gly Ser Thr Gly Ala Asn Gly Lys Ser Gln Arg Ser
1      5      10      15
Arg Ala Lys Ala Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln
      20      25      30
Val Leu Pro Gln Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser
      35      40      45
Cys Asp Asp Pro Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr
      50      55      60
Thr Thr Val Lys Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp
      65      70      75      80
Lys His Pro Glu Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg
      85      90      95
Leu Asp Ile Cys Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala
      100     105     110
Arg Ala Ala Leu Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His
      115     120     125
Leu Ile Tyr Ile Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu
      130     135     140
His Leu Ala Ala Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser
      145     150     155     160
Leu Leu Phe Leu Gly Cys Ser Gly Gly Ala Ala Ala Leu Arg Thr Ala
      165     170     175
Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala
      180     185     190
Ala Glu Thr Thr Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro
      195     200     205
Tyr Asp Leu Val Gly Xaa Arg Cys Leu Val Met Val His Gln Pro
      210     215     220
```

(2) INFORMATION FOR SEQ ID NO:3242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1576147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3242:

```
Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln Val Leu Pro Gln
1      5      10      15
Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser Cys Asp Asp Pro
      20      25      30
Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr Thr Val Lys
      35      40      45
Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp Lys His Pro Glu
      50      55      60
Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg Leu Asp Ile Cys
      65      70      75      80
Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala Arg Ala Ala Leu
      85      90      95
Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His Leu Ile Tyr Ile
      100     105     110
Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu His Leu Ala Ala
```

115	120	125
Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser Leu Leu Phe Leu		
130	135	140
Gly Cys Ser Gly Gly Ala Ala Leu Arg Thr Ala Lys Asp Ile Ala		
145	150	155
Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala Ala Glu Thr Thr		
165	170	175
Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro Tyr Asp Leu Val		
180	185	190
Gly Xaa Arg Cys Leu Val Met Val His Gln Pro		
195	200	

(2) INFORMATION FOR SEQ ID NO:3243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3243:

gagaganana ngcgargaar gavggagaga gcacgggggc ttgatcggaag atggatgccg	60
gagcaaaaggt ggtgaagaag gccgcggcgcg ggcgtcgcg cggggggcaag tacttcttcc	120
acgagcagat ttcaagggcat ccacaccatca tgaatatctt tgacaaaaacc cctcatgtgc	180
ataaagacgc atttgttctt ccaagtgcct ccttatttgg tgatgttcaa gtcgggtcag	240
gagcttccat ttggtatggg tgcgtcttaa gaggggatgc aaacatcata caaatggat	300
ctgggaccaa tatacaagac aattctctta tacatgtggc taaatctaatt ctaagtggga	360
aggtctttcc aacaaccatt ggtaataacg tcacagttag tcatagtgtc ggtttacaag	420
gatgcacggt tgaggatgag gcttttggtt gcatgtgggc aaccctatta gatgtgtgtg	480
ttgttgaaaa gcacgggaatg gtggcttgct ggagccctcg tacggcagaa tactaggatc	540
ccttgtggag aggtatgggg agggaaaccCt gccaaatttc tgaggaaagct cacagatgac	600
gagatcagtt tcattgcgga atcagctgcc aactattcca atctgtccaa ggtccatgct	660
gctgagaatg ccaaacctct tgaaaagatt gagtttgaga aggtgttggg caagaagttt	720
gctcaccagg atgagtatga ttccctgatt ggcgtcacgt aaggggcacc accagagctc	780
acgtccccc aaacagccca atgaacctct gtctctgttt tctctttggc gccttaatca	840
tttctgttg gacagtgctg gatcgttgat cggggtaact ttccatgaca ctgggtgttt	900
atgtttactt ttccctccca ataactctfg atcgagcgat gttataaagc tggccatgca	960
cttcttccag attctgtatt cggatgtttt aagatgtgct cctcttcaata acctcaagag	1020
tagttttagc acggtccata ttctgtcatga gttctgtact atgctttctg gccccggcgtg	1080
tatgaacat ctttataaaa atctctt	

(2) INFORMATION FOR SEQ ID NO:3244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3244:

Met Asp Ala Gly Ala Lys Val Val Lys Lys Ala Ala Ala Gly Arg Arg			
1	5	10	15
Gly Gly Gly Lys Tyr Phe Phe His Glu Gln Ile Ser Arg His Arg Thr			
20	25	30	
Ile Met Asn Ile Phe Asp Lys Thr Pro His Val His Lys Asp Ala Phe			
35	40	45	
Val Ala Pro Ser Ala Ser Leu Ile Gly Asp Val Gln Val Gly Ser Gly			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3246:

Met Leu Leu Arg Met Pro Asn Leu Leu Lys Arg Leu Ser Leu Arg Arg
1 5 10 15
Cys Trp Ala Arg Ser Leu Leu Thr Arg Met Ser Met Ile Pro Arg Leu
20 25 30
Ala Ser Leu Lys Gly His His Gln Ser Ser Arg Pro Gln Ile Gln Pro
35 40 45
Asn Glu Pro Leu Phe Leu Phe Ser Leu Trp Arg Leu Asn His Phe Leu
50 55 60
Leu Asp Ser Ala Gly Ser Leu Ile Gly Val Leu Phe His Asp Thr Gly
65 70 75 80
Gly Leu Cys Leu Leu Phe Leu Pro Asn Asn Leu Gly Ser Ser Asp Val
85 90 95
Ile Lys Leu Ala Met His Phe Phe Gln Ile Leu Tyr Ser Val Cys Leu
100 105 110
Arg Cys Ala Pro Phe His Asn Leu Lys Ser Ser Phe Ser Thr Val His
115 120 125
Ile Arg His Glu Phe Cys Thr Met Leu Ser Gly Pro Ala Cys Met Asn
130 135 140
His Leu Tyr Lys Asn Leu
145 150

(2) INFORMATION FOR SEQ ID NO:3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3247:

aaaactgttc	tgcttcgctc	gorggcgctc	atctccactc	ctccgatggc	gcgcgccacc	60
accagccccc	cattctcccg	ccgcgcgcgc	ctgcacaccc	accgcacccc	tcgctctctt	120
ttgcgacctc	cctccgcctc	tttccgcgtc	gcggaataac	tcggcgctgc	gggcctctgc	180
aatggtgagg	tcggcgctcg	caaagaactc	gcacccggct	ccaccacctc	ctcgcccgcg	240
ccctctctct	ctccttcgac	agattctcct	ccgcgcgcgc	cttgatccgga	cgcgcttcgag	300
aaggagatga	tgggcctcac	agggcgcttc	cctggcggtg	aggtcgccct	caaggacttc	360
gtagccaaga	accgcctccc	tcaccaagaaa	tcagaatccc	agcccccaag	cacgctctcc	420
gcgcgcgcgc	ggcgcgcgga	gctgcccgctg	ttcttgcccc	gcacgtgtgt	gctgtgtcaag	480
aaccccaaca	acgcctacca	catgtactgc	ggtatcgtgc	agcgcgtcag	CGacggcaag	540
gNtcgcggtg	ctcttcgagg	gaggagtgtg	ggacaggctc	atcaccttca	acctcgacga	600
gctcgagggc	aggagaagg	gacccctat	ggccaacccc	aagtcocgtg	tgctagagga	660
ttctgttcgc	gagctcgagg	atgacgatga	tgataaggag	gacgaagcgc	ccaagaagaa	720
ggaacccgag	ggcgcggcgc	cggcgcgcgc	atgaccaagg	ttcttgttcc	tggtatacac	780
atctctctga	tgtatgcatg	tatacagctc	aaataaaata	tttgagacta	attaaaaagg	840
aacgataata	taactcttat	tatgaagtat	atagtttgaa	tgtttagtgt	aattggggca	900
tggaagaatt	gccatacgtt	tg				

(2) INFORMATION FOR SEQ ID NO:3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3248:

Lys Thr Val Leu Leu Arg Ser Xaa Ala Leu Ile Ser Thr Pro Pro Met

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1          5          10          15
Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu Pro
20          25          30
His His Pro His Pro Arg Leu Leu Arg Pro Pro Ser Ala Ser Phe
35          40          45
Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu Val
50          55          60
Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro Ala
65          70          75          80
Pro Ser Pro Pro Pro Ser Thr Asp Ser Pro Pro Ala Val Asp Pro
85          90          95
Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro Gly
100          105          110
Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro
115          120          125
Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg
130          135          140
Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val Lys
145          150          155          160
Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg Val
165          170          175
Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly Gln
180          185          190
Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr
195          200          205
Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg Gly
210          215          220
Ala Arg Gly
225

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(2) INFORMATION FOR SEQ ID NO:3249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1576161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3249:

```

Met Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu
1          5          10          15
Pro His His Pro His Pro Arg Leu Leu Arg Pro Pro Ser Ala Ser
20          25          30
Phe Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu
35          40          45
Val Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro
50          55          60
Ala Pro Ser Pro Pro Ser Thr Asp Ser Pro Pro Ala Val Asp
65          70          75          80
Pro Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro
85          90          95
Gly Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro
100          105          110
Pro Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro
115          120          125
Arg Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val
130          135          140
Lys Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg
145          150          155          160

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Val Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly
165 170 175
Gln Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly
180 185 190
Thr Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg
195 200 205
Gly Ala Arg Gly
210

(2) INFORMATION FOR SEQ ID NO:3250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1576162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3250:

Met Met Gly Leu Thr Gly Gly Phe Pro Gly Gly Glu Val Gly Leu Lys
1 5 10 15
Asp Phe Val Ala Lys Asn Pro Pro Pro Lys Lys Ser Glu Ser Gln
20 25 30
Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg Pro Pro Glu Leu Pro Leu
35 40 45
Phe Leu Pro Gly Met Val Val Leu Val Lys Asn Pro Asn Asn Ala Tyr
50 55 60
His Met Tyr Cys Gly Ile Val Gln Arg Val Ser Asp Gly Lys Xaa Arg
65 70 75 80
Gly Ala Leu Arg Gly Arg Ser Val Gly Gln Ala His His Leu Gln Pro
85 90 95
Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr Pro Tyr Gly Gln Pro Gln
100 105 110
Val Arg Gly Ala Arg Gly Ser Cys Arg Gly Ala Arg Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:3251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..627

(D) OTHER INFORMATION: / Ceres Seq. ID 1576221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3251:

aagggtgtttt gccctcttct tcgcgarcnc cccgcgcgca acccgcagcc gcatacgggag 60
accgcagccgc gccgatggcg aagaagcaca gggacccagc ctctgargcc gcgagcggcg 120
actccccgcgc cgcgtccatc cgcctccctct tctccgcgga caaMccccgtt ccgcgcggag 180
gcctctacgg aggagccccc cgcgactctt gcacccgccca cgacgcacct ccccatgcaa 240
cccagccgctg acgccagggga tcccgcgccc tctcgaaga agaataagaa gagcaaggag 300
gaggggccgc ggcgcaagcg gaagcgrgac gaggttggagg ccggccggga gcggcgggca 360
ggcgcgaggga atccgtcgag agttggggag aaggagaaag ctccccacga cgcggcacga 420
ggggcggggg aggacgagga ggaggcttcc cgcagccgga gcaagctgct caggaccgtg 480
ttcgtgggga acctgcgct gcggwccaag cgcaaggtgc tcatcaagga gttcgtctaa 540
aaaggacagg caggcagctg cctcccccca tgttatgatg acaaaaactct agtagctagg 600
aaaggaaatca cagtgacctt ttgtttc

(2) INFORMATION FOR SEQ ID NO:3252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..209
(D) OTHER INFORMATION: / Ceres Seq. ID 1576222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3252:

Lys Val Phe Cys Pro Leu Leu Arg Xaa Xaa Pro Arg Arg Asn Pro Gln
1 5 10 15
Pro His Arg Glu Thr Arg Ser Arg Arg Trp Arg Arg Ser Thr Gly Thr
20 25 30
Gln Pro Leu Xaa Pro Arg Ala Ala Thr Pro Arg Pro Arg Pro Ser Ala
35 40 45
Pro Ser Ser Pro Arg Thr Xaa Pro Phe Arg Arg Lys Ala Ser Thr Glu
50 55 60
Glu Pro Pro Ala Thr Pro Ala Pro Ala Thr Thr Pro Leu Pro Met Gln
65 70 75 80
Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys Asn Lys
85 90 95
Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp Glu Leu
100 105 110
Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser Arg Val
115 120 125
Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala Gly Glu
130 135 140
Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg Thr Val
145 150 155 160
Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu Ile Lys
165 170 175
Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro Cys Tyr
180 185 190
Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr Phe Cys
195 200 205
Phe

(2) INFORMATION FOR SEQ ID NO:3253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1576223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3253:

Met Gln Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys
1 5 10 15
Asn Lys Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp
20 25 30
Glu Leu Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser
35 40 45
Arg Val Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala
50 55 60
Gly Glu Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg
65 70 75 80
Thr Val Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu

85 90 95
Ile Lys Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro
100 105 110
Cys Tyr Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr
115 120 125
Phe Cys Phe
130

(2) INFORMATION FOR SEQ ID NO:3254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3254:

Met Pro Ser Arg Pro Arg Arg Arg Ile Arg Arg Ala Arg Arg Ala
1 5 10 15
Arg Gly Ala Ser Gly Ser Xaa Thr Ser Trp Arg Pro Ala Gly Ser Gly
20 25 30
Gly Glu Ala Arg Arg Ile Arg Arg Glu Leu Gly Arg Arg Gly Arg Leu
35 40 45
Pro Thr Thr Arg His Arg Gly Pro Gly Arg Thr Arg Arg Arg Leu Ser
50 55 60
Thr Thr Arg Ala Ser Cys Ser Gly Pro Cys Ser Trp Gly Thr Cys Arg
65 70 75 80
Cys Xaa Pro Ser Ala Arg Cys Ser Ser Arg Ser Ser Leu Lys Lys Asp
85 90 95
Arg Gln Ala Ala Ala Ser Pro His Val Met Thr Lys Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:3255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3255:

gcttccacca tcgcaccac cgggagcgcc tctctttct cagcgtccga tccccattcc 60
ccacctctcc tcctccgcc gccagctccc gcmeccctct ctcccctct cgcctcccgc 120
cgcgcgcggt ttataaaggg tttaaagcga ggcccccggg cgtggtcgcat ggccgagmac 180
ggcgggagcc acgagggcag cggcgggcgc ggagggcgctc gggagcagga ccggttctgt 240
cccatcgcca acatcagccg gatcatgaag aargCgctcc cggccaacgg caagatcgcc 300
aaggacgcta aggagaccgc tgcaaaaccg agggtgctga aacagagatg attctggttt 360
ggcccgtaca agcgatgcaa aaggtcgtct cccaaggtaa cgacgaatga tggAcagcgg 420
gggtgctctt gctctctaca agttgatgac aactagctgg ttgcctttgg aaagcaccgc 480
tgcatgtgat ctgcagaaatg aaaaacaaagt gatgggtgta aacgtgtaaa gactttaaac 540
gtgtgccaat aaatattacg tatattatgta aatgcacgga tctgatggaa tgcacatatg 600
gtgcccatca atctgggcat tgccgcgctgc cgaattgtctg gtaaacgcgc ctatttcattg 660
gttggtgtgc tcgcagaaaaa gccaatggcc gtgcaaaagt ttcttcgacg gatggttgca 720
gatgttagca gtacaggatg ttttctctgt

(2) INFORMATION FOR SEQ ID NO:3256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..116
(D) OTHER INFORMATION: / Ceres Seq. ID 1576230
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3256:
Ala Ser Thr Ile Ala Pro Thr Arg Ser Ala Ser Ser Pro Ala Ser
1 5 10 15
Asp Pro His Ser Pro Pro Leu Leu Pro Pro Pro Ala Pro Xaa Pro
20 25 30
Phe Ser Pro Leu Leu Ala Ser Pro Arg Ala Arg Phe Tyr Lys Gly Leu
35 40 45
Ser Gly Gly Ala Arg Ser Leu Ala Met Ala Xaa Asp Gly Gly Ser His
50 55 60
Glu Gly Ser Gly Gly Gly Gly Val Arg Glu Gln Asp Arg Phe Leu
65 70 75 80
Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Xaa Ala Val Pro Ala Asn
85 90 95
Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Ala Ala Lys Pro Arg Val
100 105 110
Leu Lys Gln Arg
115
(2) INFORMATION FOR SEQ ID NO:3257:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1576231
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3257:
Met Ala Xaa Asp Gly Gly Ser His Glu Gly Ser Gly Gly Gly Gly
1 5 10 15
Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
20 25 30
Met Lys Xaa Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
35 40 45
Glu Thr Ala Ala Lys Pro Arg Val Leu Lys Gln Arg
50 55 60
(2) INFORMATION FOR SEQ ID NO:3258:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..59
(D) OTHER INFORMATION: / Ceres Seq. ID 1576232
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3258:
Met His Gly Ser Asp Gly Met His Ile Trp Cys Pro Ser Ile Trp Ala
1 5 10 15
Leu Arg Ala Ala Glu Cys Leu Val Lys Arg Ala Ile Ser Trp Leu Cys
20 25 30

Ala Ser Glu Lys Arg Gln Trp Pro Cys Lys Ser Phe Phe Asp Gly Trp
35 40 45
Leu Gln Met Leu Ala Val Gln Asp Val Phe Leu
50 55

(2) INFORMATION FOR SEQ ID NO:3259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..934
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3259:

aaaaattgca	aaaatctctg	cogtgcctct	cgtctctctt	ctcargcgcc	acgcaaaacg	60
gtctccggtt	tcctctctcg	gataccggcc	gcgggagcca	ggagccatcg	atgatccgga	120
ccgcaacggt	gcgagcggt	ctctctctat	cgcgctccta	cgtagcacag	gcaaaaggcag	180
cttctcgctg	gcctctcgct	cgtcggaagg	cttcgcatct	tggatctgta	cgctctttct	240
atcacagtga	cattacaagg	caatacaaaa	ataaaatttt	gactgcaaga	gggtgccata	300
gctccctcga	gagtcaagaa	ttagcaatga	aaagctgtgt	tccatgcaac	tctaaggatt	360
taggtcccat	gtcagaagat	tctgctaaaa	agttgcttga	acagggtgaat	ggttgggaac	420
tgatcacatga	aggtgggtgt	ctgaaattac	atagaacatg	gaaggtgaag	aactttgtta	480
aaggacttga	gttctttcag	ctgtgtgtgt	ctatogctga	ggaagaaggt	caccatccag	540
atcttcatct	tgttggttgg	aataatgtga	aaattgatgt	ttggactcat	tctgtcaagag	600
gtttaacaag	taatgatctc	atccttgctg	cgaagatcaa	tcattctcact	ttagacggca	660
ttataaggaa	gaaagctaaa	tagccaatgt	ctcagaagca	actcaaatat	gcagctcgta	720
ttgttttgga	attttgtatg	cgcagcgatg	gagaagccaa	atgttgagga	cacctcgccc	780
ttgtgtagat	taacttgctg	aaatgtagt	ccttattcag	tagctcattt	taccttggtta	840
ttcaattagta	atttgcatga	gtagacgttg	aatccatcat	tgtactttgt	tacctaacta	900
ccttacctgt	cagttttgaa	aagacacatg	gtcg			

(2) INFORMATION FOR SEQ ID NO:3260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3260:

Lys	Leu	Gln	Lys	Ser	Leu	Pro	Cys	Leu	Ser	Ser	Leu	Phe	Ser	Xaa	Ala
1			5					10						15	
Thr	Gln	Asn	Gly	Leu	Arg	Phe	Pro	Ser	Pro	Asp	Pro	Ala	Arg	Gly	Ser
			20					25						30	
Gln	Glu	Pro	Ser	Met	Ile	Arg	Thr	Ala	Thr	Val	Arg	Ala	Arg	Leu	Leu
			35					40						45	
Leu	Ser	Arg	Ser	Tyr	Val	Ala	Gln	Ala	Lys	Ala	Ala	Ser	Arg	Trp	Pro
			50					55						60	
Leu	Val	Arg	Trp	Lys	Ala	Ser	His	Leu	Gly	Ser	Val	Arg	Ser	Phe	Tyr
65								70						75	
Gln	Met	Asp	Ile	Thr	Arg	Gln	Tyr	Lys	Asn	Lys	Ile	Leu	Thr	Ala	Arg
								85						90	
Gly	Cys	His	Ser	Ser	Pro	Glu	Ser	Gln	Glu	Leu	Ala	Met	Lys	Ser	Cys
								100						105	
Val	Pro	Cys	Asn	Ser	Lys	Asp	Leu	Gly	Pro	Met	Ser	Glu	Asp	Ser	Ala
								110						115	
Lys	Lys	Leu	Leu	Glu	Gln	Val	Asn	Gly	Trp	Glu	Leu	Ile	Thr	Glu	Gly
								120						125	

130	135	140
Gly Val Leu Lys Leu His Arg Thr Trp Lys Val Lys Asn Phe Val Lys		
145	150	155
Gly Leu Glu Phe Phe Gln Leu Val Ala Ala Ile Ala Glu Glu Glu Gly		
	165	170
His His Pro Asp Leu His Leu Val Gly Trp Asn Asn Val Lys Ile Asp		
	180	185
Val Trp Thr His Ser Val Arg Gly Leu Thr Ser Asn Asp Phe Ile Leu		
	195	200
Ala Ala Lys Ile Asn His Leu Thr Leu Asp Gly Ile Ile Arg Lys Lys		
	210	215
Ala Lys		220

(2) INFORMATION FOR SEQ ID NO:3261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3261:

Met	Ile	Arg	Thr	Ala	Thr	Val	Arg	Ala	Arg	Leu	Leu	Ser	Arg	Ser
1				5					10				15	
Tyr	Val	Ala	Gln	Ala	Lys	Ala	Ala	Ser	Arg	Trp	Pro	Leu	Val	Arg
		20						25				30		Trp
Lys	Ala	Ser	His	Leu	Gly	Ser	Val	Arg	Ser	Phe	Tyr	Gln	Met	Asp
		35					40				45			Ile
Thr	Arg	Gln	Tyr	Lys	Asn	Lys	Ile	Leu	Thr	Ala	Arg	Gly	Cys	His
		50				55					60			Ser
Ser	Pro	Glu	Ser	Gln	Glu	Leu	Ala	Met	Lys	Ser	Cys	Val	Pro	Cys
		65				70				75				Asn
Ser	Lys	Asp	Leu	Gly	Pro	Met	Ser	Glu	Asp	Ser	Ala	Lys	Lys	Leu
			85						90				95	
Glu	Gln	Val	Asn	Gly	Trp	Glu	Leu	Ile	Thr	Glu	Gly	Gly	Val	Leu
			100						105				110	Lys
Leu	His	Arg	Thr	Trp	Lys	Val	Lys	Asn	Phe	Val	Lys	Gly	Leu	Glu
			115					120				125		Phe
Phe	Gln	Leu	Val	Ala	Ala	Ile	Ala	Glu	Glu	Glu	Gly	His	His	Pro
		130					135				140			Asp
Leu	His	Leu	Val	Gly	Trp	Asn	Asn	Val	Lys	Ile	Asp	Val	Trp	Thr
		145					150				155			His
Ser	Val	Arg	Gly	Leu	Thr	Ser	Asn	Asp	Phe	Ile	Leu	Ala	Ala	Lys
			165						170				175	Ile
Asn	His	Leu	Thr	Leu	Asp	Gly	Ile	Ile	Arg	Lys	Lys	Ala	Lys	
			180						185				190	

(2) INFORMATION FOR SEQ ID NO:3262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3262:

(2) INFORMATION FOR SEQ ID NO:3263:

(1) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..698

(D) OTHER INFORMATION: / Ceres Seq. ID 1576245

(X1)	SEQUENCE DESCRIPTION	SEQ	60			
aaagaaagaag	aaggaagaag	ggcctctctg	atctctctcac	ttcctctcgt	cctgtctcgt	60
ctgtctccctc	ctctctctctas	ctagctctctc	ctgtagcgcgt	cagagatggc		120
tgccctctctc	tcaccacacac	cggcgccggc	ggcagcgctg	tgtgtctgtc	ttctctctgc	180
gctgcgcggc	gtacgcggmac	atctgcgatc	tgtctcaccg	ggagcgcgacg	brcraggagg	240
cgccggcgat	gttcggcgga	tggatggcgg	cgacgcggcg	cgactacaaam	gcgctgcgGK	300
aggagaagcgc	cggttaccag	gtgtctctcc	acaactctcc	ctacatcagc	cgccacaacg	360
ccgcgcgcga	cgcggtcgctc	caactctctc	ggcctgAgcc	tcacacgcGtt	cgcgacactc	420
accacacgac	agttaccgcg	caactaacctc	ggcgcggaga	ccaggcgcga	gagggagagg	480
aagctcgcgc	ccaggtacca	cgccgcggcc	aacgagacc	tgcggagacc	cgctgcagctg	540
aggggcoagg	gcgcgcgcgc	cgaggtcaag	gaccagggca	gctcggggag	ctgttgggct	600
ttctcaacaa	tagcagctgt	ggaaggcatc	aacagcattg	ttacaggcca	cttgatctcc	660
ttgtctgaac	aaagccttgt	cgactgtgac	mytgctac			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1576246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3264:

Arg	Lys	Gly	Arg	Lys	Lys	Gly	Leu	Leu	Tyr	Pro	Leu	Thr	Ser	Leu	Ser
1				5					10					15	
Pro	Arg	Pro	Ser	Ala	Pro	Ser	Ser	Xaa	Xaa	Leu	Ala	Leu	Ala	Ser	Leu
			20					25					30		
Pro	Val	Ala	Arg	Gln	Arg	Trp	Leu	Pro	Leu	Pro	Pro	Pro	Arg	Arg	Arg

Arg	Arg	Gln	Arg	Cys	Cys	Cys	Cys	Ser	Ser	Cys	Arg	Ser	Pro	Arg	Arg
50						55				60					
Arg	Xaa	Met	Ser	Ile	Val	Ser	Tyr	Gly	Glu	Arg	Ser	Xaa	Xaa	Glu	Ala
65					70					75				80	
Arg	Arg	Met	Tyr	Ala	Glu	Trp	Met	Ala	Ala	His	Gly	Arg	Thr	Tyr	Xaa
				85						90				95	
Ala	Val	Gly	Xaa	Glu	Glu	Arg	Arg	Tyr	Gln	Val	Phe	Arg	Asp	Asn	Leu
				100				105					110		
Arg	Tyr	Ile	Asp	Ala	His	Asn	Ala	Ala	Ala	Asp	Ala	Gly	Val	His	Ser
		115				120						125			
Phe	Arg	Leu	Glu	Pro	Gln	Pro	Leu	Arg	Arg	Pro	His	Gln	Arg	Arg	Val
		130				135					140				
Pro	Arg	His	Leu	Pro	Arg	Arg	Gln	Asp	Gln	Ala	Glu	Gly	Glu	Glu	
145					150					155				160	
Ala	Arg	Arg	Gln	Val	Pro	Arg	Arg	Arg	Gln	Arg	Gly	Pro	Ala	Gly	Val
				165					170					175	
Arg	Arg	Leu	Glu	Gly	Gln	Gly	Arg	Arg	Arg	Arg	Gly	Gln	Gly	Pro	Gly
			180					185					190		
Gln	Leu	Arg	Glu	Leu	Leu	Gly	Phe	Leu	Asn	Asn	Ser	Ser	Cys	Gly	Arg
			195					200					205		
His	Gln	Pro	Asp	Cys	Tyr	Arg	Arg	Leu	Asp	Leu	Leu	Val			
		210				215						220			

(2) INFORMATION FOR SEQ ID NO:3265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1576247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3265:

Met	Ala	Ala	Pro	Ala	Ser	Thr	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu
1			5					10						15	
Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Ala	Ala	Xaa	His	Val	Asp	Arg	
			20				25					30			
Val	Leu	Arg	Gly	Ala	Gln	Xaa	Xaa	Gly	Gly	Ala	Ala	Asp	Val	Arg	Gly
			35				40					45			
Val	Asp	Gly	Gly	Ala	Arg	Pro	Asp	Leu	Gln	Xaa	Arg	Arg	Xaa	Gly	Gly
		50				55				60					
Ala	Ala	Val	Pro	Gly	Val	Pro	Gly	Gln	Pro	Pro	Leu	His	Arg	Arg	Ala
65				70					75					80	
Gln	Arg	Arg	Arg	Arg	Arg	Gly	Arg	Pro	Leu	Leu	Pro	Pro	Arg	Ala	Ser
				85				90					95		
Thr	Ala	Ser	Pro	Thr	Ser	Pro	Thr	Thr	Ser	Thr	Ala	Pro	Pro	Thr	Ser
			100					105				110			
Ala	Pro	Gly	Pro	Gly	Arg	Arg	Gly	Arg	Gly	Ser	Ser	Ala	Pro	Gly	Thr
			115				120					125			
Thr	Pro	Pro	Thr	Thr	Arg	Thr	Cys	Arg	Ser	Pro	Ser	Thr	Gly	Gly	Pro
		130				135					140				
Arg	Ala	Pro	Ser	Pro	Arg	Ser	Arg	Thr	Arg	Ala	Ala	Gly	Ala	Val	
145					150				155					160	
Gly	Leu	Ser	Gln	Gln											
				165											

(2) INFORMATION FOR SEQ ID NO:3266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1576248
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3266:
Met Ser Ile Val Ser Tyr Gly Glu Arg Ser Xaa Xaa Glu Ala Arg Arg
1 5 10 15
Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Xaa Ala Val
20 25 30
Gly Xaa Glu Glu Arg Arg Tyr Gln Val Phe Arg Asp Asn Leu Arg Tyr
35 40 45
Ile Asp Ala His Asn Ala Ala Ala Asp Ala Gly Val His Ser Phe Arg
50 55 60
Leu Glu Pro Gln Pro Leu Arg Arg Pro His Gln Arg Arg Val Pro Arg
65 70 75 80
His Leu Pro Arg Arg Gln Asp Gln Ala Ala Glu Gly Glu Glu Ala Arg
85 90 95
Arg Gln Val Pro Arg Arg Arg Gln Arg Gly Pro Ala Gly Val Arg Arg
100 105 110
Leu Glu Gly Gln Gly Arg Arg Arg Gly Gln Gly Pro Gly Gln Leu
115 120 125
Arg Glu Leu Leu Gly Phe Leu Asn Asn Ser Ser Cys Gly Arg His Gln
130 135 140
Pro Asp Cys Tyr Arg Arg Leu Asp Leu Leu Val
145 150 155
(2) INFORMATION FOR SEQ ID NO:3267:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 988 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..988
(D) OTHER INFORMATION: / Ceres Seq. ID 1576267
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3267:
cgatagtatg ctaggaaagga gagaaaatcc agggcgatgc gcaagatgaa 60
gaatgaattt atggtaaattt gggatggggtt gcgcactaaa gataaggagc gtgtgcttgtt 120
tcttggtgctt acaaaatagct cttttgacct cgaacgaggt gtgattagga gggtccccgcg 180
cagggttaatg gtaaaacttgc ccgatgcatc aaataggagg aaaattctaa aagtaattttt 240
ggcaaaagaa gagctgggat ctgatgttga tatggactcg cttggcaata tgactgatgg 300
ttattccaggaa agcgacctga agaattctgtg tgtvacccgc gcgcattacc ccacccgagc 360
aattctggag aaggaaaaga aggagaagag tttggctaaa acagaaggta ggcccgagcc 420
tgcatatatg ggaagcgaag acatccgcgc ccttagcata gatgacttca aaAtctgcgc 480
atgagcaggt gtgtgcgasc gtttcgtccg actcggcgaa catgaacgag ctcttccaat 540
ggaacgacyt gtacgktgaa ggcgggtcaa ggaagaagaa agcgcgtgagc tacttcatgt 600
gatgtggtga gagcatagaa tcacagaagga tcacagccgt ggcataagat cagaaggaac 660
acagagcggc catagtacca caccacaccc cactatggcc ctaaaatccag tcaggttttc 720
gctccttccc cctccctcag tagccgcgcg cgccccaccg ccgcctgggt taattagaa 780
tgtgtaccga gtgcagttgg ttgtccagct gtctcaggt tacagagttg agatttggaa 840
ttacaatggc gcgattgccc tctccaacc cccctttttt ctctctctca taagttgcg 900
tcactgtcct tcttggactc tctggccttt gttctgttaa atgcgaagt aagggatgtg 960
aaataagaac attctcgttc tgttgttg
(2) INFORMATION FOR SEQ ID NO:3268:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..160
(D) OTHER INFORMATION: / Ceres Seq. ID 1576268
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3268:
Asp Ser Met Leu Gly Arg Arg Glu Asn Pro Gly Glu His Glu Ala Met
1 5 10 15
Arg Lys Met Lys Asn Glu Phe Met Val Asn Trp Asp Gly Leu Arg Thr
20 25 30
Lys Asp Lys Glu Arg Val Leu Val Leu Gly Ala Thr Asn Arg Pro Phe
35 40 45
Asp Leu Asp Glu Ala Val Ile Arg Arg Phe Pro Arg Arg Leu Met Val
50 55 60
Asn Leu Pro Asp Ala Ser Asn Arg Glu Lys Ile Leu Lys Val Ile Leu
65 70 75 80
Ala Lys Glu Glu Leu Gly Ser Asp Val Asp Met Asp Ser Leu Ala Asn
85 90 95
Met Thr Asp Gly Tyr Ser Gly Ser Asp Leu Lys Asn Leu Cys Xaa Thr
100 105 110
Ala Ala His Tyr Pro Ile Arg Glu Ile Leu Glu Lys Glu Lys Lys Glu
115 120 125
Lys Ser Leu Ala Lys Thr Glu Gly Arg Pro Glu Pro Ala Leu Tyr Gly
130 135 140
Ser Glu Asp Ile Arg Pro Leu Ser Ile Asp Asp Phe Lys Ile Cys Xaa
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:3269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1576269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3269:

Met Leu Gly Arg Arg Glu Asn Pro Gly Glu His Glu Ala Met Arg Lys
1 5 10 15
Met Lys Asn Glu Phe Met Val Asn Trp Asp Gly Leu Arg Thr Lys Asp
20 25 30
Lys Glu Arg Val Leu Val Leu Gly Ala Thr Asn Arg Pro Phe Asp Leu
35 40 45
Asp Glu Ala Val Ile Arg Arg Phe Pro Arg Arg Leu Met Val Asn Leu
50 55 60
Pro Asp Ala Ser Asn Arg Glu Lys Ile Leu Lys Val Ile Leu Ala Lys
65 70 75 80
Glu Glu Leu Gly Ser Asp Val Asp Met Asp Ser Leu Ala Asn Met Thr
85 90 95
Asp Gly Tyr Ser Gly Ser Asp Leu Lys Asn Leu Cys Xaa Thr Ala Ala
100 105 110
His Tyr Pro Ile Arg Glu Ile Leu Glu Lys Glu Lys Lys Glu Lys Ser
115 120 125
Leu Ala Lys Thr Glu Gly Arg Pro Glu Pro Ala Leu Tyr Gly Ser Glu
130 135 140
Asp Ile Arg Pro Leu Ser Ile Asp Asp Phe Lys Ile Cys Xaa

145 150 155

(2) INFORMATION FOR SEQ ID NO:3270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1576270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3270:

Met	Arg	Lys	Met	Lys	Asn	Glu	Phe	Met	Val	Asn	Trp	Asp	Gly	Leu	Arg
1				5					10					15	
Thr	Lys	Asp	Lys	Glu	Arg	Val	Leu	Val	Leu	Gly	Ala	Thr	Asn	Arg	Pro
			20					25					30		
Phe	Asp	Leu	Asp	Glu	Ala	Val	Ile	Arg	Arg	Phe	Pro	Arg	Arg	Leu	Met
		35					40					45			
Val	Asn	Leu	Pro	Asp	Ala	Ser	Asn	Arg	Glu	Lys	Ile	Leu	Lys	Val	Ile
	50					55				60					
Leu	Ala	Lys	Glu	Glu	Leu	Gly	Ser	Asp	Val	Asp	Met	Asp	Ser	Leu	Ala
	65				70				75					80	
Asn	Met	Thr	Asp	Gly	Tyr	Ser	Gly	Ser	Asp	Leu	Lys	Asn	Leu	Cys	Xaa
			85					90					95		
Thr	Ala	Ala	His	Tyr	Pro	Ile	Arg	Glu	Ile	Leu	Glu	Lys	Glu	Lys	Lys
			100				105						110		
Glu	Lys	Ser	Leu	Ala	Lys	Thr	Glu	Gly	Arg	Pro	Glu	Pro	Ala	Leu	Tyr
			115				120					125			
Gly	Ser	Glu	Asp	Ile	Arg	Pro	Leu	Ser	Ile	Asp	Asp	Phe	Lys	Ile	Cys
		130				135						140			

Xaa
145

(2) INFORMATION FOR SEQ ID NO:3271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..824

(D) OTHER INFORMATION: / Ceres Seq. ID 1576273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3271:

accagccacc	gccaaagccgc	attacaaaga	acgcgaaccg	ctgccagtc	aaaccctacg	60
gcgcgcgcga	gcatacaagt	ccccgaccaa	accctactcg	taccccgccg	cgcgcgcagc	120
cgcagccgcg	gccacaccag	caagcagaac	tagcagccat	gccgcgccaa	ttggaccctt	180
ctcaggtggt	ggaggtcttc	gtccgcgtga	cgggagcgga	ggtcggcgcg	gcgtcgtcgc	240
tggcccccaa	gaticggccc	ctcggctctc	ccccgaagaa	gaticggcag	gacatcgcca	300
aggagaccgc	caaggaactgg	aagggcctcc	gcgtcaaccgt	caagctcaacc	gtgcagaacc	360
ggcagggcca	gtctctccgtc	gtcccctccg	cgcgcggcgt	cgtcataaag	gcgctcaagg	420
aaocccagag	ggacaggaag	aaggtcaaga	acatcaagca	cagcGggcga	catcagcctc	480
gacgaogtca	tcagagatcgc	caagaCccat	cggaacacag	tccatggcca	aggagttggc	540
cgggaccgct	aaggagatcc	tggggacctg	cgtcaGcgct	gggtgcaccg	tcgatgggaa	600
ggaccccaag	gaacttcgacg	aggagatcga	tgatgttgag	gtcgagatcc	cctcagctta	660
aaggctatac	aactagaaat	catcgacac	tattaaaagt	tggtgttttg	ttccaakksa	720
gttcctgcac	ctcaatcgcc	tattattgtc	tgctttagtt	ccttcaagtc	ttgtgagaga	780
cctaactcagt	accttgtgcc	ttataaaatt	acatcttcgc	attc		

(2) INFORMATION FOR SEQ ID NO:3272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..219
(D) OTHER INFORMATION: / Ceres Seq. ID 1576274
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3272:
Pro Ala Thr Ala Lys Pro His Tyr Lys Glu Arg Glu Pro Leu Pro Val
1 5 10 15
Gln Thr Leu Arg Pro Pro Pro Ala Ser Ser Ser Pro Thr Lys Pro Tyr
20 25 30
Ser Tyr Pro Ala Ala Ala Ala Ala Ala Ala Thr Pro Ala Ser
35 40 45
Arg Thr Ser Ser His Ala Ala Gln Ile Gly Pro Leu Ser Gly Gly Gly
50 55 60
Gly Leu Arg Pro Arg Asp Gly Arg Arg Gly Arg Gly Val Val Ala
65 70 75 80
Gly Pro Gln Asp Arg Pro Ala Arg Ser Leu Pro Glu Glu Asp Arg Arg
85 90 95
Gly His Arg Gln Gly Asp Arg Gln Gly Leu Glu Gly Pro Pro Arg His
100 105 110
Arg Gln Ala His Arg Ala Glu Pro Ala Gly Gln Gly Leu Arg Arg Pro
115 120 125
Leu Arg Arg Gly Ala Arg His Gln Gly Ala Gln Gly Thr Arg Glu Gly
130 135 140
Gln Glu Glu Gly Gln Glu His Gln Ala Gln Arg Ala Thr Ser Ala Ser
145 150 155 160
Thr Thr Ser Ser Arg Ser Pro Arg Pro Met Arg Asn Arg Ser Met Ala
165 170 175
Lys Glu Leu Ala Gly Thr Val Lys Glu Ile Leu Gly Thr Cys Val Ser
180 185 190
Val Gly Cys Thr Val Asp Gly Lys Asp Pro Lys Asp Leu Gln Gln Glu
195 200 205
Ile Asp Asp Gly Glu Val Glu Ile Pro Ser Ala
210 215
(2) INFORMATION FOR SEQ ID NO:3273:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..251
(D) OTHER INFORMATION: / Ceres Seq. ID 1576275
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3273:
Gln Pro Pro Pro Ser Arg Ile Thr Lys Asn Ala Asn Arg Cys Gln Ser
1 5 10 15
Lys Pro Tyr Gly Arg Arg Gln His Gln Ala Pro Arg Pro Asn Pro Thr
20 25 30
Arg Thr Pro Pro Pro Pro Gln Pro Gln Pro Arg Pro His Gln Gln Ala
35 40 45
Glu Leu Ala Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu
50 55 60
Val Phe Val Arg Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu
65 70 75 80
Ala Pro Lys Ile Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu

85 90 95
Asp Ile Ala Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr
100 105 110
Val Lys Leu Thr Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro
115 120 125
Ser Ala Ala Ala Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp
130 135 140
Arg Lys Lys Val Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg
145 150 155 160
Arg Arg His Arg Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro
165 170 175
Arg Ser Trp Pro Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala
180 185 190
Ser Gly Ala Pro Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg
195 200 205
Ser Met Met Val Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr
210 215 220
Arg Asn His Arg Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser
225 230 235 240
Ser Cys Thr Ser Ile Ala Tyr Tyr Cys Leu Leu
245 250

(2) INFORMATION FOR SEQ ID NO:3274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1576276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3274:

Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val Arg
1 5 10 15
Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys Ile
20 25 30
Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala Lys
35 40 45
Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu Thr
50 55 60
Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro Ser Ala Ala Ala
65 70 75 80
Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp Arg Lys Lys Val
85 90 95
Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg Arg Arg His Arg
100 105 110
Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro Arg Ser Trp Pro
115 120 125
Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala Ser Gly Ala Pro
130 135 140
Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg Ser Met Met Val
145 150 155 160
Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr Arg Asn His Arg
165 170 175
Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser Ser Cys Thr Ser
180 185 190
Ile Ala Tyr Tyr Cys Leu Leu
195

(2) INFORMATION FOR SEQ ID NO:3275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..573
(D) OTHER INFORMATION: / Ceres Seq. ID 1576315
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3275:
acgaagcacaca caacaaacct gcagatcccc catggcaggc tccacctccc tcgtwccctc 60
tcccgtmccc gccctcccat ctgcgccacg cttccacacg tccacgtccg catccccccg 120
ccacctgcgc cccctcccctg ctacacgcct ccgcgcgtgcc cggcgtcggc atccccgacg 180
cgtcgtgtgc gtccagatg cccgcccctg ggtcggcgat ctatcgggcg ccgcgcggtc 240
ctaccgggac ggaagtgaag aggacgaaga cgacgcagat gaagatgagg acgaagacga 300
ggaccgcagc ctggacctac tggcccgggt cctgcactcc gtattcagga aggcctcacg 360
ccGgcSgcg ccgCgctgcc aggtccgtgc tgccgccttc cgtccccgcc gagctggtag 420
agttttcggt caatggcggt ctgtcctcga cgttcttatg gatcctgaag ggtcttctcg 480
aggtagtctg cacatttgga agcatgggtg ttggtAattc gattcaagaT tactgtacgc 540
tgccagctct tggagaaaaa aggttttcgg tgc
(2) INFORMATION FOR SEQ ID NO:3276:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..171
(D) OTHER INFORMATION: / Ceres Seq. ID 1576316
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3276:
Arg Ser Thr Gln Gln Thr Cys Arg Ser Pro Met Ala Gly Ser Thr Ser
1 5 10 15
Leu Xaa Pro Leu Pro Xaa Pro Ala Pro Pro Ser Arg His Arg Phe His
20 25 30
Thr Ser Thr Ser Ala Ser Pro Arg His Leu Arg Pro Ser Pro Ala Thr
35 40 45
Arg Leu Arg Ala Ala Arg Arg Arg His Pro Asp Ala Val Val Val Val
50 55 60
Pro Asp Ala Arg Pro Trp Val Gly Asp Leu Ser Gly Ala Ala Ala Ser
65 70 75 80
Tyr Arg Asp Gly Ser Glu Glu Asp Glu Asp Asp Ala Asp Glu Asp Glu
85 90 95
Asp Glu Asp Glu Asp Arg Ser Leu Asp Leu Leu Ala Arg Phe Leu His
100 105 110
Ser Val Phe Arg Lys Ala Ser Arg Arg Xaa Ala Pro Arg Cys Gln Val
115 120 125
Arg Ala Ala Ala Phe Arg Pro Arg Arg Ala Gly Glu Val Phe Gly Gln
130 135 140
Trp Arg Ala Cys Pro Asp Val Leu Met Asp Pro Glu Gly Ser Ser Arg
145 150 155 160
Gly Gly Leu His Ile Trp Lys His Gly Val Trp
165 170
(2) INFORMATION FOR SEQ ID NO:3277:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1576317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3277:

```
Glu Ala His Asn Lys Pro Ala Asp Pro Pro Trp Gln Ala Pro Pro Pro
1      5      10      15
Ser Xaa Pro Phe Pro Xaa Pro Pro Leu His Leu Ala Thr Ala Ser Thr
      20      25      30
Arg Pro Arg Pro His Pro Pro Ala Thr Cys Ala Pro Pro Leu Leu His
      35      40      45
Ala Ser Ala Leu Pro Gly Val Gly Ile Pro Thr Pro Ser Leu Ser Ser
50      55      60
Gln Met Pro Ala Pro Gly Ser Ala Ile Tyr Arg Ala Pro Pro Arg Pro
65      70      75      80
Thr Gly Thr Glu Val Arg Arg Thr Lys Thr Thr Gln Met Lys Met Arg
      85      90      95
Thr Lys Thr Arg Thr Ala Ala Trp Thr Tyr Trp Pro Gly Ser Cys Thr
      100      105      110
Pro Tyr Ser Gly Arg Pro His Ala Ala Xaa Arg Arg Ala Ala Arg Ser
      115      120      125
Val Leu Pro Pro Ser Val Pro Ala Glu Leu Val Lys Phe Ser Val Asn
130      135      140
Gly Val Leu Val Leu Thr Phe Leu Trp Ile Leu Lys Gly Leu Leu Glu
145      150      155      160
Val Val Cys Thr Phe Gly Ser Met Val Phe Gly Asn Ser Ile Gln Asp
      165      170      175
Tyr Cys Thr Leu Pro Ala Leu Gly Glu Lys Arg Phe Ser Val
      180      185      190
```

(2) INFORMATION FOR SEQ ID NO:3278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3278:

```
Met Ala Gly Ser Thr Ser Leu Xaa Pro Leu Pro Xaa Pro Ala Pro Pro
1      5      10      15
Ser Arg His Arg Phe His Thr Ser Thr Ser Ala Ser Pro Arg His Leu
      20      25      30
Arg Pro Ser Pro Ala Thr Arg Leu Arg Ala Ala Arg Arg Arg His Pro
      35      40      45
Asp Ala Val Val Val Val Pro Asp Ala Arg Pro Trp Val Gly Asp Leu
50      55      60
Ser Gly Ala Ala Ala Ser Tyr Arg Asp Gly Ser Glu Glu Asp Glu Asp
65      70      75      80
Asp Ala Asp Glu Asp Glu Asp Glu Asp Arg Ser Leu Asp Leu
      85      90      95
Leu Ala Arg Phe Leu His Ser Val Phe Arg Lys Ala Ser Arg Arg Xaa
      100      105      110
Ala Pro Arg Cys Gln Val Arg Ala Ala Ala Phe Arg Pro Arg Arg Ala
      115      120      125
Gly Glu Val Phe Gly Gln Trp Arg Ala Cys Pro Asp Val Leu Met Asp
130      135      140
Pro Glu Gly Ser Ser Arg Gly Gly Leu His Ile Trp Lys His Gly Val
145      150      155      160
```

Trp

(2) INFORMATION FOR SEQ ID NO:3279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3279:

aagacctcct	cgcggtctatg	gcgaaGcgctc	tgatcccgctc	gctgaaccgg	gttctggtgg	60
agaagctgct	gaagcccaagc	aagagcgccg	gcggcatcct	cctcccgagg	accaccaagc	120
agctgaacgc	cgctaaagtc	gttgctgttg	gccctggtga	tcgtgatagg	gatggcaagc	180
tgatccctgt	atctctgagc	gaaggcgaca	ctgttctgct	tccggagtac	ggtgggaacg	240
aagtgaagct	tgcaagaaaa	gagtagcttc	ttttcagaga	gcacgacata	ctgggggaagc	300
tcgaggaagta	gctctggact	gttaaaatgg	agttgtttga	aagtaggtat	gcaagagttt	360
tgccacggct	tatctttttt	ttttgtacgg	gggaacaaat	gagaacacata	acccttgtga	420
gaatgcaata	acactgcctc	attcttg				

(2) INFORMATION FOR SEQ ID NO:3280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3280:

Asp	Leu	Leu	Ala	Ala	Met	Ala	Lys	Arg	Leu	Ile	Pro	Ser	Leu	Asn	Arg
1			5							10				15	
Val	Leu	Val	Glu	Lys	Leu	Leu	Lys	Pro	Ser	Lys	Ser	Ala	Gly	Gly	Ile
			20					25					30		
Leu	Leu	Pro	Glu	Thr	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Lys	Val	Val	Ala
			35				40					45			
Val	Gly	Pro	Gly	Asp	Arg	Asp	Arg	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser
			50				55				60				
Leu	Ser	Glu	Gly	Asp	Thr	Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Glu
			65			70				75				80	
Val	Lys	Leu	Ala	Glu	Lys	Glu	Tyr	Leu	Leu	Phe	Arg	Glu	His	Asp	Ile
			85					90						95	
Leu	Gly	Lys	Leu	Glu	Glu										
			100												

(2) INFORMATION FOR SEQ ID NO:3281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3281:

Met Ala Lys Arg Leu Ile Pro Ser Leu Asn Arg Val Leu Val Glu Lys

1	5	10	15
Leu Leu Lys Pro Ser Lys Ser Ala Gly Gly Ile Leu Leu Pro Glu Thr			
20	25	30	35
Thr Lys Gln Leu Asn Ala Ala Lys Val Val Ala Val Gly Pro Gly Asp			
40	45	50	55
Arg Asp Arg Asp Gly Lys Leu Ile Pro Val Ser Leu Ser Glu Gly Asp			
60	65	70	75
Thr Val Leu Leu Pro Glu Tyr Gly Gly Thr Glu Val Lys Leu Ala Glu			
80	85	90	95
Lys Glu Tyr Leu Leu Phe Arg Glu His Asp Ile Leu Gly Lys Leu Glu			
Glu			

(2) INFORMATION FOR SEQ ID NO:3282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..798
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3282:

gcaaaacccct	aacctgtgtct	tgtgcgcast	ccgctattaa	agctctgcgta	cagtcgccgcg	60
cggtcaggcg	acgcgatccg	catctcccct	acgtctctctc	gccggctgcg	cacgggcataa	120
gcagcgatgg	ctacagcgac	ggcagtttgt	ggaccgcgaca	ggtggagact	gcggcgctcgt	180
ccgcggcgcc	agtcgtcgcc	gtcgcgcttg	cctcgcagag	tgtctcaggt	ctgcctcgctc	240
ttgcggttca	aactgttaaat	gttggagcag	aaatatataa	taaagatcag	cgggccaatat	300
acaagtattt	atctGggaag	aatcaaatct	gaaaatgtcc	ctgaaaaataa	ggatgggttca	360
gacgacgacg	atgatgaaga	cgacgatgaa	gacaatgacg	atgagggttg	tgacgacgat	420
gatgatcctg	aggaggaatt	ctctggagaa	gaagatgggg	gtgatgacga	tgatgaagat	480
gatgatcctg	aagctaattg	tgaaggagga	agtgacaacg	acaatgatga	cgacgaagat	540
ggtgatgatg	atggcgatga	ggacgatgaa	ggtgatgagg	acgacgaaga	cgaggacgat	600
gatgaagatg	acgaagacca	gccaccttcc	aagaagaaga	aatgatttgc	tcattccatgg	660
atttaacctca	gctctccat	gctgttagtt	gtgtgtgtta	gatcatggac	agcttttgga	720
tcaatgtagc	ttgtgtcttg	tcattggtatc	gtagtgtagg	aaaatttgac	atctgatgtt	780
aaatcactat	ctgccttt					

(2) INFORMATION FOR SEQ ID NO:3283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3283:

Met Leu Glu Gln Lys Tyr Ile Ile Lys Ile Ser Gly Gln Tyr Thr Ser			
1	5	10	15
Tyr Tyr Leu Gly Arg Ile Lys Ser Glu Asn Val Pro Glu Asn Lys Asp			
20	25	30	35
Gly Ser Asp Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Asp Asp			
40	45	50	55
Glu Gly Gly Asp Asp Asp Asp Asp Ala Glu Glu Glu Phe Ser Gly Glu			
60	65	70	75
Glu Asp Gly Gly Asp Asp Asp Asp Glu Asp Asp Asp Pro Glu Ala Asn			
80			

Gly	Glu	Gly	Gly	Ser	Asp	Asn	Asp	Asn	Asp	Asp	Asp	Glu	Asp	Gly	Asp
				85							90			95	
Asp	Asp	Gly	Asp	Glu	Asp	Asp	Glu	Gly	Asp	Glu	Asp	Glu	Asp	Glu	
				100				105						110	
Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gln	Pro	Pro	Ser	Lys	Lys	Lys	
				115				120						125	

(2) INFORMATION FOR SEQ ID NO:3284:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1576336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3284:

Met	Ser	Leu	Lys	Ile	Arg	Met	Gly	Gln	Thr	Thr	Thr	Met	Met	Thr	Thr
1				5				10						15	
Thr	Met	Lys	Thr	Met	Thr	Met	Arg	Val	Val	Thr	Thr	Met	Met	Met	Leu
				20				25						30	
Arg	Arg	Asn	Ser	Leu	Glu	Lys	Lys	Met	Gly	Val	Met	Thr	Met	Met	Lys
				35				40						45	
Met	Met	Ile	Leu	Lys	Leu	Met	Val	Lys	Glu	Glu	Val	Thr	Thr	Thr	Met
				50				55						60	
Met	Thr	Thr	Lys	Met	Val	Met	Met	Met	Ala	Met	Arg	Thr	Met	Lys	Val
65				70						75				80	
Met	Arg	Thr	Thr	Lys	Thr	Arg	Thr	Met	Met	Lys	Met	Thr	Lys	Thr	Ser
				85						90				95	
His	Leu	Pro	Arg	Arg	Arg	Asn	Asp	Leu	Leu	Ile	His	Gly	Phe	Thr	Ser
				100				105						110	
Ala	Ser	Pro	Cys	Cys											
				115											

(2) INFORMATION FOR SEQ ID NO:3285:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1576337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3285:

Met	Gly	Gln	Thr	Thr	Thr	Met	Met	Thr	Thr	Thr	Met	Lys	Thr	Met	Thr
1								10						15	
Met	Arg	Val	Val	Thr	Thr	Met	Met	Met	Leu	Arg	Arg	Asn	Ser	Leu	Glu
				20				25						30	
Lys	Lys	Met	Gly	Val	Met	Thr	Met	Met	Lys	Met	Met	Ile	Leu	Lys	Leu
				35				40						45	
Met	Val	Lys	Glu	Glu	Val	Thr	Thr	Met	Met	Thr	Thr	Lys	Met	Val	
				50				55						60	
Met	Met	Met	Ala	Met	Arg	Thr	Met	Lys	Val	Met	Arg	Thr	Thr	Lys	Thr
65				70						75				80	
Arg	Thr	Met	Met	Lys	Met	Thr	Lys	Thr	Ser	His	Leu	Pro	Arg	Arg	Arg
				85						90				95	
Asn	Asp	Leu	Leu	Ile	His	Gly	Phe	Thr	Ser	Ala	Ser	Pro	Cys	Cys	

100 105 110

(2) INFORMATION FOR SEQ ID NO:3286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..646

(D) OTHER INFORMATION: / Ceres Seq. ID 1576347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3286:

gacggggagaa aatctccaaa cgcagcaran mcccctgcgc cgcgcagctc ttcagcctcg	60
cagcacacccg ccgcccagccc gactgaccgc tgcagcctag ggtttccgtc ggcatgaggc	120
ggtaargrag ggaagggtct gctggcgccc aagacgacgg cggccaagag caccgacaag	180
gacaaggaca ggaagaargc ccccggtgtcg cgtcctccc gcgcccgcct ccagttcccg	240
gtgggtcgca tccaccgcca gctcaagtgc cgtgcctctg cgcacggccc cgtcggcgcc	300
accgcgcgcg tctattccgc cgccatctc gagtacctca ccgccgaggt cctcgagctg	360
gGccggcaac gccagcaagg acctcaaggt caagcgcatc accccgcgcc acctgcagct	420
cgccatccgc ggggacgagg agctcgacac cctcatcaag gccaccatcg ccggggcgcg	480
cgtcatcccg cacatccaca agtcgctcat caacaagacc gccaaaggag gaatacaagg	540
cgtgctgctg ctctgcctg actacagctc catctcgttc tgtactgtg caatctgagt	600
ttaagtgcag gttggcagc ttctagtaaa ctcctcgtg tcacct	

(2) INFORMATION FOR SEQ ID NO:3287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1576348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3287:

Asp Gly Arg Lys Ser Pro Asn Ala Ala Xaa Xaa Leu Ala Pro Pro Thr	
1 5 10 15	
Ser Ser Ala Ser Gln His Thr Ala Ala Ser Pro Ser Asp Arg Cys Ser	
20 25 30	
Leu Gly Phe Pro Ser Ala Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu	
35 40 45	
Ala Ala Lys Thr Thr Ala Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg	
50 55 60	
Lys Xaa Ala Pro Val Ser Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro	
65 70 75 80	
Val Gly Arg Ile His Arg Gln Leu Lys Ser Arg Ala Ser Ala His Gly	
85 90 95	
Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr	
100 105 110	
Leu Thr Ala Glu Val Leu Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro	
115 120 125	
Gln Gly Gln Ala His His Pro Ala Pro Pro Ala Ala Arg His Pro Arg	
130 135 140	
Gly Arg Gly Ala Arg His Pro His Gln Gly His His Arg Arg Gly Arg	
145 150 155 160	
Arg His Pro Ala His Pro Gln Val Ala His Gln Gln Asp Arg Gln Gly	
165 170 175	
Val Asn Gln Gly Arg Ala Ala Ala Ser Ala	
180 185	

(2) INFORMATION FOR SEQ ID NO:3288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576349
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3288:

Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala
1 5 10 15
Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg Lys Xaa Ala Pro Val Ser
20 25 30
Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Ile His Arg
35 40 45
Gln Leu Lys Ser Arg Ala Ser Ala His Gly Arg Val Gly Ala Thr Ala
50 55 60
Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu
65 70 75 80
Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro Gln Gly Gln Ala His His
85 90 95
Pro Ala Pro Pro Ala Ala Arg His Pro Arg Gly Arg Gly Ala Arg His
100 105 110
Pro His Gln Gly His His Arg Arg Gly Arg Arg His Pro Ala His Pro
115 120 125
Gln Val Ala His Gln Gln Asp Arg Gln Gly Val Asn Gln Gly Arg Ala
130 135 140
Ala Ala Ser Ala
145

- (2) INFORMATION FOR SEQ ID NO:3289:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..454
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576358
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3289:

tatccaaatt caaatttcag acaatgagtg atgcagacaa gctagctgct ggcattgcag 60
cacctgtggg tggagtgtat acagagtggt gtaccaatcc tcctgtcgaa catattctct 120
cagctgaggga tgcagagtgc tgtatctgcc tatgcccgta tgaagatggc gtggaaactac 180
gtgagcttcc ttgcaaccac cattttcact gcagctgcac tgacaagtgg cttcacataa 240
atgtctacatg cccattgtgc aagttcgaca tcatcaagag caaccgtgac atagaagagg 300
tctaggtcac taaggaaaaa acgcccgaas acttttgtca tgtctctgct gtgttcttca 360
gtactaccgc taccacattt gcgatcctga gttgtgatta ccggtccctt aggtgatgca 420
caaatggtac tcgGtgaata ttccttttat tagc

- (2) INFORMATION FOR SEQ ID NO:3290:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1576359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3290:

Ser Lys Phe Lys Phe Gln Thr Met Ser Asp Ala Asp Lys Leu Ala Ala
1 5 10 15
Gly Ile Ala Ala Pro Val Gly Gly Val Met Thr Glu Cys Gly Thr Asn
20 25 30
Pro Pro Val Glu His Ile Leu Ser Ala Glu Asp Ala Glu Cys Cys Ile
35 40 45
Cys Leu Cys Pro Tyr Glu Asp Gly Val Glu Leu Arg Glu Leu Pro Cys
50 55 60
Asn His His Phe His Cys Ser Cys Ile Asp Lys Trp Leu His Ile Asn
65 70 75 80
Ala Thr Cys Pro Leu Cys Lys Phe Asp Ile Ile Lys Ser Asn Arg Asp
85 90 95
Ile Glu Glu Val
100

(2) INFORMATION FOR SEQ ID NO:3291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1576360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3291:

Met Ser Asp Ala Asp Lys Leu Ala Ala Gly Ile Ala Ala Pro Val Gly
1 5 10 15
Gly Val Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu
20 25 30
Ser Ala Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp
35 40 45
Gly Val Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser
50 55 60
Cys Ile Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys
65 70 75 80
Phe Asp Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val
85 90

(2) INFORMATION FOR SEQ ID NO:3292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1576361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3292:

Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu Ser Ala
1 5 10 15
Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp Gly Val
20 25 30
Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser Cys Ile
35 40 45
Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys Phe Asp
50 55 60
Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val

65

70

75

(2) INFORMATION FOR SEQ ID NO:3293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3293:

aacaacagcg	aacacaNtct	gCttgcatt	tcttccatc	cccttcgca	acccaaaccc	60
caacNtcgCt	ccgcctcgat	ggcgcccaag	gccgagaaga	agcccgcgcc	gaagaagccg	120
gcggaggagg	agcccgcgcc	tgagaaggcg	ccgcgggga	agaagcagag	gtgggggttg	180
ttcattgcc	ccaagtgtatt	tggcctggca	gcaggaggcc	tcttcggaat	aagaatggat	240
gtgctgttaa	ctctgcctct	agaccgggtga	tggttcagct	tagaagcagg	ggatcttcac	300
catcagaata	aaaacgtgtg	ctgttgtgtt	gctgtgtcc			

(2) INFORMATION FOR SEQ ID NO:3294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3294:

Asn	Asn	Ser	Glu	His	Xaa	Leu	Leu	Arg	Ile	Ser	Ser	His	Pro	Pro	Ser	
1				5					10					15		
Gln	Pro	Lys	Pro	Gln	Xaa	Arg	Ser	Ala	Ser	Met	Ala	Pro	Lys	Ala	Glu	
				20				25					30			
Lys	Lys	Pro	Ala	Ala	Lys	Lys	Pro	Ala	Glu	Glu	Glu	Pro	Ala	Ala	Glu	
				35				40					45			
Lys	Ala	Pro	Ala	Gly	Lys	Lys	Gln	Arg	Trp	Gly	Leu	Phe	Ile	Ala	Thr	
				50			55					60				

Lys

65

(2) INFORMATION FOR SEQ ID NO:3295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3295:

Thr	Thr	Ala	Asn	Thr	Xaa	Cys	Phe	Ala	Phe	Leu	Pro	Ile	Pro	Leu	Arg	
1				5					10					15		
Asn	Pro	Asn	Pro	Asn	Xaa	Ala	Pro	His	Arg	Trp	Arg	Pro	Arg	Pro	Arg	
				20				25					30			
Arg	Ser	Pro	Arg	Arg	Arg	Ser	Arg	Arg	Arg	Arg	Ser	Pro	Arg	Leu	Arg	
				35				40					45			
Arg	Arg	Pro	Pro	Gly	Arg	Ser	Arg	Gly	Gly	Gly	Cys	Ser	Leu	Pro	Pro	
				50			55					60				

Ser Asp Leu Ala Trp Gln Gln Glu Gly Ser Ser Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3296:

Gln Gln Arg Thr Xaa Ser Ala Ser His Phe Phe Pro Ser Pro Phe Ala
1 5 10 15
Thr Gln Thr Pro Xaa Ser Leu Arg Ile Asp Gly Ala Gln Gly Arg Glu
20 25 30
Glu Ala Arg Gly Glu Glu Ala Gly Gly Gly Ala Arg Gly
35 40 45

(2) INFORMATION FOR SEQ ID NO:3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..634
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3297:

acccaagtcc aagcaccttc ccaaaaaaat cccccatttt cttcgaggcg aggagagcgt 60
gaaagacagg gcaccggcag cgacgatgtc ggggcgcggc aagggcgcca aaggtctggs 120
caagggcgga Gcaaaagcgcc accgtaaggT gctccgtgac aacatccagg gcatacaccaa 180
gcccgcgatc cgtaggctgg ctcggagggg cggcgtgaag cgcatttcgg ggcttatcta 240
cgaggagggt aagactgtgg acctctatgt ccccaggaag tgctcgggcca caaacaggat 300
catcactgcc aaggaccatg cctctgtcca gatcaacatt ggccacttgg atgcgaatgg 360
cctgtatgat ggtaacttca caacgtttgc tctctctggg ttgtctcgtg ctcagggtga 420
cgcagacagc tccttggaca ggctgtggca aaagaagaag gctgatataca agcagtagat 480
tttacatcta gtttaccag aattggacac cgccttagct atgttttgaa ttcatgtcac 540
tatatgcAat gttgtgattt cagctggtag cttaaatotg aagatttagt atctttgttg 600
ggttccttct gagtttgatg tgggtgttgc gttt

(2) INFORMATION FOR SEQ ID NO:3298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3298:

Pro Lys Ser Lys His Leu Pro Lys Lys Ile Pro His Phe Leu Arg Gly
1 5 10 15
Glu Glu Ser Val Lys Asp Arg Ala Pro Ala Ala Thr Met Ser Gly Arg
20 25 30
Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala Lys Arg His Arg
35 40 45

Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg
50 55 60
Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr
65 70 75 80
Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys Cys Ser Ala
85 90 95
Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val Gln Ile Asn
100 105 110
Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly His Phe Thr Thr
115 120 125
Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala Asp Ser Ser
130 135 140
Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile Lys Gln
145 150 155

(2) INFORMATION FOR SEQ ID NO:3299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1576374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3299:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala
1 5 10 15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
20 25 30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
35 40 45
Gly Leu Ile Tyr Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg
50 55 60
Lys Cys Ser Ala Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser
65 70 75 80
Val Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly
85 90 95
His Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp
100 105 110
Ala Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile
115 120 125
Lys Gln
130

(2) INFORMATION FOR SEQ ID NO:3300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847

(D) OTHER INFORMATION: / Ceres Seq. ID 1576379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3300:

acaaaatgaa gatgaagatg aagaagtgtg	tgaagaagttaa gaagctgcag atgattcacg	60
caagcctgca acatcaattg gctcagcata	cagactgctt actccatcag taaaggtcca	120
gttggtgata tacttcatgc tgaataacgc	aatggagatt ttgctttcag agtctagtgt	180
tatcactaat cactatttca gttggaacac	aagcgcagtg gncaattttt ctagcaatcc	240
ttgggttgac ggtgcttcc	gttaatgctg ttgttggaac atacatcagc aatatgtttg	300

aggacaggca actgctcatg gtctctcaaa ttacgttgct agtaggcatt atcttcagct 360
tcaaggttac gactacatac tctgtgtgcc agtatgttg ctcagcactt gtcacatttg 420
ttctgcaga agttcttgaa ggtgtgaacc ttccctcct atcaagcgtg atgtcatctc 480
gcctctcccg tggcacatac aacggtggcc tcctctcgac ggaggccVgg gacctggcg 540
aggggtgctg ctgactgcac cateactgcg gcgggggtacc tggcggtggg gaagcttctc 600
aacgtcaacc tgctaccatc cctgggtgata tgtgttgctg ccattgctcg caccttctcg 660
acataaact cgcttttctg atggagcttc acaatgtatt tgtgtcatca tgattcgctc 720
catattagcg caaatcaagg cagctgggag accgcatcg ccattgcccg aaggggctat 780
tgtattacta ttattatatg ttcgtcgatt tgattgctat aaattgattg ataaaatgat 840
tgtagcg

(2) INFORMATION FOR SEQ ID NO:3301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1576380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3301:

Gln Asn Glu Asp Glu Asp Glu Glu Val Asp Glu Ser Glu Ala Ala
1 5 10 15
Asp Asp Ser Arg Lys Pro Ala Thr Ser Ile Gly Ser Ala Tyr Arg Leu
20 25 30
Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr Phe Met Leu Lys
35 40 45
Tyr Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val Ile Thr Asn His
50 55 60
Tyr Phe Ser Trp Asn Thr Ser Ala Val Xaa Asn Phe Ser Ser Asn Pro
65 70 75 80
Trp Val Asp Gly Ala Ser Cys
85

(2) INFORMATION FOR SEQ ID NO:3302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1576381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3302:

Met Phe Glu Asp Arg Gln Leu Leu Met Val Ser Gln Ile Thr Leu Leu
1 5 10 15
Val Gly Ile Ile Phe Ser Phe Lys Val Thr Ser Thr Tyr Ser Val Val
20 25 30
Gln Tyr Val Val Ser Ala Leu Val Thr Phe Val Ser Ala Glu Val Leu
35 40 45
Glu Gly Val Asn Leu Ser Leu Leu Ser Ser Val Met Ser Ser Arg Leu
50 55 60
Ser Arg Gly Thr Tyr Asn Gly Gly Leu Leu Ser Thr Glu Ala Xaa Asp
65 70 75 80
Pro Gly Glu Gly Gly Arg
85

(2) INFORMATION FOR SEQ ID NO:3303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1576382
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3303:
Met Val Ser Gln Ile Thr Leu Leu Val Gly Ile Ile Phe Ser Phe Lys
1 5 10 15
Val Thr Ser Thr Tyr Ser Val Val Gln Tyr Val Val Ser Ala Leu Val
20 25 30
Thr Phe Val Ser Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
35 40 45
Ser Ser Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly
50 55 60
Leu Leu Ser Thr Glu Ala Xaa Asp Pro Gly Glu Gly Gly Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:3304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..688
(D) OTHER INFORMATION: / Ceres Seq. ID 1576401
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3304:
ccaccacccc ccacacccac gagcccgccg gcgtgctctc tctgtctcgc tctgcaccca 60
ggaccttcgg ccacaggagc tcagccctat ccctcgacgg tgcctcgccg cgccgcccgg 120
cggtctgacc cttccccatc tccagctcca ccgcgtctcc accgctgga atccagggcc 180
tcgcagcgcca cccacacctc accgcctgga atcgaggacc gtccggctcc ttcatgatcag 240
cgccgagcgc aacaaggagc agggaggagaa gacggacacc tggcaccgcg tggagcggag 300
cagcggggaga ttccctgcgc ggttcgcgact gcccgagaac gccaaagcgg agcagatcac 360
ggccgcatcg gagaacggcg tgcttacagt cactgtgccc aaggaggagc ccaagaagcc 420
CCtgaagtga agtccattca gatctccggc tagacctcgg tctgcggtcg tctgacctgc 480
gtggttttag gaacggcagt tcgcctcggc cggtctgtga aataaaattg gggtacaaga 540
attatgcgct ttgtcaatat gatcgtaatg tcgtaggatg gtggaatgtg gtcacaaact 600
ttcgctatgt tgggtctact ggtggtgtct actctgaatc tatgtatgga tgcacatgat 660
tccagtctct gtggtgttcg tatgatgc

(2) INFORMATION FOR SEQ ID NO:3305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1576402
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3305:
Pro Pro Thr Pro Thr Ser Pro Ala Ala Cys Ser Leu Leu Ser
1 5 10 15
Ala Leu His Pro Gly Pro Ser Ala Thr Gly Ala Gln Pro Tyr Pro Ser
20 25 30
Thr Val Leu Ala Ala Gly Ala Arg Arg Leu Asp Pro Ser Pro Ser Pro
35 40 45

Ala Pro Arg Arg Leu His Arg Leu Glu Ser Arg Ala Ser Asp Ala Thr
50 55 60
Pro Pro Pro Pro Gly Ile Glu Asp Arg Arg Pro Ser Asp Gln
65 70 75 80
Arg Arg Ala Gln Gln Gly Ala Gly Gly Glu Asp Gly His Leu Ala Pro
85 90 95
Arg Gly Ala Glu Gln Arg Glu Ile Pro Ala Gln Val Pro Thr Ala Arg
100 105 110
Glu Arg Gln Asp Gly Ala Asp Gln Gly Arg His Gly Glu Arg Arg Ala
115 120 125
Tyr Ser His Cys Ala Gln Gly Gly Arg Gln Glu Ala Pro Glu Val Lys
130 135 140
Ser Ile Gln Ile Ser Gly
145 150

(2) INFORMATION FOR SEQ ID NO:3306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1576403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3306:

His Pro Pro Pro His Pro Arg Ala Arg Arg Ala Leu Cys Cys Leu
1 5 10 15
Leu Cys Thr Gln Asp Leu Arg Pro Gln Glu Leu Ser Pro Ile Pro Arg
20 25 30
Arg Cys Ser Arg Pro Ala Arg Gly Gly Ser Thr Leu Pro His Leu Gln
35 40 45
Leu His Ala Val Ser Thr Ala Trp Asn Pro Gly Pro Pro Thr Pro Pro
50 55 60
His Leu His Arg Leu Glu Ser Arg Thr Val Gly Val Leu Gln Ile Ser
65 70 75 80
Gly Glu Arg Asn Lys Glu Gln Glu Glu Lys Thr Asp Thr Trp His Arg
85 90 95
Val Glu Arg Ser Ser Gly Arg Phe Leu Arg Arg Phe Arg Leu Pro Glu
100 105 110
Asn Ala Lys Thr Glu Gln Ile Arg Ala Ala Met Glu Asn Gly Val Leu
115 120 125
Thr Val Thr Val Pro Lys Glu Asp Ala Lys Lys Pro Leu Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:3307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1576404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3307:

Thr His Pro His Thr His Glu Pro Gly Gly Val Leu Ser Ala Val Cys
1 5 10 15
Ser Ala Pro Arg Thr Phe Gly His Arg Ser Ser Ala Leu Ser Leu Asp
20 25 30
Gly Ala Arg Gly Arg Arg Ala Ala Arg Pro Phe Pro Ile Ser Ser

1	Leu	Gln	Leu	Gln	Ser	Gly	Val	Trp	Leu	Val	Leu	Arg	Met	Phe	Val	Leu
				5					10						15	
Phe	Thr	Pro	Thr	Glu	Ile	Asn	Leu	Arg	Arg	Cys	Leu	Leu	Arg	Ser	Arg	
			20						25					30		
Arg	Arg	Leu	Arg	Leu	Arg	Cys	Arg	Arg	Ala	Gly	Gln	Gly	His	Val	Asp	
			35				40						45			
Leu	Arg	Val	Gln	Arg	Glu	Arg	Arg	Gly	Gly	Asp	Gly	Gly	Glu	Glu	Leu	
			50			55					60					
Leu	Arg	Asp	Arg	Gln	Arg	Pro	Pro	Arg	Arg	Ala	Ala	Ala	Asp	Asp		
65					70				75					80		
Arg	His	Arg	Leu	Pro	Thr	Gly	Val	Gln	Gly	Pro	Arg	Gln	Ala	Leu	His	
			85						90					95		
Arg	Ala	Leu	Gly	Ala	Arg	His	Arg	Arg	Pro	Asp	Ala	Val	Ser	Ala	Ala	
			100					105					110			
Gly	Val	Gln	Ala	Gln	Val	Val	Pro	Ala	Glu	Gly	Gly	Glu	Gly	His	Glu	
			115				120					125				

Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:3310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3310:

```
Pro Val Thr Val Arg Ser Leu Val Ser Thr Pro His Val Arg Ser Phe
1      5      10      15
Tyr Ala Asp Gly Asn Gln Pro Ala Pro Leu Pro Ser Pro Phe Ser Pro
20      25      30
Ser Pro Pro Pro Pro Leu Pro Pro Arg Arg Ser Gly Ser Cys Arg Ser
35      40      45
Ser Ser Thr Thr Gly Ala Pro Trp Trp Arg Trp Gly Arg Thr Ala
50      55      60
Ser Arg Ser Pro Ala Thr Ala Ala Ser Ala Cys Ser Cys Arg Arg Ser
65      70      75      80
Pro Pro Thr Ser Asp Gly Cys Ser Arg Ser Thr Thr Ser Ser Thr Ser
85      90      95
Gly Ser Arg Gly Ser Pro Pro Thr Pro Arg Arg Cys Ile Ser Gly Trp
100      105      110
Cys Ser Gly Thr Ser Cys Thr Ser
115      120
```

(2) INFORMATION FOR SEQ ID NO:3311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3311:

```
Met Phe Val Leu Phe Thr Pro Thr Glu Ile Asn Leu Arg Arg Cys Leu
1      5      10      15
Leu Arg Ser Arg Arg Arg Leu Arg Leu Arg Cys Arg Arg Ala Gly Gln
20      25      30
Gly His Val Asp Leu Arg Val Gln Arg Glu Arg Arg Gly Gly Asp Gly
35      40      45
Gly Glu Glu Leu Leu Arg Asp Arg Gln Arg Pro Pro Pro Arg Arg Ala
50      55      60
Ala Ala Asp Asp Arg His Arg Leu Pro Thr Gly Val Gln Gly Pro Arg
65      70      75      80
Gln Ala Leu His Arg Ala Leu Gly Ala Arg His Arg Arg Pro Asp Ala
85      90      95
Val Ser Ala Ala Gly Val Gln Ala Gln Val Val Pro Ala Glu Gly Gly
100      105      110
Glu Gly His Glu Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro
115      120      125
Leu
```

(2) INFORMATION FOR SEQ ID NO:3312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 986 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..986
(D) OTHER INFORMATION: / Ceres Seq. ID 1576429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3312:

aacgtgcct	tcgcgcgctt	atcctttccc	acgaactcctc	tcgccgcgtg	gagaacatgc	60
cccggtcct	tgtccaggca	ccattgcgcg	cgccgcgtcg	ctcccttgca	ccatcgccct	120
ctacagatga	agctcaaaag	aagtgaactc	aaattatcac	tcaagaatct	caagagcatt	180
tggtagaag	tgttctcctg	attttgtgaa	tgtccagtat	gcagtgaaat	tctagaagtt	240
tttatttatg	tatgcattgt	ttaataactt	tgatcaatgg	atgcttataa	agattctatg	300
gaatttctgg	aggagttatc	tgtctttgat	cttcactctg	ggaggccgtg	gtggccggtt	360
cgccgcggcg	ttccgcgacg	aggggccgcc	cgcagaggtc	gtcgaggtgt	cgacgttctg	420
gcacgcgtgc	gaggggagacg	cggtgacgaa	actcaccaac	gagaaGgtgc	cctacttcaa	480
cgcccccata	tacctgcaga	acaagactca	ggtcggcaag	gtcgacgaga	tcttcggccc	540
catcaacgaa	tcttatttct	ctgtgaagat	gatggaaggg	atcattgcaa	catcgtacaa	600
ggaaggcgac	aagttctata	tcgaccccat	gaaattgctg	cctctttcgc	gcttctctgc	660
gcaaccaaaag	ggacaattctc	aaggagcacc	tagagttggt	ggccgtgtgg	aagggtgtgt	720
ggccgaggcc	gtgtgtgttc	gttccggggt	ggaagaggac	caccaagggg	tgtgtggcga	780
ggtccaaaggg	gtggaaagccg	tggtgtgttt	agaggcgag	gaaggttcta	ggtgtagttt	840
gagtttgatg	atgttttttt	ttgttgaggc	atcatagcta	cccaattgga	aacttccatg	900
ttcttgtaac	ctgatattgt	taaggtagca	gaacactttg	ttgtggaac	ttggattctc	960
aattgaaaca	aagggtttgt	actcgt				

(2) INFORMATION FOR SEQ ID NO:3313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..209
(D) OTHER INFORMATION: / Ceres Seq. ID 1576430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3313:

Met	Tyr	Ala	Cys	Phe	Lys	Tyr	Phe	Asp	Gln	Trp	Met	Leu	Ile	Lys	Ile
1			5						10					15	
Leu	Trp	Asn	Phe	Trp	Arg	Ser	Tyr	Leu	Ser	Leu	Ile	Phe	Ile	Cys	Gly
			20					25					30		
Gly	Arg	Gly	Gly	Arg	Phe	Gly	Gly	Phe	Arg	Asp	Glu	Gly	Pro	Pro	
			35				40				45				
Ala	Glu	Val	Val	Glu	Val	Ser	Thr	Phe	Val	His	Ala	Cys	Glu	Gly	Asp
			50				55				60				
Ala	Val	Thr	Lys	Leu	Thr	Asn	Glu	Lys	Val	Pro	Tyr	Phe	Asn	Ala	Pro
65					70				75					80	
Ile	Tyr	Leu	Gln	Asn	Lys	Thr	Gln	Val	Gly	Lys	Val	Asp	Glu	Ile	Phe
			85					90					95		
Gly	Pro	Ile	Asn	Glu	Ser	Tyr	Phe	Ser	Val	Lys	Met	Met	Glu	Gly	Ile
			100					105					110		
Ile	Ala	Thr	Ser	Tyr	Lys	Glu	Gly	Asp	Lys	Phe	Tyr	Ile	Asp	Pro	Met
			115				120					125			
Lys	Leu	Leu	Pro	Leu	Ser	Arg	Phe	Leu	Pro	Gln	Pro	Lys	Gly	Gln	Ser
			130				135				140				
Gln	Gly	Ala	Pro	Arg	Gly	Gly	Gly	Arg	Val	Glu	Gly	Val	Val	Ala	Glu
145					150				155					160	
Ala	Val	Val	Val	Arg	Ser	Gly	Val	Glu	Glu	Asp	His	Gln	Gly	Val	Val

			165						170							175
Ala	Glu	Val	Gln	Gly	Val	Glu	Ala	Val	Val	Leu	Glu	Gly	Glu	Glu		
			180							185			190			
Gly	Ser	Arg	Cys	Ser	Leu	Ser	Leu	Met	Met	Phe	Phe	Phe	Val	Glu	Ala	
			195					200					205			
Ser																

(2) INFORMATION FOR SEQ ID NO:3314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3314:

Met	Asp	Ala	Tyr	Lys	Asp	Ser	Met	Glu	Phe	Leu	Glu	Glu	Leu	Ser	Val	
1			5					10					15			
Phe	Asp	Leu	His	Leu	Trp	Arg	Pro	Trp	Trp	Pro	Val	Arg	Arg	Arg	Val	
			20					25					30			
Pro	Arg	Arg	Gly	Pro	Ala	Arg	Arg	Gly	Arg	Arg	Gly	Val	Asp	Val	Arg	
			35					40					45			
Ala	Arg	Val	Arg	Gly	Arg	Arg	Gly	Asp	Glu	Thr	His	Gln	Arg	Glu	Gly	
			50					55				60				
Ala	Leu	Leu	Gln	Arg	Ala	His	Ile	Pro	Ala	Glu	Gln	Asp	Ser	Gly	Arg	
65				70						75				80		
Gln	Gly	Arg	Arg	Asp	Leu	Arg	Pro	His	Gln	Arg	Ile	Leu	Phe	Leu	Cys	
				85				90					95			
Glu	Asp	Asp	Gly	Arg	Asp	His	Cys	Asn	Ile	Val	Gln	Gly	Arg	Arg	Gln	
			100					105					110			
Val	Leu	Tyr	Arg	Pro	His	Glu	Ile	Ala	Ala	Ser	Phe	Ala	Leu	Pro	Ala	
			115					120				125				
Ala	Thr	Lys	Gly	Thr	Ile	Ser	Arg	Ser	Thr							
			130					135								

(2) INFORMATION FOR SEQ ID NO:3315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3315:

Met	Leu	Ile	Lys	Ile	Leu	Trp	Asn	Phe	Trp	Arg	Ser	Tyr	Leu	Ser	Leu	
1			5					10					15			
Ile	Phe	Ile	Cys	Gly	Gly	Arg	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Phe	Arg	
			20					25					30			
Asp	Glu	Gly	Pro	Pro	Ala	Glu	Val	Val	Glu	Val	Ser	Thr	Phe	Val	His	
			35					40					45			
Ala	Cys	Glu	Gly	Asp	Ala	Val	Thr	Lys	Leu	Thr	Asn	Glu	Lys	Val	Pro	
			50					55				60				
Tyr	Phe	Asn	Ala	Pro	Ile	Tyr	Leu	Gln	Asn	Lys	Thr	Gln	Val	Gly	Lys	
65				70					75					80		
Val	Asp	Glu	Ile	Phe	Gly	Pro	Ile	Asn	Glu	Ser	Tyr	Phe	Ser	Val	Lys	
				85				90						95		

Met Met Glu Gly Ile Ile Ala Thr Ser Tyr Lys Glu Gly Asp Lys Phe
100 105 110
Tyr Ile Asp Pro Met Lys Leu Leu Pro Leu Ser Arg Phe Leu Pro Gln
115 120 125
Pro Lys Gly Gln Ser Gln Gly Ala Pro Arg Gly Gly Arg Val Glu
130 135 140
Gly Val Val Ala Glu Ala Val Val Val Arg Ser Gly Val Glu Glu Asp
145 150 155 160
His Gln Gly Val Val Ala Glu Val Gln Gly Val Glu Ala Val Val Val
165 170 175
Leu Glu Gly Glu Glu Gly Ser Arg Cys Ser Leu Ser Leu Met Met Phe
180 185 190
Phe Phe Val Glu Ala Ser
195

(2) INFORMATION FOR SEQ ID NO:3316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..582

(D) OTHER INFORMATION: / Ceres Seq. ID 1576433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3316:

atccaggcgt	acagccctcc	gcctcgtgaa	ggcaaaagcac	gcgcaaagcc	accacagcgt	60
cgctcctttc	gtctccagtc	caagcaagcg	aagagcacc	ctcgagatct	ctccctcccc	120
gcgcgcgat	ggacgcagtT	gactcggtag	tcgaccgcgt	ccgggaagttc	gccaaaggaca	180
gcatecgcc	cgtaacgcg	tgccacaagc	cggaccgcga	ggagttcacc	aaggtcgccg	240
cgcgactgc	gateggttc	gtcgtcatgg	gattcgtcgg	ctctctttgc	aagctcatct	300
tcatcccat	caacaacatc	atcgtcggct	ccggtcgatc	cgttcacctc	aggctagtgg	360
ctgcaggagt	ggacaatggc	gtcactacct	tggaggcagc	accgttttca	gctctgattt	420
ccgcaagca	attcctttag	gacttgtgtt	gttaaggggc	aactccctta	tcttttcttc	480
tcttgaggtc	gtgtggtaga	tctggaaact	ttttgtacct	gggtccgaat	agtctttttg	540
ggatcagcgg	gtgacaaaat	tTaaatgggt	actgtctttg	gg		

(2) INFORMATION FOR SEQ ID NO:3317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1576434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3317:

Ile	Gln	Ala	Tyr	Ser	Pro	Pro	Pro	Arg	Glu	Gly	Lys	Ala	Arg	Ala	Lys
1		5						10			15				
Pro	Pro	Gln	Arg	Arg	Pro	Leu	Arg	Leu	Gln	Ser	Lys	Gln	Ala	Lys	Ser
		20					25				30				
Thr	Pro	Arg	Asp	Leu	Ser	Leu	Pro	Ala	Pro	Pro	Trp	Thr	Gln	Leu	Thr
		35					40				45				

Arg

(2) INFORMATION FOR SEQ ID NO:3318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..46
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576435
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3318:
Ser Arg Arg Thr Ala Leu Arg Leu Val Lys Ala Lys His Ala Gln Ser
1 5 10 15
His His Ser Val Val Leu Phe Val Ser Ser Pro Ser Lys Arg Arg Ala
 20 25 30
Pro Leu Glu Ile Ser Pro Ser Pro Arg Arg His Gly Arg Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1576436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3319:

Met Asp Ala Val Asp Ser Val Val Asp Pro Leu Arg Glu Phe Ala Lys
1 5 10 15
Asp Ser Ile Arg Leu Val Lys Arg Cys His Lys Pro Asp Arg Lys Glu
 20 25 30
Phe Thr Lys Val Ala Ala Arg Thr Ala Ile Gly Phe Val Val Met Gly
 35 40 45
Phe Val Gly Phe Phe Val Lys Leu Ile Phe Ile Pro Ile Asn Asn Ile
 50 55 60
Ile Val Gly Ser Gly
65

(2) INFORMATION FOR SEQ ID NO:3320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..810
(D) OTHER INFORMATION: / Ceres Seq. ID 1576437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3320:

aacgacccaa	gtcccaacgg	aacttagctg	cgcagcgccc	aaagcccccac	cgccgctccc	60
atcaagcggc	gctaaagggt	tctctgcgcc	caacgcgatg	cgaagaagaa	agggaagggg	120
aggcaagaac	cggaaagcgg	gcaagaacga	rgcggacgac	gagaagcggg	agctggntgt	180
tcaaggagga	cgggcaggag	tacgcgcagg	tgacgcggat	gctggggcaa	ggccgctgcg	240
aggcgcctcg	catcgacggc	accaagcgcc	tctgccacat	ccggggcaag	atgcacaaga	300
agggtgtgat	cgccgcgggg	gacatcgtgc	tcgtccggct	gcgcgactac	caGggacgac	360
aaaggcgagc	tcaactctaa	gtacatgaac	gaagaggccc	gcctgctcaa	gGCctacggc	420
gagatccccg	tcactcgtag	gctcaacgag	ggcgtgcttg	atgaggagga	agccggcgcg	480
caggatgact	atatacagtt	cgaggcagag	gacatcgaca	agatctgatg	atccgctctt	540
ccacacggtc	cctttccatg	gtaaaactaaa	cgtatgcmaa	acaattgtat	ccctctgttt	600
tgtgttggtc	accatgactg	aagaatggta	gtcgttggtg	tggtataatg	atttgggcgg	660
agagtactgt	gtataatgat	tgtggggcac	ttgttgtgcc	caataacccc	atatggtgat	720
atagcaagta	tgggactgaa	cgaaccgttc	ctctcccttt	ctgttaatat	gatataattg	780
gttgggcgatg	atccaatatt	ttttttttct				

(2) INFORMATION FOR SEQ ID NO:3321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3321:

Thr	Thr	Gln	Val	Pro	Thr	Glu	Leu	Ser	Cys	Arg	Ala	Pro	Lys	Ala	Pro
1			5						10				15		
Pro	Pro	Leu	Pro	Ser	Ser	Gly	Ala	Lys	Gly	Phe	Leu	Ala	Arg	Asn	Ala
			20					25					30		
Met	Pro	Lys	Asn	Lys	Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys
			35				40					45			
Asn	Xaa	Ala	Asp	Asp	Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg
			50			55					60				
Ala	Gly	Val	Arg	Ala	Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg
			65			70				75				80	
Gly	Ala	Leu	His	Arg	Arg	His	Gln	Ala	Pro	Leu	Pro	His	Pro	Gly	Gln
			85						90					95	
Asp	Ala	Gln	Glu	Gly	Val	Asp	Arg	Arg	Arg	Gly	His	Arg	Ala	Arg	Arg
			100				105						110		
Pro	Ala	Arg	Leu	Pro	Gly	Thr	Arg	Arg	Thr	Ser	Ser	Ser	Ser	Thr	
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:3322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3322:

Arg	Pro	Lys	Ser	Gln	Arg	Asn	Leu	Ala	Ala	Glu	Arg	Pro	Lys	Pro	His
1				5						10				15	
Arg	Arg	Ser	His	Gln	Ala	Ala	Leu	Lys	Val	Ser	Ser	Pro	Ala	Thr	Arg
			20				25					30			
Cys	Arg	Arg	Thr	Arg	Glu	Arg	Glu	Ala	Arg	Thr	Gly	Ser	Gly	Ala	Arg
			35				40				45				
Thr	Xaa	Arg	Thr	Thr	Arg	Ser	Gly	Ser	Trp	Xaa	Phe	Lys	Glu	Asp	Gly
			50			55				60					
Gln	Glu	Tyr	Ala	Gln	Val	Thr	Arg	Met	Leu	Gly	Asn	Gly	Arg	Cys	Glu
			65			70				75				80	
Ala	Leu	Cys	Ile	Asp	Gly	Thr	Lys	Arg	Leu	Cys	His	Ile	Arg	Gly	Lys
			85						90				95		
Met	His	Lys	Lys	Val	Trp	Ile	Ala	Ala	Gly	Asp	Ile	Val	Leu	Val	Gly
			100				105						110		
Leu	Arg	Asp	Tyr	Gln	Gly	Arg	Gln	Gly	Gly	Arg	His	Pro	Gln	Val	His
			115				120					125			
Glu	Arg	Arg	Gly	Pro	Pro	Ala	Gln	Gly	Leu	Arg	Arg	Asp	Pro	Arg	Gln
			130				135					140			
Arg	Gln	Ala	Gln	Arg	Gly	Arg	Arg								

145 150
(2) INFORMATION FOR SEQ ID NO:3323:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..96
(D) OTHER INFORMATION: / Ceres Seq. ID 1576440
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3323:
Met Pro Lys Asn Lys Gly Lys Gly Lys Asn Arg Lys Arg Gly Lys
1 5 10 15
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Arg
20 25 30
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg
35 40 45
Gly Ala Leu His Arg Arg His Gln Ala Pro Leu Pro His Pro Gly Gln
50 55 60
Asp Ala Gln Glu Gly Val Asp Arg Arg Arg Gly His Arg Ala Arg Arg
65 70 75 80
Pro Ala Arg Leu Pro Gly Thr Thr Arg Arg Thr Ser Ser Ser Ser Thr
85 90 95

(2) INFORMATION FOR SEQ ID NO:3324:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1030
(D) OTHER INFORMATION: / Ceres Seq. ID 1576441
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3324:
gtcggtaggt gtccctccct ttactccctc cgcctcccca cagtcaccat gccctctctc 60
tcggctccatc gcaagctcct cgggtcctgc ctacggccgt acggcgccat ccaccctctc 120
gcgcgcatcgt cttctcctcaag acgctgcccc aggtccatcg cgcttaggggt tcgccgagtc 180
cgccgcgcctc aagataatga gtgggcaccg aaacagtcct ggaagccgt acctcgatta 240
tactgaaact ggagggcggt agagaagaaa tctcggtgat gatacctatg cccctggctc 300
tgatgaacct gtgtatcgct acctctgcgc ctctagaaaa atTgggagta tcattggcag 360
gggtggagaaa atTgcaaaagc agttgaggac tgagacccaa gctaAgatca ggattgtgga 420
gagtgctccct ggatgtgaag agcgagttat taccatattt agctcaagtc gaagaactaa 480
taccatcgct gatgctgaag ataaggtttg cctcgctcag gatgcctctc ttagagttca 540
tgagaggctt gccactgatg agagtgtttg taacgaagac agcgaagaaa tttaacctca 600
agttactggt cgctcgtgtg tgccatcaga ccagattgga tgcattcttg gaaaagggtg 660
gcacatcctc caaggaaatcc gcagtggagc tgggtgcgcaa atacgcgtcg ttagtgaagg 720
tcatatccct gcatgtgcga ttagtggcga tgaacttctc cagatatctg gggacatggt 780
agttgtcaaa aaggctcttt gtcaagtgct atctcgctc catacaacc catccaagtc 840
acagcatctt cttgctacca gottgaccga accgtatcca gggggtaacc atttggtg 900
ttctctctgt gcaactgttg tagggatcac tccagtaatt cctccttatg gaggtacaa 960
aggtagctg gcaggagatt ggcctcttt ataccaacc cgacgggatg agagctctgc 1020
aaaggagttt

(2) INFORMATION FOR SEQ ID NO:3325:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..343
(D) OTHER INFORMATION: / Ceres Seq. ID 1576442
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3325:

Ser	Val	Gly	Val	Pro	Pro	Phe	Thr	Pro	Ser	Ala	Leu	Pro	Gln	Ser	His
1			5						10				15		
Cys	Pro	Ser	Pro	Arg	Ser	Ile	Ala	Ser	Ser	Cys	Gly	Pro	Ala	Tyr	Gly
			20					25					30		
Arg	Thr	Ala	Ala	Ser	Thr	Leu	Leu	Pro	His	Arg	Leu	Ser	Gln	Asp	Ala
			35				40					45			
Ala	Pro	Gly	Pro	Ser	Arg	Leu	Gly	Phe	Ala	Glu	Ser	Gly	Gly	Ala	Lys
			50			55					60				
Ile	Met	Ser	Gly	His	Arg	Asn	Ser	His	Gly	Lys	Arg	Tyr	Ser	Asp	Tyr
65				70					75					80	
Thr	Glu	Thr	Gly	Gly	Gly	Lys	Arg	Arg	Asn	Pro	Gly	Asp	Asp	Thr	Tyr
			85						90					95	
Ala	Pro	Gly	Pro	Asp	Asp	Thr	Val	Tyr	Arg	Tyr	Leu	Cys	Ala	Ser	Arg
			100					105					110		
Lys	Ile	Gly	Ser	Ile	Ile	Gly	Arg	Gly	Gly	Glu	Ile	Ala	Lys	Gln	Leu
			115				120					125			
Arg	Thr	Glu	Thr	Gln	Ala	Lys	Ile	Arg	Ile	Gly	Glu	Ser	Val	Pro	Gly
			130			135					140				
Cys	Glu	Glu	Arg	Val	Ile	Thr	Ile	Phe	Ser	Ser	Ser	Arg	Arg	Thr	Asn
145				150					155						160
Thr	Ile	Asp	Asp	Ala	Glu	Asp	Lys	Val	Cys	Pro	Ala	Gln	Asp	Ala	Leu
			165						170					175	
Phe	Arg	Val	His	Glu	Arg	Leu	Ala	Thr	Asp	Glu	Ser	Phe	Gly	Asn	Glu
			180				185						190		
Asp	Ser	Glu	Glu	Ile	Ser	Pro	Gln	Val	Thr	Val	Arg	Leu	Leu	Val	Pro
			195				200					205			
Ser	Asp	Gln	Ile	Gly	Cys	Ile	Leu	Gly	Lys	Gly	Gly	His	Ile	Ile	Gln
			210			215						220			
Gly	Ile	Arg	Ser	Glu	Thr	Gly	Ala	Gln	Ile	Arg	Val	Leu	Ser	Lys	Asp
225				230					235					240	
His	Ile	Pro	Ala	Cys	Ala	Ile	Ser	Gly	Asp	Glu	Leu	Leu	Gln	Ile	Ser
			245						250				255		
Gly	Asp	Met	Val	Val	Val	Lys	Lys	Ala	Leu	Cys	Gln	Val	Ser	Ser	Arg
			260					265					270		
Leu	His	Asn	Asn	Pro	Ser	Lys	Ser	Gln	His	Leu	Leu	Ala	Ser	Ser	Leu
			275				280					285			
Thr	Gln	Pro	Tyr	Pro	Gly	Gly	Thr	His	Leu	Gly	Gly	Ser	Ser	Ala	Ala
			290			295						300			
Pro	Val	Val	Gly	Ile	Thr	Pro	Val	Ile	Pro	Pro	Tyr	Gly	Gly	Tyr	Lys
305				310						315					320
Gly	Asp	Val	Ala	Gly	Asp	Trp	Pro	Ser	Leu	Tyr	Gln	Pro	Arg	Arg	Asp
				325					330					335	
Glu	Ser	Ser	Ala	Lys	Glu	Phe									
			340												

(2) INFORMATION FOR SEQ ID NO:3326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1576443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3326:

Met	Ser	Gly	His	Arg	Asn	Ser	His	Gly	Lys	Arg	Tyr	Ser	Asp	Tyr	Thr
1				5					10					15	
Glu	Thr	Gly	Gly	Gly	Lys	Arg	Arg	Asn	Pro	Gly	Asp	Asp	Thr	Tyr	Ala
			20					25					30		
Pro	Gly	Pro	Asp	Asp	Thr	Val	Tyr	Arg	Tyr	Leu	Cys	Ala	Ser	Arg	Lys
		35					40					45			
Ile	Gly	Ser	Ile	Ile	Gly	Arg	Gly	Gly	Glu	Ile	Ala	Lys	Gln	Leu	Arg
		50				55					60				
Thr	Glu	Thr	Gln	Ala	Lys	Ile	Arg	Ile	Gly	Glu	Ser	Val	Pro	Gly	Cys
65				70					75					80	
Glu	Glu	Arg	Val	Ile	Thr	Ile	Phe	Ser	Ser	Ser	Arg	Arg	Thr	Asn	Thr
				85				90						95	
Ile	Asp	Asp	Ala	Glu	Asp	Lys	Val	Cys	Pro	Ala	Gln	Asp	Ala	Leu	Phe
			100				105						110		
Arg	Val	His	Glu	Arg	Leu	Ala	Thr	Asp	Glu	Ser	Phe	Gly	Asn	Glu	Asp
		115					120					125			
Ser	Glu	Glu	Ile	Ser	Pro	Gln	Val	Thr	Val	Arg	Leu	Leu	Val	Pro	Ser
		130				135					140				
Asp	Gln	Ile	Gly	Cys	Ile	Leu	Gly	Lys	Gly	Gly	His	Ile	Ile	Gln	Gly
145				150						155					160
Ile	Arg	Ser	Glu	Thr	Gly	Ala	Gln	Ile	Arg	Val	Leu	Ser	Lys	Asp	His
				165					170					175	
Ile	Pro	Ala	Cys	Ala	Ile	Ser	Gly	Asp	Glu	Leu	Leu	Gln	Ile	Ser	Gly
			180				185						190		
Asp	Met	Val	Val	Val	Lys	Lys	Ala	Leu	Cys	Gln	Val	Ser	Ser	Arg	Leu
		195					200					205			
His	Asn	Asn	Pro	Ser	Lys	Ser	Gln	His	Leu	Leu	Ala	Ser	Ser	Leu	Thr
		210				215					220				
Gln	Pro	Tyr	Pro	Gly	Gly	Thr	His	Leu	Gly	Gly	Ser	Ser	Ala	Ala	Pro
225				230						235				240	
Val	Val	Gly	Ile	Thr	Pro	Val	Ile	Pro	Pro	Tyr	Gly	Gly	Tyr	Lys	Gly
			245						250					255	
Asp	Val	Ala	Gly	Asp	Trp	Pro	Ser	Leu	Tyr	Gln	Pro	Arg	Arg	Asp	Glu
		260					265						270		
Ser	Ser	Ala	Lys	Glu	Phe										
			275												

(2) INFORMATION FOR SEQ ID NO:3327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1576444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3327:

taggataaatt	ctcgttgctg	ctgcaacaga	aataagagctg	gcaaaagagat	tgaaggaggtt	60
ctctttgaaag	gaaacacgggt	tggacacagta	tgctgttgcg	aaattttgctg	aaattttgaa	120
atgggttccaa	gaacctctggc	agaaaatgcc	ggacttagcg	caatggatgt	aatatcctct	180
ctttatgctg	agcatgctag	tggcaatgtg	aaagtggcca	ttgacctgga	ggaagggtgcc	240
tgcaaggagca	tcacgacctt	gaaaaatagg	gaccttttat	tcacaaaagt	ctttgcctta	300
aaatattctg	ccgatgccgc	atgcaccgtg	gcctgggttg	accagatcat	tatggcggaG	360
csggcaggag	gtccaagaag	agatgccacg	ctcgttggtg	ggatgggacg	ggactagttt	420
gactgagatt	gtctctcttg	tgatcacagt	acgcaagggt	tcagagcagg	gaacatcatg	480
tcttatttag	ggtttgggtc	tgtagaaggt	tttggtgcct	gtagtccacg	tttgggaagg	540
ttgcacggct	gtgctgggat	cgtatgggga	atttgcttgt	tctttctcgg	tgtattattg	600

cagtgcgcgat gtattatttca ttgcagggtt ctttctcttca gttcattcaca ccgactgagc 660
tcatatgagt sytacttcag ttttttttatt atagaagcaa aaatgttaca gcc

(2) INFORMATION FOR SEQ ID NO:3328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3328:

Met	Val	Pro	Arg	Thr	Leu	Ala	Glu	Asn	Ala	Gly	Leu	Ser	Ala	Met	Asp
1															
Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val	Lys	Val
Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr	Leu	Lys
Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr	Ser	Ala
Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met	Ala	Lys
Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly	Met	Asp
Glu	Asp														

(2) INFORMATION FOR SEQ ID NO:3329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3329:

Met	Asp	Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val
1															
Lys	Val	Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr
Leu	Lys	Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr
Ser	Ala	Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met
Ala	Lys	Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly
Met	Asp	Glu	Asp												

(2) INFORMATION FOR SEQ ID NO:3330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1576447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3330:

Met	Ser	Tyr	Leu	Gly	Phe	Gly	Ser	Val	Glu	Gly	Phe	Gly	Ala	Cys	Ser
1			5						10					15	
Ser	Arg	Leu	Glu	Gly	Leu	His	Gly	Cys	Ala	Gly	Ile	Val	Trp	Gly	Ile
			20						25					30	
Cys	Leu	Phe	Phe	Pro	Gly	Val	Leu	Leu	Gln	Cys	Arg	Cys	Ile	Ile	His
			35						40					45	
Ser	Arg	Val	Leu	Ser	Phe	Ser	Ser	Ser	His	Arg	Leu	Ser	Ser	Tyr	Glu
			50						55					60	
Xaa	Tyr	Phe	Ser	Phe	Phe	Ile	Ile	Glu	Ala	Lys	Met	Leu	Gln		
65						70					75				

(2) INFORMATION FOR SEQ ID NO:3331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..927

(D) OTHER INFORMATION: / Ceres Seq. ID 1576470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3331:

atttgcattct	gagttccctga	ttgttgtatt	ccagtttctt	ctgtgagttt	tgtgggagtc	60
craggaagaa	ctagaaggat	gtcgtgctgc	rgargcaact	rcrggtvcvg	cgccggctgc	120
aagtrcgga	rcggctcgcg	agggtgcaag	atgtaccg	acatggctga	rcaggtgacc	180
accactacc	agactctcat	catgggtgtw	gcacctctct	rmcgccgcgc	ccgctccgcg	240
tcocagctcg	gtttccgctt	cttgcagcgc	tcgcccgcga	gctccagaga	acttccgtca	300
acatggggaa	racacgtggt	atggrarcgc	ggcgcaagct	caagaccacc	cgagaaacca	360
gcggtgggct	gacaaggcat	acaagaagag	ccatttgggS	caatgagtg	agaaaacctt	420
tcgctgggtc	atccccatgcc	aagggcattg	ycctggagaa	gatttgtatt	gaggccaagc	480
agcccaactc	cgctatccgt	aagtgtgctc	gtgttcagct	tgtaaagaat	ggcaagaaga	540
ttgctgcctt	cgtgccaaat	gacggttgtt	tgaactacat	tgaggaaaat	gatgaggtct	600
tgattgtctg	atttggctgt	aaggggccag	ctgtgggaga	tattcctggt	gtccgggttca	660
aggtcgtaaa	ggtttccggt	gtgtctctgc	ttgccctttt	caaggagaa	aaagagaagc	720
caaggtctta	gattgtctct	gctacaaaaa	tcagcaagcg	tggagtgaa	acgggagggc	780
gttagatgat	taagaagaat	ggttgcttgc	tatgtttgca	gtgcattcgt	gcaattgtta	840
acctaaagatt	ttgttgtgtga	aaacgatttc	tttccagact	tgcttctggt	gagtgctatc	900
attccataac	aatgtacttc	ctctctt				

(2) INFORMATION FOR SEQ ID NO:3332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1576471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3332:

Met	Ser	Cys	Cys	Xaa	Asn	Xaa	Xaa	Xaa	Ala	Gly	Cys	Lys	Xaa
1				5					10				15
Gly	Xaa	Gly	Cys	Gly	Gly	Cys	Lys	Met	Tyr	Pro	Asp	Met	Ala
				20					25				30
Val	Thr	Thr	Thr	Thr	Gln	Thr	Leu	Ile	Met	Gly	Xaa	Ala	Pro
				35					40				45
Arg	Arg	Arg	Arg	Ser	Arg	Ser	Gln	Leu	Val	Phe	Arg	Phe	Leu
				50					55				60

Ser Pro Arg Ser Ser Arg Glu Leu Pro Ser Thr Trp Gly Xaa His Val
65 70 75 80
Val Trp Xaa Pro Gly Ala Ser Ser Arg Pro Thr Ala Glu Pro Ala Val
85 90 95
Gly

(2) INFORMATION FOR SEQ ID NO:3333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1576472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3333:

Met Gly Xaa Thr Arg Gly Met Xaa Xaa Gly Arg Lys Leu Lys Thr His
1 5 10 15
Arg Arg Thr Ser Gly Gly Leu Thr Arg His Thr Arg Arg Ala Ile Trp
20 25 30
Xaa Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45
Ile Xaa Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65 70 75 80
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125
Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:3334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1576473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3334:

Met Xaa Xaa Gly Arg Lys Leu Lys Thr His Arg Arg Thr Ser Gly Gly
1 5 10 15
Leu Thr Arg His Thr Arg Arg Ala Ile Trp Xaa Asn Glu Trp Lys Lys
20 25 30
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Xaa Leu Glu Lys Ile
35 40 45
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg
50 55 60
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn
65 70 75 80
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala
85 90 95
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg

100 105 110
Phe Lys Val Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys
115 120 125
Glu Lys Lys Glu Lys Pro Arg Ser
130 135

(2) INFORMATION FOR SEQ ID NO:3335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440

(D) OTHER INFORMATION: / Ceres Seq. ID 1576485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3335:

aaacccctagc	cgccgccaga	ccattcggtt	ctgcgcagcc	atcgcttctg	taattctcag	60
gcctccggaa	gaaatggcca	agtcgaagaa	ccacacggcg	cacaaccagt	cgttcaaggc	120
gcacaagaac	ggcattaaga	aaccacaagcg	ccaccgccag	acctccacca	aggggatgga	180
ccccaagtgc	ctgaggaacc	tgaggtattc	taggaaggcg	aacaaaaaga	gtggtgaggc	240
tgaagctgag	gagtaggaag	gaaagcatgg	ctttgtttcc	tctgttttta	gctcagttcc	300
acctttagga	cctgggggtt	tgctaaagat	ggGaacttaa	gtggtgtttc	tgtatgatgg	360
caaggacctt	ttgctgccga	agGttatggt	ttgaagtcca	tgctaccttt	taaagtaacg	420
attaccttgt	gcctatgttc					

(2) INFORMATION FOR SEQ ID NO:3336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1576486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3336:

Asn	Pro	Ser	Arg	Arg	Gln	Thr	Ile	Arg	Phe	Ser	Arg	Ala	Ile	Ala	Ser	
1				5				10					15			
Val	Ile	Leu	Arg	His	Pro	Glu	Glu	Met	Ala	Lys	Ser	Lys	Asn	His	Thr	
				20				25					30			
Ala	His	Asn	Gln	Ser	Phe	Lys	Ala	His	Lys	Asn	Gly	Ile	Lys	Lys	Pro	
				35				40				45				
Lys	Arg	His	Arg	Gln	Thr	Ser	Thr	Lys	Gly	Met	Asp	Pro	Lys	Phe	Leu	
				50				55			60					
Arg	Asn	Leu	Arg	Tyr	Ser	Arg	Lys	Gly	Asn	Lys	Lys	Ser	Gly	Glu	Ala	
				65				70			75			80		
Glu	Ala	Glu	Glu													

(2) INFORMATION FOR SEQ ID NO:3337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1576487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3337:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1 5 10 15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
20 25 30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys
35 40 45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..577

(D) OTHER INFORMATION: / Ceres Seq. ID 1576491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3338:

gagccgaact	caacccaact	tctctccctc	tccctcgcc	gcctgccgtt	ccgcgtttga	60
ccaactcccc	cgacccgtaa	ccctagcagc	agatcggcca	tggagagctg	ggcgacactgg	120
gtggggacaa	cgctcacctc	cgcttctctc	gcctccctcg	agcgtgtctc	ctgcatcaac	180
ctctccaccg	acgacgacga	cgacgacgag	gaccacgacg	aggccaagga	ccggcccttc	240
atcctcgccg	ccgccccacg	ccaagactcc	gccgccaaagc	ccgatccaga	ctccgcgcgc	300
gaggaccagc	acgaccagaa	ccaagacgag	ccgccMgctg	ccgcgctatg	aatcaaaacc	360
gattcccttc	ttgtactagc	tgctactgct	gttatgtcgc	caataaagt	cgtgtgtgcg	420
tgctcagtc	gtactactgc	tctgtcgtca	ctatcctagt	cctagtatat	tagtatatta	480
tacagtcttc	tctgtgaaat	ttgaatcgac	tcaaaaatca	aacccccacca	atatgagcgtt	540
gttaaatatt	gtctcccgga	atcaaccagc	gcttggtt			

(2) INFORMATION FOR SEQ ID NO:3339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1576492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3339:

Ser Arg Thr Gln Pro Asn Phe Ser Pro Ser Pro Ser Pro Ala Cys Arg	
1 5 10 15	
Ser Ala Phe Asp Gln Leu Pro Arg Thr Val Thr Leu Ala Ala Asp Arg	
20 25 30	
Pro Trp Arg Ala Gly Arg Pro Gly Trp Gly Gln Ala Ser Pro Pro Pro	
35 40 45	
Ser Ser Pro Pro Ser Ser Ala Ala Pro Ala Ser Thr Ser Pro Pro Thr	
50 55 60	
Thr Thr Thr Thr Thr Arg Thr Thr Thr Arg Pro Arg Thr Gly Pro Ser	
65 70 75 80	
Ser Ser Pro Pro Pro His Ala Thr Thr Pro Pro Pro Ser Pro Ile Gln	
85 90 95	
Thr Pro Pro Pro Arg Thr Arg Thr Thr Arg Ser Lys Ser Ser Arg Xaa	
100 105 110	
Leu Pro Pro Tyr Glu Ser Asn Pro Ile Pro Cys Leu Tyr	
115 120 125	

(2) INFORMATION FOR SEQ ID NO:3340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..83
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576493
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3340:
Met Glu Ser Trp Ala Thr Trp Val Gly Thr Ser Val Thr Ser Ala Phe
1 5 10 15
Phe Ala Ser Leu Glu Arg Cys Ser Cys Ile Asn Leu Ser Thr Asp Asp
 20 25 30
Asp Asp Asp Asp Glu Asp His Asp Glu Ala Lys Asp Arg Pro Leu Ile
 35 40 45
Leu Ala Ala Ala Pro Arg His Asp Ser Ala Lys Pro Asp Pro Asp
 50 55 60
Ser Ala Ala Glu Asp Gln Asp Asp Gln Lys Gln Glu Gln Pro Xaa Ala
65 70 75 80
Ala Ala Val

(2) INFORMATION FOR SEQ ID NO:3341:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..618
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3341:
agccgactga atcttccacc tcgcttcgcy cctccgggtc cgcgcggggc cgcataatc 60
tgtgtctggg atcgccctct cccgcggcaa atggggggcg actccgagga cgcgctcaag 120
cagctcagcc tctctcatgga gcaagtdgag gccccgctga agagatcggt tcagaaatag 180
caccagggct atcctaaaga aacactgggt cgtttcctta aggctagaga gtggaatgta 240
gcaaaaggctc ataaaaatgat tgtagaatgt ttgaattgga ggattcaaaa tgaaattgat 300
agtgtgctag agaggcctat agtcccagta gatttataca ggtaaatatcg tgattcacaa 360
cttattggcc tgtcaggata cacaaaggag ggtctcccaa tttttggcat tgggtgtgga 420
catagcacat atgacaaagc ttcggtccac tactatgtgc aatctcatat ccagattaac 480
gagtagcgtg atcgtataat tttgcctagg ctgacacaac agtttggggc gcctgttacc 540
agctgtataa aagtgtctga tatgactggt ttgaagctat cagcactaag ccaataaag 600
atgttgactT ccatatcg

(2) INFORMATION FOR SEQ ID NO:3342:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..206
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576495
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3342:
Ser Arg Leu Asn Leu Pro Pro Arg Phe Ala Pro Pro Ala Pro Arg Arg
1 5 10 15
Ala Arg Ile Ile Cys Ala Arg Asp Arg Leu Phe Pro Arg Gln Met Gly
 20 25 30
Ala Asp Ser Glu Asp Ala Val Lys Gln Leu Ser Leu Leu Met Glu Gln

(2) INFORMATION FOR SEO ID NO:3343:

(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(A) NAME/KEY: peptide
(B) LOCATION: 1..176
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3343:

(2) INFORMATION FOR SEQ ID NO:3344:

(A) LENGTH: 161 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1576497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3344:
Met Glu Gln Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His
1 5 10 15
Gln Gly Tyr Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu
20 25 30
Trp Asn Val Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp
35 40 45
Arg Ile Gln Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro
50 55 60
Val Asp Leu Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser
65 70 75 80
Gly Tyr Thr Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His
85 90 95
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile
100 105 110
Gln Ile Asn Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln
115 120 125
Gln Phe Gly Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr
130 135 140
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile
145 150 155 160
Ser

- (2) INFORMATION FOR SEQ ID NO:3345:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..768
(D) OTHER INFORMATION: / Ceres Seq. ID 1576508
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3345:
ttccttcggt attgccacag ccacaccggg ccgctctctc tctccctcgc gacaggggaga 60
gaccctttcc atccaagcta gccaaaccct agccaccgtc ggttccaatc tgccaacgtc 120
tcgtccgctg gttggttggt cggcgccatg gcctcgtccg cctacgccgc ttgggacgcc 180
gcggaggagg cggacatcga cgcctccgca tcgcaggagg agtcctatcg ccgcgccccg 240
ttcatctccc gtgacaatga ggaggagggg gaggggaggg gggaggaggga ggaggaggtc 300
gaggtgttca gcacgcgcgc tctcacgcac caggaccgcc agagtccagg ggaagaagtc 360
atcgtcatgt gctccatccc ctccacccag cctgacccca cccctccccc cgctcccgct 420
ccctcccttc cctcggacag taagagtcgc cgtccggagc ggttcaaat gaagccggg 480
aagaaggctg gcaagaggaa gaggggtctg aagaggaaag tgagaagagc caacaagatc 540
aggctctcga ctccgagccg cagcccccga ctggaccytc tcgccagggc cgtgctcatg 600
atcccaaccg ctcccttctac aatcacccgt ggtgaggata tctcagaggt tgctcgacgc 660
cgcggcatct tctagatcta ctagtgcct gtgtattttg tcgattgtag cgtagtcctc 720
tgtgtttctg ccgatcaatc catatgctat ggcctggctg gattttgt

- (2) INFORMATION FOR SEQ ID NO:3346:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1576509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3346:

```
Ser Phe Arg Ile Ala Thr Ala Thr Pro Gly Arg Leu Ser Ser Ser Leu
1      5      10      15
Gly Gln Gly Glu Thr Leu Ser Ile Gln Ala Ser Gln Thr Leu Ala Thr
20      25      30
Val Gly Ser Asn Leu Pro Thr Ser Arg Pro Leu Val Gly Gly Ser Ala
35      40      45
Ala Trp Pro Arg Pro Pro Thr Pro Leu Gly Thr Pro Arg Arg Arg Arg
50      55      60
Thr Ser Thr Pro Pro His Arg Arg Arg Ser Ser Ser Ala Ala Pro Ala
65      70      75      80
Ser Ser Pro Val Thr Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Arg
85      90      95
Arg Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg Ile Arg Thr
100      105      110
Arg Arg Val Arg Gly Lys Lys Ser Ser Ser Cys Ala Pro Ser Pro Ser
115      120      125
Pro Ser Leu Thr Pro Pro Leu Pro Xaa Leu Pro Leu Pro Pro Leu Pro
130      135      140
Arg Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn
145      150      155
```

(2) INFORMATION FOR SEQ ID NO:3347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1576510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3347:

```
Met Ala Ser Ser Ala Tyr Ala Ala Trp Asp Ala Ala Glu Glu Ala Asp
1      5      10      15
Ile Asp Ala Ser Ala Ser Gln Glu Glu Leu Ile Gly Arg Ala Arg Phe
20      25      30
Ile Ser Arg Asp Asn Glu Glu Glu Gly Glu Gly Glu Glu Glu
35      40      45
Glu Glu Val Glu Val Phe Ser Thr Pro Pro Leu Thr His Gln Asp Pro
50      55      60
Gln Ser Gln Gly Glu Glu Val Ile Val Met Cys Ser Ile Pro Phe Thr
65      70      75      80
Gln Pro Asp Pro Thr Pro Pro Xaa Ala Pro Ala Pro Ser Pro Pro Ser
85      90      95
Asp Ser Lys Ser Arg Arg Pro Glu Arg Val Lys Leu Lys Pro Arg Lys
100      105      110
Lys Val Cys Lys Arg Lys Arg Val Cys Lys Arg Lys Val Arg Arg Ala
115      120      125
Asn Lys Ile Arg Ser Pro Thr Pro Ser Arg Ser Pro Glu Leu Asp Xaa
130      135      140
Leu Ala Arg Ala Val Leu Met Ile Pro Thr Ala Pro Ser Thr Ile Thr
145      150      155      160
Gly Gly Glu Asp Ile Leu Glu Val Ala Arg Ser Arg Gly Ile Phe
165      170      175
```

(2) INFORMATION FOR SEQ ID NO:3348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1576511
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3348:
Met Cys Ser Ile Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Xaa Ala
1 5 10 15
Pro Ala Pro Ser Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg
20 25 30
Val Lys Leu Lys Pro Arg Lys Lys Val Cys Lys Arg Lys Arg Val Cys
35 40 45
Lys Arg Lys Val Arg Arg Ala Asn Lys Ile Arg Ser Pro Thr Pro Ser
50 55 60
Arg Ser Pro Glu Leu Asp Xaa Leu Ala Arg Ala Val Leu Met Ile Pro
65 70 75 80
Thr Ala Pro Ser Thr Ile Thr Gly Gly Glu Asp Ile Leu Glu Val Ala
85 90 95
Arg Ser Arg Gly Ile Phe
100

(2) INFORMATION FOR SEQ ID NO:3349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..663
(D) OTHER INFORMATION: / Ceres Seq. ID 1576523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3349:
agggtgtgtct agtctctagt ctagtctaggc actactctag ctcccaagtg gccaaagtata 60
ctcgccagag tacgtagagt gtaGbtgagc gtcgtcgag gatggcggtGg acytcccgc 120
gcatggctgc gtccgcgcctc gtcttctctg tgaatgctgt cgccgcctca gagatggggga 180
cgacgaggkt ggcggaggcg aggcactgca cgtcgagag caaccggttc gtccggcgctt 240
gcagtagcaa gcgaactcgc gagaacgtct cgaggacgga gggtttcccg tggggcgagt 300
gcaggtggca cggcatagag cgcaagtgc actgcaagcg gatctgctag taattaacta 360
gcccgtctggc cagcgcatgc atgcacgacg accgacctac ctgctgtggg tccgttttgcg 420
ttgtttttt gtccctttggg ccttctgtgt ggcgcgagtc ttgcgtacgt gcgtgtgcgt 480
tgtgttttt agttactctc aattagtcac agcagacgtg cgtgggtgcg agcgtgtgtc 540
ctgtgtgcat gatgaaccgg cttcacgtgc tgtgtgttta cagtttctga tgtgttttag 600
ctaactcgca ataataaata taaggccccc gtcttcacgc agttgcgtac tgggtgctta 660
cgt

(2) INFORMATION FOR SEQ ID NO:3350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1576524
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3350:

Met Ala Trp Xaa Ser Arg Arg Met Val Ala Ser Ala Leu Val Phe Leu
1 5 10 15
Leu Met Leu Leu Ala Ala Ser Glu Met Gly Thr Thr Arg Xaa Ala Glu
20 25 30
Ala Arg His Cys Thr Ser Gln Ser His Arg Phe Val Gly Ala Cys Met
35 40 45
Ser Lys Ser Asn Cys Glu Asn Val Cys Arg Thr Glu Gly Phe Pro Trp
50 55 60
Gly Glu Cys Arg Trp His Gly Ile Glu Arg Lys Cys His Cys Lys Arg
65 70 75 80
Ile Cys

(2) INFORMATION FOR SEQ ID NO:3351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3351:

Met Val Ala Ser Ala Leu Val Phe Leu Leu Met Leu Leu Ala Ala Ser
1 5 10 15
Glu Met Gly Thr Thr Arg Xaa Ala Glu Ala Arg His Cys Thr Ser Gln
20 25 30
Ser His Arg Phe Val Gly Ala Cys Met Ser Lys Ser Asn Cys Glu Asn
35 40 45
Val Cys Arg Thr Glu Gly Phe Pro Trp Gly Glu Cys Arg Trp His Gly
50 55 60
Ile Glu Arg Lys Cys His Cys Lys Arg Ile Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:3352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3352:

Met His Ala Arg Arg Pro Thr Tyr Leu Leu Leu Val Arg Leu Arg Leu
1 5 10 15
Phe Leu Val Leu Trp Ala Leu Leu Trp Arg Ala Val Leu Arg Thr Cys
20 25 30
Val Cys Val Cys Leu Phe Ser Tyr Ser Gln Leu Val Ile Ala Asp Val
35 40 45
Arg Gly Cys Glu Arg Val Ser Arg Cys Ile Asp Glu Pro Ala Ser Arg
50 55 60
Ala Val Val Leu Gln Phe Leu Met Cys Phe Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:3353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..906
(D) OTHER INFORMATION: / Ceres Seq. ID 1576535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3353:

ctcgctcaaaa	accctagacc	tcgcgcgcgc	gcgcgcgcgc	ccagcgctgc	arctcctcgc	60
ctgcgcgcgc	ctgcgcgcgc	aacgcccacca	tgaagtccaa	catcgcggaac	ccgtctaccg	120
gggtgccagaa	gaagctggaa	atcgatgacg	accagaaact	acgtgccttt	tatgaccgaa	180
gatctccacg	gaggtcagtg	gtgatgctct	gggtgaggag	tttaagggtt	atgtcttcaa	240
gatcatgggt	ggatgtgagc	caagacctat	ctgttatcaa	cttggttaatt	gttaagaagg	300
gtgagaacga	tctgcctggg	ttaactgaca	ctgagaagcc	aaggatgagg	gggtcccaaaa	360
ggggctccaa	gacaggaag	ctgttcaatc	ttgcaaaagg	tgacgacgtg	cgcaagtacg	420
tgaacacgta	ccgcagggaca	ttcactacca	agaatggcaa	gaaggtgagc	aaggcacccta	480
agatccagcg	gcttgtgacc	cccttgacc	tccagaggaa	gcgtgctaga	attgctgaca	540
agaagaagag	gatcgctaag	aagaagcttg	aggctgctga	gtaccagaa	cttcttgccc	600
agaggtcgaa	agaacagagg	gaccgcgcga	gtgagagctt	ggccaagagg	aggtctaaag	660
tttctgcgc	cgccaaggct	ctgtgtgcca	ccctgccta	agaatgatca	gtgctttgag	720
atgttttcaa	ggcctatttt	gttacagctt	ataagtacct	tatgctgccc	tggctgtggt	780
gcatacagtg	accctcccta	cttagactta	tgagtaattg	ttgcaatttt	gtatggacat	840
ggatactggct	tgctcggtt	ttttgagtac	cgaggtttg	atatgttggt	ttattctgtg	900

(2) INFORMATION FOR SEQ ID NO:3354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..203
(D) OTHER INFORMATION: / Ceres Seq. ID 1576536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3354:

Met	Lys	Phe	Asn	Ile	Ala	Asn	Pro	Ser	Thr	Gly	Cys	Gln	Lys	Lys	Leu
1			5						10					15	
Glu	Ile	Asp	Asp	Asp	Gln	Lys	Leu	Arg	Ala	Phe	Tyr	Asp	Arg	Arg	Ser
			20					25					30		
Pro	Arg	Arg	Ser	Val	Val	Met	Leu	Trp	Val	Arg	Ser	Leu	Arg	Val	Met
			35				40					45			
Ser	Ser	Arg	Ser	Trp	Val	Asp	Val	Ser	Gln	Asp	Leu	Ser	Val	Ile	Asn
			50				55				60				
Leu	Val	Ile	Val	Lys	Lys	Gly	Glu	Asn	Asp	Leu	Pro	Gly	Leu	Thr	Asp
			65			70			75					80	
Thr	Glu	Lys	Pro	Arg	Met	Arg	Gly	Pro	Lys	Arg	Ala	Ser	Lys	Ile	Arg
					85				90					95	
Lys	Leu	Phe	Asn	Leu	Ala	Lys	Asp	Asp	Val	Arg	Lys	Tyr	Val	Asn	
			100					105					110		
Thr	Thr	Arg	Arg	Thr	Phe	Thr	Thr	Lys	Asn	Gly	Lys	Lys	Val	Ser	Lys
					115			120				125			
Ala	Pro	Lys	Ile	Gln	Arg	Leu	Val	Thr	Pro	Leu	Thr	Leu	Gln	Arg	Lys
					130			135				140			
Arg	Ala	Arg	Ile	Ala	Asp	Lys	Lys	Lys	Arg	Ile	Ala	Lys	Lys	Lys	Ser
					145			150			155				160
Glu	Ala	Ala	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Gln	Arg	Leu	Lys	Glu	Gln
					165			170						175	
Arg	Asp	Arg	Arg	Ser	Glu	Ser	Leu	Ala	Lys	Arg	Arg	Ser	Lys	Leu	Ser
					180			185					190		
Ala	Ala	Ala	Lys	Ala	Ser	Ala	Ala	Thr	Ser	Ala					
					195			200							

(2) INFORMATION FOR SEQ ID NO:3355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1576537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3355:

Met	Leu	Trp	Val	Arg	Ser	Leu	Arg	Val	Met	Ser	Ser	Arg	Ser	Trp	Val
1															
			5						10					15	
Asp	Val	Ser	Gln	Asp	Leu	Ser	Val	Ile	Asn	Leu	Val	Ile	Val	Lys	Lys
			20					25						30	
Gly	Glu	Asn	Asp	Leu	Pro	Gly	Leu	Thr	Asp	Thr	Glu	Lys	Pro	Arg	Met
			35				40					45			
Arg	Gly	Pro	Lys	Arg	Ala	Ser	Lys	Ile	Arg	Lys	Leu	Phe	Asn	Leu	Ala
			50			55				60					
Lys	Asp	Asp	Asp	Val	Arg	Lys	Tyr	Val	Asn	Thr	Tyr	Arg	Arg	Thr	Phe
65					70				75					80	
Thr	Thr	Lys	Asn	Gly	Lys	Lys	Val	Ser	Lys	Ala	Pro	Lys	Ile	Gln	Arg
			85					90						95	
Leu	Val	Thr	Pro	Leu	Thr	Leu	Gln	Arg	Lys	Arg	Ala	Arg	Ile	Ala	Asp
			100					105					110		
Lys	Lys	Lys	Arg	Ile	Ala	Lys	Lys	Ser	Glu	Ala	Ala	Glu	Tyr	Gln	
			115				120					125			
Lys	Leu	Leu	Ala	Gln	Arg	Leu	Lys	Glu	Gln	Arg	Asp	Arg	Arg	Ser	Glu
			130			135					140				
Ser	Leu	Ala	Lys	Arg	Arg	Ser	Lys	Leu	Ser	Ala	Ala	Ala	Lys	Ala	Ser
145				150					155						160
Ala	Ala	Thr	Ser	Ala											
			165												

(2) INFORMATION FOR SEQ ID NO:3356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1576538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3356:

Met	Ser	Ser	Arg	Ser	Trp	Val	Asp	Val	Ser	Gln	Asp	Leu	Ser	Val	Ile
1															
				5					10					15	
Asn	Leu	Val	Ile	Val	Lys	Lys	Gly	Glu	Asn	Asp	Leu	Pro	Gly	Leu	Thr
			20					25						30	
Asp	Thr	Glu	Lys	Pro	Arg	Met	Arg	Gly	Pro	Lys	Arg	Ala	Ser	Lys	Ile
			35				40					45			
Arg	Lys	Leu	Phe	Asn	Leu	Ala	Lys	Asp	Asp	Asp	Val	Arg	Lys	Tyr	Val
			50			55					60				
Asn	Thr	Tyr	Arg	Arg	Thr	Phe	Thr	Thr	Lys	Asn	Gly	Lys	Lys	Val	Ser
65					70				75					80	
Lys	Ala	Pro	Lys	Ile	Gln	Arg	Leu	Val	Thr	Pro	Leu	Thr	Leu	Gln	Arg
			85						90					95	
Lys	Arg	Ala	Arg	Ile	Ala	Asp	Lys	Lys	Lys	Arg	Ile	Ala	Lys	Lys	Lys
			100					105					110		
Ser	Glu	Ala	Ala	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Gln	Arg	Leu	Lys	Glu

115 120 125
Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Arg Arg Ser Lys Leu
130 135 140
Ser Ala Ala Ala Lys Ala Ser Ala Ala Thr Ser Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3357:

agtgggtcgt	ccactgtgac	gtgaagccgg	agaacatact	tctgaccocgg	gatttcgatg	60
ccaagatagc	agactttggg	ctggccaagc	tcgcgaacaa	gggagcacta	gtctgaactt	120
caccccatatg	agaggcacca	tgggctacat	ggcgccggaa	tggcgctcca	actcgccgat	180
carcgcgaag	gttgatgtgt	acarcctacgg	ggctcrtggtt	ctrgagatcg	tractgggat	240
carggcttcg	artggcatag	tgctagatga	gagRgcagat	agactttcgg	cagtttgtac	300
aggaggctaa	gcatactctg	tctactggga	gtgtcagtga	tatcgttgat	gatagattgc	360
aaggccattt	tcaagcggac	caagcgggtg	cgatggtcaa	aatagccttt	tcattgcctcg	420
aggaagacg	caagagggcca	acgatggatg	agattgtcaa	gggtctcatg	tcgtgtgggtg	480
atgacgatga	taccattcct	gcttattcat	attgacttgc	aacagatgtg	aaggtttccc	540
aaaagaaaaa	agatgcgaag	atttgagagg	cgagggcaag	tgtacctttg	atcaaatgata	600
gaagctgaac	tgaactgact	gatgaaatat	attcgaaaagc	gtgcctcaat	tgatattttg	660
tgtagagtat	gttggggtag	ctccatatct	ggtagattaa	aattgagtaa	tggtgttttg	720
ctctatttct	aaggggagtg	tcttgcccta	taagtggaat	actataatat	tctctccggtt	780

cc

(2) INFORMATION FOR SEQ ID NO:3358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3358:

Met	Arg	Gly	Thr	Met	Gly	Tyr	Met	Ala	Pro	Glu	Trp	Ala	Leu	Asn	Ser
1				5				10					15		
Pro	Ile	Xaa	Ala	Lys	Val	Asp	Val	Tyr	Xaa	Tyr	Gly	Val	Xaa	Xaa	Xaa
			20					25					30		
Glu	Ile	Xaa	Thr	Gly	Ile	Xaa	Ala	Ser	Xaa	Gly	Ile	Val	Leu	Asp	Glu
			35					40					45		
Xaa	Ala	Asp	Arg	Leu	Ser	Ala	Val	Cys	Thr	Gly	Gly				
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:3359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1576545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3359:

Met Gly Tyr Met Ala Pro Glu Trp Ala Leu Asn Ser Pro Ile Xaa Ala
1 5 10 15
Lys Val Asp Val Tyr Xaa Tyr Gly Val Xaa Xaa Glu Ile Xaa Thr
20 25 30
Gly Ile Xaa Ala Ser Xaa Gly Ile Val Leu Asp Glu Xaa Ala Asp Arg
35 40 45
Leu Ser Ala Val Cys Thr Gly Gly
50 55

(2) INFORMATION FOR SEQ ID NO:3360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1576546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3360:

Met Arg Xaa Gln Ile Asp Phe Arg Gln Phe Val Gln Ala Lys His
1 5 10 15
Ile Leu Ser Thr Gly Ser Val Ser Asp Ile Val Asp Asp Arg Leu Gln
20 25 30
Gly His Phe His Ala Asp Gln Ala Val Ala Met Val Lys Ile Ala Phe
35 40 45
Ser Cys Leu Glu Glu Arg Arg Lys Arg Pro Thr Met Asp Glu Ile Val
50 55 60
Lys Val Leu Met Ser Cys Gly Asp Asp Asp Asp Tyr His Pro Ala Tyr
65 70 75 80
Ser Tyr

(2) INFORMATION FOR SEQ ID NO:3361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..746

(D) OTHER INFORMATION: / Ceres Seq. ID 1576564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3361:

gccgtgtgca tagcagcaaa tagtggctcg cctgttggtg ctctatatcg tcccttccag 60
tgtaccgctc ctccagccca ttatacatca tacttgctcc agataagacc aagagcatca 120
tggccaacgc cttgcctctc atcgtcgccg tggctgcgcg cgccgggtgc gcggcgctgg 180
cttcggccac gtgctacacc gtccggcact cgcagggtcg gacgaccacc ggcgtcgact 240
acacgagctg ggccagcccg aacactttcg tcgtcggaga cacactagtg ttcaactacg 300
tgagcaagtc gcacacggtg acggaggtga gcaaggcccg ctacgacgcc tgctccggcg 360
ccaacgcgct cagcgacgac gacacgggct ccaccaccat cagcgtccag accccgggca 420
cgcaactatt catctgcaac gtcccgggcc actgcgccag cgcatgaag ctacggtgct 480
ccgtctccgc ctgcgcctcg ggcaaggccc ctccaccagg agccctgcag gttccggcga 540
tggcatccgt cgtcgcgcgg ccgcccggcg tgccatcaag tgcacgcaga ctacgttctt ggccggtgat 600
cacggccggg tgcgtctcagg ggagagacag tgcacgcaga ctacgttctt ggccggtgat 660
agtttcccg tggcgatgtg tcggcgccga gttcatgtac gtatgtatgt gtgatgtgta 720
ctctcggtg gccaatgctt ttcttg

(2) INFORMATION FOR SEQ ID NO:3362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1576565
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3362:
Ala Val Cys Ile Ala Ala Asn Ser Gly Arg Pro Val Gly Thr Leu Tyr
1 5 10 15
Arg Pro Phe Gln Cys Thr Arg Pro Pro Ala His Tyr Thr Ser Tyr Leu
20 25 30
Leu Gln Ile Arg Pro Arg Ala Ser Trp Pro Thr Pro Cys Leu Ser Ser
35 40 45
Ser Arg Trp Ser Pro Pro Pro Gly Ala Arg Arg Trp Leu Arg Pro Arg
50 55 60
Arg Thr Pro Ser Ala Thr Arg Arg Ala Gly Arg Pro Pro Ala Ser Thr
65 70 75 80
Thr Ala Ala Gly Pro Ala Ala Thr Leu Ser Ser Ser Glu Thr His
85 90 95
(2) INFORMATION FOR SEQ ID NO:3363:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1576566
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3363:
Met Ala Asn Ala Leu Pro Leu Ile Val Ala Leu Val Ala Ala Ala Gly
1 5 10 15
Cys Ala Ala Leu Ala Ser Ala Thr Ser Tyr Thr Val Gly Asp Ser Gln
20 25 30
Gly Trp Thr Thr Thr Gly Val Asp Tyr Ser Ser Trp Ala Ser Arg Asn
35 40 45
Thr Phe Val Val Gly Asp Thr Leu Val Phe Asn Tyr Val Ser Lys Ala
50 55 60
His Thr Val Thr Glu Val Ser Lys Ala Gly Tyr Asp Ala Cys Ser Gly
65 70 75 80
Ala Asn Ala Leu Ser Asp Asp Asp Thr Gly Ser Thr Thr Ile Thr Leu
85 90 95
Gln Thr Pro Gly Thr His Tyr Phe Ile Cys Asn Val Pro Gly His Cys
100 105 110
Ala Ser Gly Met Lys Leu Ala Val Ala Val Ser Ala Ser Pro Ser Gly
115 120 125
Thr Ala Pro Ser Thr Gly Ala Leu Gln Val Pro Ala Met Ala Ser Val
130 135 140
Val Ala Arg Pro Arg Ala Leu Pro Ser Ser Ser Arg Ser Ser Asp Gly
145 150 155 160
Ala Arg Pro Gly Arg Leu Arg Gly Glu Thr Val His Ala Asp Tyr Val
165 170 175
Leu Gly Gly

(2) INFORMATION FOR SEQ ID NO:3364:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..782
(D) OTHER INFORMATION: / Ceres Seq. ID 1576575
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3364:
actcgccccc caaccttccc gtccccgatg gcgatcatgg cggccaccgc cactgcccgtg 60
gccttccccct ccagctccac ctgcgccagt cccctccaac ccagccccgc ctctctccct 120
cccgctccca cgcccgctcg ctgccatctc ctccccaagc cgccggcggtg gtgcgcgcgc 180
ctccacatcg agcgtcgggt ggccgtcggc agcgacgtgt cctcgtccca tgacgtggct 240
gcmgaggagg ccgctgtctg gtccaaggto gggaaagcscg tgcgcgtcMa cggtgccogt 300
ccgctccac caggttgcca agcgcccggt cctggacctg cgcggcatgg agggcgctgt 360
caagcagtac atcgcggttt ggaaggggaa gcgcctcacg gccaatctcc ccttcaaggt 420
ggagttcgag ctcaagctgg acggccatga caagccggtc cggttcacca cccaactccg 480
cgagcaagag ttogagatcc tcggggagga atagagctct ggactagaga ataacgcgct 540
ctcatcgccg gctgtggcat ctgtatacta ttgtgtctgc gctaaagaag aacgtggctg 600
agggtcgggg gagaatagga gattgcaact ttgctagtaa gtctcgtttt gtttgcctat 660
ttgcggtgcg ctctccccct ctccaccctt taacattgaa attttcatat gtgaggattg 720
aggaattggt cgattgttga tacttatgat ccaaagtaat taaactgagg aatctgttca 780
gc

(2) INFORMATION FOR SEQ ID NO:3365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1576576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3365:

Thr Arg Pro Pro Thr Phe Pro Ser Pro Met Ala Ile Met Ala Thr
1 5 10 15
Ala Thr Ala Val Ala Ser Pro Ser Ser Ser Thr Ser Pro Gly Pro Leu
20 25 30
Gln Pro Ser Pro Arg Phe Leu Pro Pro Val Ser Thr Pro Ala Arg Cys
35 40 45
His Leu Leu Pro Lys Pro Arg Arg Trp Cys Ala Arg Leu His Ile Glu
50 55 60
Arg Arg Val Ala Val Gly Ser Asp Val Ser Ser His Asp Val Ala
65 70 75 80
Xaa Glu Glu Ala Ala Ala Ala Ser Lys Val Gly Lys Xaa Val Arg Val
85 90 95
Xaa Gly Ala Arg Pro Arg Pro Pro Arg Cys Gln Gly Ala Arg Pro Gly
100 105 110
Pro Ala Arg His Gly Gly Arg Arg Gln Ala Val His Arg Arg Leu Glu
115 120 125
Gly Glu Ala His His Gly Gln Ser Pro Leu Gln Gly Gly Val Arg Ala
130 135 140
Gln Ala Gly Arg Pro
145

(2) INFORMATION FOR SEQ ID NO:3366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1576577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3366:

Leu	Ala	His	Gln	Pro	Ser	Arg	Pro	Arg	Trp	Arg	Ser	Trp	Arg	Pro	Pro
1			5					10					15		
Pro	Leu	Pro	Trp	Leu	Pro	Pro	Pro	Ala	Pro	Pro	Arg	Gln	Val	Pro	Ser
			20					25					30		
Asn	Pro	Ala	Pro	Ala	Ser	Ser	Leu	Pro	Ser	Pro	Arg	Pro	Leu	Ala	Ala
			35				40					45			
Ile	Ser	Ser	Pro	Ser	Arg	Gly	Gly	Gly	Ala	Arg	Ala	Ser	Thr	Ser	Ser
			50				55					60			
Val	Gly	Trp	Pro	Ser	Ala	Ala	Thr	Cys	Pro	Arg	Pro	Met	Thr	Trp	Leu
			65			70			75					80	
Xaa	Arg	Arg	Pro	Leu	Leu	Arg	Pro	Arg	Ser	Gly	Ser	Xaa	Cys	Ala	Xaa
						85			90					95	
Thr	Val	Pro	Val	Arg	Val	His	His	Val	Ala	Lys	Ala	Pro	Gly	Leu	Asp
						100			105				110		
Leu	Arg	Gly	Met	Glu	Gly	Val	Val	Lys	Gln	Tyr	Ile	Gly	Val	Trp	Lys
			115				120					125			
Gly	Lys	Arg	Ile	Thr	Ala	Asn	Leu	Pro	Phe	Lys	Val	Glu	Phe	Glu	Leu
			130				135					140			
Lys	Leu	Asp	Gly	His	Asp	Lys	Pro	Val	Arg	Phe	Ile	Thr	His	Leu	Arg
			145			150				155					160
Glu	Gln	Glu	Phe	Glu	Ile	Leu	Gly	Glu	Glu						
						165			170						

(2) INFORMATION FOR SEQ ID NO:3367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1576578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3367:

Met	Ala	Ile	Met	Ala	Ala	Thr	Ala	Thr	Ala	Val	Ala	Ser	Pro	Ser	Ser
1			5					10						15	
Ser	Thr	Ser	Pro	Gly	Pro	Leu	Gln	Pro	Ser	Pro	Arg	Phe	Leu	Pro	Pro
			20					25					30		
Val	Ser	Thr	Pro	Ala	Arg	Cys	His	Leu	Leu	Pro	Lys	Pro	Arg	Arg	Trp
			35				40					45			
Cys	Ala	Arg	Leu	His	Ile	Glu	Arg	Arg	Val	Ala	Val	Gly	Ser	Asp	Val
			50				55					60			
Ser	Ser	Ser	His	Asp	Val	Ala	Xaa	Glu	Glu	Ala	Ala	Ala	Ser	Lys	
			65			70			75					80	
Val	Gly	Lys	Xaa	Val	Arg	Val	Xaa	Gly	Ala	Arg	Pro	Arg	Pro	Pro	Arg
						85			90					95	
Cys	Gln	Gly	Ala	Arg	Pro	Gly	Pro	Ala	Arg	His	Gly	Gly	Arg	Arg	Gln
			100					105					110		
Ala	Val	His	Arg	Arg	Leu	Glu	Gly	Glu	Ala	His	His	Gly	Gln	Ser	Pro
			115				120					125			
Leu	Gln	Gly	Gly	Val	Arg	Ala	Gln	Ala	Gly	Arg	Pro				
			130				135				140				

(2) INFORMATION FOR SEQ ID NO:3368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..810
(D) OTHER INFORMATION: / Ceres Seq. ID 1576582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3368:

acaggcaagc	atctggccac	atgtgcactc	acacgactca	gggcgagagg	acagcagggc	60
acaataaacc	ttccactttg	gtccatagga	gcgcatagca	cagcacaagg	agaggccgag	120
aagcgcttta	gcgctagccg	tagcgataag	agtgagctag	ctgggtgcaca	ccggcatggc	180
ggccacggcg	tactccgtgg	cgctccctcg	cgccgcgcgc	ctccccccgc	ctccgcgcctc	240
cgccctctct	cctcgccgcr	sgtctgccag	Cttcgcttcc	aagatgcacc	gaggctctcc	300
ctgctccgtg	cgaaggcccg	ttccgaggac	acatcgccCt	ccggcgacga	gttgatcgag	360
gacctcaaa	cgaagtggga	cgccgcttag	gacaagccca	ccgtctcttt	gtacggcgcc	420
ggcgcCgtg	tcgcccctatg	gctgacgtcc	gtggtcgtag	gcgccatcaa	cgccgtgccg	480
ctgctcccca	agatccttga	gctcgttggg	ctcggtctaca	ccggctggtt	cgtgtaccgc	540
tacctttctc	ttaaggaaag	caggaaagag	ttggccgcgc	acattgagac	cttgaagaaa	600
aaaatagctg	gaacagaata	aacgctcatg	gaaagtttta	gagcgctcct	tcttcttttg	660
aaagagatct	attcgatcgg	agaaccaata	tgcaactact	tgagtactat	tattgcccat	720
gtattgtgtg	ctgtatatct	tctgtataca	aaggaaaggtt	cgtttgttat	gtacgtagta	780
gcattgtagt	ttaaatgtat	cgtattacct				

(2) INFORMATION FOR SEQ ID NO:3369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..206
(D) OTHER INFORMATION: / Ceres Seq. ID 1576583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3369:

Thr	Gly	Lys	His	Leu	Ala	Thr	Cys	Ala	Leu	Thr	Arg	Leu	Arg	Ala	Arg
1				5					10				15		
Gly	Gln	Gln	Gly	Thr	Ile	Thr	Val	Pro	Leu	Trp	Ser	Ile	Gly	Ala	His
				20				25					30		
Ser	Thr	Ala	Gln	Gly	Glu	Ala	Glu	Lys	Arg	Phe	Ser	Arg	Ser	Arg	Ser
				35			40					45			
Asp	Lys	Ser	Glu	Leu	Ala	Gly	Ala	His	Arg	His	Gly	Gly	His	Gly	Val
				50			55				60				
Leu	Arg	Gly	Ala	Pro	Arg	Arg	Arg	Ala	Pro	Pro	Arg	Arg	Ser	Ala	Leu
				65			70			75			80		
Arg	Pro	Pro	Pro	Ser	Ala	Xaa	Val	Cys	Gln	Leu	Arg	Phe	Gln	Asp	Ala
				85			90						95		
Pro	Arg	Leu	Ser	Leu	Leu	Arg	Ala	Lys	Ala	Ala	Ser	Glu	Asp	Thr	Ser
				100			105					110			
Ala	Ser	Gly	Asp	Glu	Leu	Ile	Glu	Asp	Leu	Lys	Ala	Lys	Trp	Asp	Ala
				115			120					125			
Val	Glu	Asp	Lys	Pro	Thr	Val	Leu	Leu	Tyr	Gly	Gly	Gly	Ala	Val	Val
				130			135				140				
Ala	Leu	Trp	Leu	Thr	Ser	Val	Val	Val	Gly	Ala	Ile	Asn	Ala	Val	Pro
				145			150			155			160		
Leu	Leu	Pro	Lys	Ile	Leu	Glu	Leu	Val	Gly	Leu	Gly	Tyr	Thr	Gly	Trp
				165			170					175			
Phe	Val	Tyr	Arg	Tyr	Leu	Leu	Phe	Lys	Glu	Ser	Arg	Lys	Glu	Leu	Ala
				180			185					190			
Ala	Asp	Ile	Glu	Thr	Leu	Lys	Lys	Lys	Ile	Ala	Gly	Thr	Glu		
				195			200				205				

(2) INFORMATION FOR SEQ ID NO:3370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3370:

aactcagatt	cagtacaagc	tcaagccagg	cacacagcaa	gacatcgacc	atggctgcct	60
accaacaagc	tcccgcctctc	ctgtgcgcct	gcctgatgct	cgctctcatg	gcggcgccgg	120
catccgcggc	ccgcgtagac	gtggaagaca	tgctgatgat	ggaccggttc	cgccgctggc	180
aagccacgta	caaccgctcg	tacctgaccg	ccgcggagyg	Tctgcgcggc	ttcgaggtgt	240
accgccagaa	catggagctc	atcgaggcca	cgaaccgcgc	cgccgagctc	tcgtaccagc	300
tcggcgagac	cccgttcacc	gacctcacca	gcgaggagtt	cctcgccaca	cacaccatgt	360
ccacgcgcct	gcctgcgtcc	gaggccgctc	ggcgccacgc	ggagctcatc	acgacgcacg	420
caggccccgt	cagcgacgGc	ggtcgcCagt	ggaaccgcgc	g		

(2) INFORMATION FOR SEQ ID NO:3371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3371:

Thr	Gln	Ile	Gln	Tyr	Lys	Leu	Lys	Pro	Gly	Thr	Gln	Gln	Asp	Ile	Asp	
1				5				10					15			
His	Gly	Cys	Leu	Pro	Thr	Ser	Ser	Arg	Ser	Pro	Val	Arg	Leu	Pro	Asp	
			20					25					30			
Ala	Arg	Ala	His	Gly	Gly	Arg	Gly	Ile	Arg	Arg	Pro	Arg	Arg	Arg	Gly	
			35				40					45				
Arg	His	Ala	Asp	Asp	Gly	Pro	Val	Pro	Arg	Val	Ala	Ser	His	Val	Gln	
			50			55					60					
Pro	Leu	Val	Pro	Asp	Arg	Arg	Gly	Xaa	Ser	Ala	Pro	Val	Arg	Gly	Val	
			65			70				75				80		
Pro	Pro	Glu	His	Gly	Ala	His	Arg	Gly	His	Glu	Pro	Pro	Arg	Arg	Ala	
			85					90					95			
Leu	Val	Pro	Ala	Arg	Arg	Asp	Pro	Val	His	Arg	Pro	His	Gln	Arg	Gly	
			100				105						110			
Val	Pro	Arg	His	Thr	His	His	Val	His	Ala	Pro	Ala	Cys	Val	Arg	Gly	
			115			120						125				
Arg	Ser	Ala	Ala	Pro	Gly	Ala	His	His	Asp	Ala	Arg	Arg	Pro	Arg	Gln	
			130			135					140					
Arg	Arg	Arg	Ser	Pro	Val	Glu	Pro	Ala								
			145			150										

(2) INFORMATION FOR SEQ ID NO:3372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres, Seq. ID 1576594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3372:

Leu Arg Phe Ser Thr Ser Ser Ser Gln Ala His Ser Lys Thr Ser Thr
1 5 10 15
Met Ala Ala Tyr Gln Gln Ala Pro Ala Leu Leu Cys Ala Cys Leu Met
20 25 30
Leu Val Leu Met Met Ala Gly Ala Ala Ser Gly Gly Arg Val Asp Val Glu
35 40 45
Asp Met Leu Met Met Asp Arg Phe Arg Ala Trp Gln Ala Thr Tyr Asn
50 55 60
Arg Ser Tyr Leu Thr Ala Ala Glu Xaa Leu Arg Arg Phe Glu Val Tyr
65 70 75 80
Arg Gln Asn Met Glu Leu Ile Glu Ala Thr Asn Arg Arg Ala Glu Leu
85 90 95
Ser Tyr Gln Leu Gly Glu Thr Pro Phe Thr Asp Leu Thr Ser Glu Glu
100 105 110
Phe Leu Ala Thr His Thr Met Ser Thr Arg Leu His Ala Ser Glu Ala
115 120 125
Ala Arg Arg His Arg Glu Leu Ile Thr Thr His Ala Gly Pro Val Ser
130 135 140
Asp Gly Gly Arg Gln Trp Asn Arg Arg
145 150

(2) INFORMATION FOR SEQ ID NO:3373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1576595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3373:

Met Ala Ala Tyr Gln Gln Ala Pro Ala Leu Leu Cys Ala Cys Leu Met
1 5 10 15
Leu Val Leu Met Met Ala Gly Ala Ala Ser Gly Gly Arg Val Asp Val Glu
20 25 30
Asp Met Leu Met Met Asp Arg Phe Arg Ala Trp Gln Ala Thr Tyr Asn
35 40 45
Arg Ser Tyr Leu Thr Ala Ala Glu Xaa Leu Arg Arg Phe Glu Val Tyr
50 55 60
Arg Gln Asn Met Glu Leu Ile Glu Ala Thr Asn Arg Arg Ala Glu Leu
65 70 75 80
Ser Tyr Gln Leu Gly Glu Thr Pro Phe Thr Asp Leu Thr Ser Glu Glu
85 90 95
Phe Leu Ala Thr His Thr Met Ser Thr Arg Leu His Ala Ser Glu Ala
100 105 110
Ala Arg Arg His Arg Glu Leu Ile Thr Thr His Ala Gly Pro Val Ser
115 120 125
Asp Gly Gly Arg Gln Trp Asn Arg Arg
130 135

(2) INFORMATION FOR SEQ ID NO:3374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..677

(D) OTHER INFORMATION: / Ceres Seq. ID 1576618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3374:

aattgcgatt	gcgagtcctc	caaacatgg	cgctcgccct	ggcctctcca	atggcgcttc	60
ttctcttcca	ctccgggagg	atctcgggcg	cgtctatcgg	aggcgtcggc	cgcaactcgca	120
ggcgcgcccc	ggtaggggta	tcgcctctcg	cgttcctcgg	gagctccttc	gtctcgtcct	180
ctccacagtc	gtccgcctcc	gcctcgcctc	ccvccgcttc	gctcgcggcg	gctgtctcgg	240
cgtctctggc	attacgtccc	tcctccgcgt	ttcggggttc	atctttggga	atcgagttca	300
gctacagtat	aatgacaaca	cggagatccc	gtggtagcca	gattagggct	ggaaaggctg	360
ccctctgcat	gaccacagag	tcaaagttct	ggaagtcaat	tgcccgtaca	catgggttcc	420
gcagGcgag	cgggactact	tctgggaagg	aggtactgaa	gGcagggcg	gccaaaggca	480
ggaaggttct	ttgcacaagg	acaaactcaa	acagtgggaa	gaaaagaatg	ttctaatatc	540
actgcaattt	gatgtgctcg	caactgtaag	tgtaatgtct	acttgcaatc	ttctaaagcg	600
ccatctatgt	gtaacaatca	tgtagcatcc	tattcctggt	taattgggta	aaaatatctg	660
gatacccttc	tgcttccc					

(2) INFORMATION FOR SEQ ID NO:3375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1576619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3375:

Leu	Arg	Leu	Arg	Val	Leu	Gln	Thr	Met	Ala	Leu	Ala	Leu	Ala	Ser	Pro	
1			5						10					15		
Met	Ala	Ser	Leu	Ser	Phe	His	Ser	Gly	Arg	Ile	Ser	Ala	Ala	Ser	Ile	
			20					25					30			
Gly	Gly	Val	Gly	Arg	Thr	Arg	Arg	Ala	Ala	Pro	Val	Gly	Val	Ser	Ala	
			35					40				45				
Ser	Pro	Phe	Leu	Arg	Ser	Ser	Phe	Val	Ser	Ser	Ser	Ser	Thr	Ser	Ser	
			50				55					60				
Ala	Ser	Ala	Ser	Ala	Ser	Xaa	Ala	Ser	Leu	Ala	Ala	Ala	Val	Ser	Ala	
			65				70			75				80		
Ser	Leu	Ala	Phe	Thr	Ser	Ser	Ser	Ala	Phe	Ala	Gly	Ser	Ser	Leu	Gly	
			85						90					95		
Ile	Glu	Phe	Ser	Tyr	Ser	Ile	Met	Thr	Thr	Arg	Arg	Ser	Arg	Gly	Met	
			100					105					110			
Gln	Ile	Arg	Ala	Gly	Lys	Ala	Ala	Leu	Cys	Met	Thr	Lys	Arg	Ser	Arg	
			115					120				125				
Ser	Arg	Lys	Ser	Leu	Ala	Arg	Thr	His	Gly	Phe	Arg	Arg	Arg	Met	Arg	
			130					135				140				
Thr	Thr	Ser	Gly	Arg	Lys	Val	Leu	Lys	Arg	Arg	Ala	Lys	Gly	Arg		
			145					150				155			160	
Lys	Val	Leu	Cys	Thr	Arg	Thr	Asn	Ser	Asn	Ser	Gly	Lys	Lys	Arg	Met	
			165					170						175		

Phe

(2) INFORMATION FOR SEQ ID NO:3376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1576620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3376:

```
Met Ala Leu Ala Leu Ala Ser Pro Met Ala Ser Leu Ser Phe His Ser
1      5      10      15
Gly Arg Ile Ser Ala Ala Ser Ile Gly Gly Val Gly Arg Thr Arg Arg
20      25      30
Ala Ala Pro Val Gly Val Ser Ala Ser Pro Phe Leu Arg Ser Ser Phe
35      40      45
Val Ser Ser Ser Ser Thr Ser Ser Ala Ser Ala Ser Ala Ser Xaa Ala
50      55      60
Ser Leu Ala Ala Ala Val Ser Ala Ser Leu Ala Phe Thr Ser Ser Ser
65      70      75      80
Ala Phe Ala Gly Ser Ser Leu Gly Ile Glu Phe Ser Tyr Ser Ile Met
85      90      95
Thr Thr Arg Arg Ser Arg Gly Met Gln Ile Arg Ala Gly Lys Ala Ala
100      105      110
Leu Cys Met Thr Lys Arg Ser Arg Ser Arg Lys Ser Leu Ala Arg Thr
115      120      125
His Gly Phe Arg Arg Arg Met Arg Thr Thr Ser Gly Arg Lys Val Leu
130      135      140
Lys Arg Arg Arg Ala Lys Gly Arg Lys Val Leu Cys Thr Arg Thr Asn
145      150      155      160
Ser Asn Ser Gly Lys Lys Arg Met Phe
165
```

(2) INFORMATION FOR SEQ ID NO:3377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3377:

```
Met Ala Ser Leu Ser Phe His Ser Gly Arg Ile Ser Ala Ala Ser Ile
1      5      10      15
Gly Gly Val Gly Arg Thr Arg Arg Ala Ala Pro Val Gly Val Ser Ala
20      25      30
Ser Pro Phe Leu Arg Ser Ser Phe Val Ser Ser Ser Ser Thr Ser Ser
35      40      45
Ala Ser Ala Ser Ala Ser Xaa Ala Ser Leu Ala Ala Ala Val Ser Ala
50      55      60
Ser Leu Ala Phe Thr Ser Ser Ser Ala Phe Ala Gly Ser Ser Leu Gly
65      70      75      80
Ile Glu Phe Ser Tyr Ser Ile Met Thr Thr Arg Arg Ser Arg Gly Met
85      90      95
Gln Ile Arg Ala Gly Lys Ala Ala Leu Cys Met Thr Lys Arg Ser Arg
100      105      110
Ser Arg Lys Ser Leu Ala Arg Thr His Gly Phe Arg Arg Arg Met Arg
115      120      125
Thr Thr Ser Gly Arg Lys Val Leu Lys Arg Arg Arg Ala Lys Gly Arg
130      135      140
Lys Val Leu Cys Thr Arg Thr Asn Ser Asn Ser Gly Lys Lys Arg Met
145      150      155      160
Phe
```

(2) INFORMATION FOR SEQ ID NO:3378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..479
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1576636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3378:

```
gttgccggtt gtgcctctct tctctattcg ttcccccgcct camcccgcgc cagccgctctc 60
gctagggttt cgccgcgcgc gccgcgcgcgc ccgcgcctat gcctcgccgc agctcaggcg 120
cgcgaaatgg caggcgcgcg ggttgcacat gctacccctca agggcccccag cgtggtgaag 180
gagatcttca ttggaactgac cctggggtct gatcgctgga ggtatgtgga agatgcacca 240
ctggaacgag cagagggaaa ctagatcctt ctacgacatg cttgacaagg gccagatgct 300
cgtcgtcgag gagtagtctc cacgtgtcac ctcacaagtt ttttttttcc agttgttttt 360
gaaaactcac tctggagagc acgacaaagt gaatgctgtg gagatttggc ttgaaaaataa 420
gcataacccat ttgagaacac cagcttctgt tgaattgtct tttcttgtca tgactatttt
```

(2) INFORMATION FOR SEQ ID NO:3379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3379:

```
Val Ala Arg Cys Ala Leu Ser Leu Tyr Ser Phe Pro Ala Ser Xaa Arg
1      5      10      15
Ala Ser Arg Leu Ala Arg Val Ser Pro Pro Pro Pro Pro Pro Pro
20     25     30
Leu Cys Leu Ala Ala Ala Gln Ala Arg Gln Met Ala Gly Gly Arg Val
35     40     45
Ala His Ala Thr Leu Lys Gly Pro Ser Val Val Lys Glu Ile Phe Ile
50     55     60
Gly Leu Thr Leu Gly Ser Asp Arg Trp Arg Tyr Val Glu Asp Ala Pro
65     70     75     80
Leu Glu Arg Ala Glu Glu Asn
85
```

(2) INFORMATION FOR SEQ ID NO:3380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3380:

```
Leu Pro Val Val Leu Ser Leu Ser Ile Arg Ser Pro Pro Xaa Pro Glu
1      5      10      15
Pro Ala Val Ser Leu Gly Phe Arg Arg Arg Arg Arg Arg Arg Arg
20     25     30
Tyr Ala Ser Pro Gln Leu Arg Arg Gly Lys Trp Gln Ala Ala Gly Leu
35     40     45
His Met Leu Pro Ser Arg Ala Pro Ala Trp
```

50 55
(2) INFORMATION FOR SEQ ID NO:3381:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..45
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576639
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3381:
Met Ala Gly Arg Val Ala His Ala Thr Leu Lys Gly Pro Ser Val
1 5 10 15
Val Lys Glu Ile Phe Ile Gly Leu Thr Leu Gly Ser Asp Arg Trp Arg
20 25 30
Tyr Val Glu Asp Ala Pro Leu Glu Arg Ala Glu Glu Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:3382:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..719
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576648
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3382:
gttgatatg cggatctcca ttacccaatc gcttctctg cgcctctccg ctgcggctcgg 60
cgaaacgcat ctgttcccca acctccgcag ccgtctccacc gtctctccact ccggtctcgg 120
aatcgaccgc ccccgatcca gatcaggagc tgagggatgg acgcgaacag gcgccagagt 180
gggatccagc agttgctggc tgcggaScag gaggctcagc aaattgtgaa tgccCgctag 240
agctgcgaag tcagcgaggc tcaggcaagc aaaagaggag gctgagcggg aaatagccga 300
ataccgtgcc cagatggagg ctgagtttca gaggaaggtt gcagagagca gcggcgactc 360
cgggtcaaac gtcaagcgct tcgaggaaga aacggcgggc aagatcgagc aactcaccga 420
gcaggccgca agcatctccc cggatgtcat tcagatgctt ctgcggcatg tcaccacagt 480
caagaactga ggagtgtgtg tcccgaaacta tgctcgcaga cttgtaccgt cgatctattt 540
attttttgca agagtggag aggttgaggaa taatatgccc gcttgatccc ataattctcg 600
ttctgaacta cgggaataagc cgccgcagct ttagcggcaa acgtgactag tactgtcaga 660
acctaccatt gttatttggg acaattggta aataattatt ttttaaacgt gatttttcg

(2) INFORMATION FOR SEQ ID NO:3383:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..75
 (D) OTHER INFORMATION: / Ceres Seq. ID 1576649
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3383:
Leu Tyr Met Arg Ile Ser Ile His Gln Ser Pro Ser Cys Arg Pro Pro
1 5 10 15
Ala Arg Leu Gly Glu Arg Asp Leu Phe Pro Asn Leu Arg Ser Arg Ser
20 25 30
Thr Val Leu His Ser Gly Cys Arg Ile Asp Pro Pro Arg Ser Arg Ser
35 40 45

Gly Ala Glu Gly Trp Thr Arg Thr Gly Ala Arg Val Gly Ser Ser Ser
50 55 60
Cys Trp Leu Arg Xaa Arg Arg Leu Ser Lys Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3384:

Cys Ile Cys Gly Ser Pro Phe Thr Asn Arg Leu Pro Val Ala Leu Pro
1 5 10 15
Leu Gly Ser Ala Asn Ala Ile Cys Ser Pro Thr Ser Ala Ala Ala Pro
20 25 30
Pro Ser Ser Thr Pro Ala Ala Glu Ser Thr Arg Pro Asp Pro Asp Gln
35 40 45
Glu Leu Arg Asp Gly Arg Glu Gln Ala Pro Glu Trp Asp Pro Ala Val
50 55 60
Ala Gly Cys Gly Xaa Gly Gly Ser Ala Asn Cys Glu Cys Pro Leu Glu
65 70 75 80
Leu Pro Ser Gln Arg Gly Ser Gly Lys Gln Lys Arg Arg Leu Ser Gly
85 90 95

Lys

(2) INFORMATION FOR SEQ ID NO:3385:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3385:

Met Pro Ala Arg Ala Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu
1 5 10 15
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu
20 25 30
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val
35 40 45
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln
50 55 60
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His
65 70 75 80
Val Thr Thr Val Lys Asn
85

(2) INFORMATION FOR SEQ ID NO:3386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..756

(D) OTHER INFORMATION: / Ceres Seq. ID 1576665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3386:

ataggggtct	aagcctcgcc	cggtttcttcg	tctccacagc	tcccgcgcgc	gcggaccagc	60
gcgtcactct	accgggttcc	ggcgctctccc	cgtaccocgta	gcgcgggcac	catggcggas	120
agacggaaag	ggctttcttg	aagcagccca	aggtgtttct	ctgttccaag	aaggccacca	180
aggtaaacaa	acctggccaag	ggaggaaaca	gattctggaa	gaacattggc	cttggtttca	240
agacaccag	ggaagccatt	gaaggaaacct	acattgataa	gaagtgtcca	ttcaccggca	300
ctgtgtctat	cagggttcgc	atcatcgccg	gaacatgcca	cagtgtctaa	atgaatagga	360
ccatcattgt	tcgtaggaa	tatcttcact	tcgtcaagaa	gtaccagagg	tatgagaaga	420
gacactccaa	catccctgcg	cacatttcac	catgcttcgc	tgtcaaggaa	ggagatcatg	480
tgatcattgg	ccagtcgag	ccagtgctga	agactgntaa	ggttcaaatg	ggtcaaatgt	540
attcctgcag	gttcgaagag	tgagcagtg	aagaaagctt	tcactgcgcg	ttaaagatcat	600
gacgagttca	tcattccatg	cccggaaaag	ctctgtgtta	taacgttttg	atgctgccta	660
ttagcctttt	tcccgcgtaac	tactatatgt	gtacttgga	ttggacttga	attacatcca	720
gaacttgaaa	tcctgaaaaa	aatcatacat	cctttg			

(2) INFORMATION FOR SEQ ID NO:3387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1576666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3387:

Met	Asn	Arg	Thr	Ile	Ile	Val	Arg	Arg	Asn	Tyr	Leu	His	Phe	Val	Lys
1			5						10				15		
Lys	Tyr	Gln	Arg	Tyr	Glu	Lys	Arg	His	Ser	Asn	Ile	Pro	Ala	His	Ile
			20					25					30		
Ser	Pro	Cys	Phe	Arg	Val	Lys	Glu	Gly	Asp	His	Val	Ile	Ile	Gly	Gln
			35					40					45		
Cys	Arg	Pro	Val	Ser	Lys	Thr	Xaa	Lys	Val	Gln	Cys	Gly	Gln	Ser	Tyr
			50			55					60				
Ser	Cys	Arg	Phe	Glu	Glu	Trp	Ser	Ser	Glu	Glu	Ser	Phe	His	Cys	Arg
						70				75				80	
Leu	Arg	Ser													

(2) INFORMATION FOR SEQ ID NO:3388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1034

(D) OTHER INFORMATION: / Ceres Seq. ID 1576671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3388:

gtgtctctta	ttcttttttg	tgtttggttg	ctggaaagg	agtggacttt	tacaacttct	60
catgtcccta	ttgttgggag	ggttcggagt	ccggactcgg	atttgccaca	accagattgt	120
tcacaactcg	gaaggctcac	caaatcgctc	tacgctcttg	cttctcctc	cacgaggtga	180
ggaaccctca	gcgactgacc	atggcggttc	ctccgcgcac	cgacagggtg	gccttctctt	240
ctaccccgcg	gtgctactcc	gcgcgcgcgc	ctgcggcgcg	ctccccgacc	tcgccagcgc	300
catacggggg	cgcgcgccca	ccggcgatgt	cgaagaggnc	cgagttctgt	gtctccaaag	360
ttgatgacct	gatgaactgg	gcgcgtaagg	gctcgatttg	gcccatgacc	tttgggctcg	420

```

cctgctgcrc  ggctcgagatg  atgcacgcgc  ggcGgtccgc  ctacgaacttc  gaccggGttc  480
ggcgctcatct  tccgtccctc  gccgcgcma  tccgattgca  tgatcgctgc  cggaacgyc  540
accaacaaaa  tgggtccagc  cctccgcaag  gtttatgacc  aaatgcctga  gctagatgg  600
gttattttcaa  tgggcagctg  tgccaacggt  ggtggatact  accattactc  ctactctgtt  660
gtacgtggat  gtgacgcgat  agtcccggt  gacatctacg  tcctggggtg  cccaccaact  720
gctgaggcac  tgctgtacgg  tgtttttcag  ctccaaaaga  agatcaacag  gcgtaaggat  780
ttccttcact  ggtggaccaa  gtgaagcatg  ctctgctgt  tgctcgcttg  ctacgtttct  840
ttgcaactga  cctacctgtc  ttatctgaaa  taaggacgga  ctttgctggg  attcacaaat  900
tgtgtgtgcc  tggaaggatg  tatgcccaag  ttgtgacgaa  catataactt  gtgtacttgg  960
agtcagttcg  cctgtaatgg  acaccagacc  tgctgtgaat  ctgtttttaa  gcttccattg  1020
taatacagca  atac

```

(2) INFORMATION FOR SEQ ID NO:3389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3389:

```

Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu
1      5      10      15
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile
20      25      30
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn
35      40      45
Arg Pro Thr Leu Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala
50      55      60
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu
65      70      75      80
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp
85      90      95
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu
100     105     110
Xaa Arg Val Arg Gly Leu Gln Gly
115     120

```

(2) INFORMATION FOR SEQ ID NO:3390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3390:

```

Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile Gly Ile Cys His
1      5      10      15
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu
20      25      30
Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly
35      40      45
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val
50      55      60
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala
65      70      75      80

```

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Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Xaa Arg Val Arg
85 90 95
Gly Leu Gln Gly
100

(2) INFORMATION FOR SEQ ID NO:3391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3391:

Met	Ala	Leu	Leu	Pro	Arg	Thr	Ala	Arg	Leu	Ala	Phe	Leu	Ser	Thr	Pro
1			5						10				15		
Arg	Ser	Tyr	Ser	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Ser	Pro	Thr	Ser	Pro
			20					25				30			
Ala	Pro	Tyr	Gly	Gly	Ala	Pro	Pro	Pro	Ala	Met	Ser	Lys	Arg	Xaa	Glu
			35				40					45			
Phe	Val	Val	Ser	Lys	Val	Asp	Asp	Leu	Met	Asn	Trp	Ala	Arg	Lys	Gly
			50			55					60				
Ser	Ile	Trp	Pro	Met	Thr	Phe	Gly	Leu	Ala	Cys	Xaa	Val	Glu	Met	
					70					75				80	
Met	His	Ala	Gly	Ala	Ser	Arg	Tyr	Asp	Phe	Asp	Arg	Val	Arg	Arg	His
					85				90					95	
Leu	Pro	Ser	Leu	Ala	Ala	Xaa	Val	Arg	Leu	His	Asp	Arg	Arg	Arg	His
			100					105				110			
Xaa	His	Gln	Gln	Asn	Gly	Ser	Ser	Pro	Pro	Gln	Gly	Leu			
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3392:

adgcctctcc	aaaattcgaa	caccctcgcc	tggaaccttc	tacgagccag	ctccgagcgg	60
ttgcgcgtcc	ataatctgag	agacgggtgcc	gtgggttttc	rgcgctcggg	tcgcagtaaa	120
agtcggggcc	gagatggagt	cctcgtcgtc	rgcgccggcg	ctggcgccgg	ggcgagtag	180
cgcgcgctcg	ggcagcttca	gcggcgacac	ggaccgcgtc	gacatccccg	cgaagggcgc	240
acccctcgag	cggcttagga	agtggcgcca	agcagccctt	gtgctgaatg	catcaagcgg	300
cttttaggtac	acactcgatt	ttggaagagc	attggccttg	gtttcaagac	tccagcgaaa	360
Gcaattgaag	ggacatcacat	tgacaagaaa	tgctccattca	ctggaacctg	ttctatcaga	420
ggcagaatta	ttgctggaac	atgccacagt	gctaagatga	acagaaacct	catgtgtctg	480
aggaactata	tcacttttgt	taagaataac	cagaggtatg	aaaagaggca	ctccaacatt	540
ccagctcaca	tctcccatcg	cttcogtgtg	aagggaaggcg	accatgtcat	cattggccag	600
tgccggcccg	tatcaaaaac	tgtgaggttc	aatgtcgtca	aagtcattcc	agctggatct	660
gtgtgtcccg	gcaagaagcg	tttcaccgca	gcctgagttt	aagactatgt	tccatgagta	720
gtttatatag	tgatgtcttt	ttttgttaaa	aaaactgcct	tctaggcttg	tgcttttcca	780
ctatggtttg	gagatgtgtc	ccatcttaat	gaagtcacat	catctgaaca	tgttactgtt	840
tattgtacct	tgctgtgcaa	agttttcc				

(2) INFORMATION FOR SEQ ID NO:3393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1576683
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3393:
Met Glu Ser Ser Ser Xaa Gly Gly Gly Leu Ala Arg Arg Arg Ser Ser
1 5 10 15
Gly Gly Trp Gly Ser Phe Ser Gly Asp Thr Asp Pro Phe Asp Ile Pro
20 25 30
Ala Lys Gly Ala Pro Leu Glu Arg Leu Arg Lys Trp Arg Gln Ala Ala
35 40 45
Leu Val Leu Asn Ala Ser Arg Arg Phe Arg Tyr Thr Leu Asp Phe Gly
50 55 60
Arg Ala Leu Ala Leu Val Ser Arg Leu Pro Ala Lys Gln Leu Lys Gly
65 70 75 80
Pro Thr Leu Thr Arg Asn Val His Ser Leu Glu Pro Phe Leu Ser Glu
85 90 95
Ala Glu Leu Leu Glu His Ala Thr Val Leu Arg
100 105
(2) INFORMATION FOR SEQ ID NO:3394:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1576684
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3394:
Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys
1 5 10 15
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile
20 25 30
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln
35 40 45
Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Val Lys Val Ile
50 55 60
Pro Ala Gly Ser Ala Ala Ala Gly Lys Lys Ala Phe Thr Ala Ala
65 70 75
(2) INFORMATION FOR SEQ ID NO:3395:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1576685
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3395:
Met Leu Pro Cys Glu Gly Arg Arg Pro Cys His His Trp Pro Val Gln
1 5 10 15
Ala Pro Ile Lys Asn Cys Glu Val Gln Cys Arg Gln Ser His Ser Ser

	20					25						30							
Trp	Ile	Cys	Cys	Arg	Gln	Glu	Gly	Phe	His	Arg	Ser	Leu	Ser	Leu					
	35					40						45							
Arg	Leu	Cys	Ser	Met	Ser	Ser	Leu	Tyr	Ser	Asp	Val	Phe	Phe	Cys					
	50					55						60							

(2) INFORMATION FOR SEQ ID NO:3396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1576713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3396:

atcctctagc	tctctctctc	tctctctctc	cacacacaca	cacagtcaca	gacaccctta	60
tcacttagac	tgtgctagta	ggtagcggcc	gcgtaatgga	gcaggagctc	agccttgagc	120
tcaccctect	ccaccctctc	gcctcgccgc	cggagccacc	gggtactctc	gtctgcatgt	180
actgcgacgc	caagttcttc	agctcgacgg	ctctcggtgg	ccaccagaa	gcgcacaagt	240
acgagcgcas	ctggcccaagc	gccgcaggga	gatagccgcc	gcctgcgcgc	cgacacgggc	300
ggccgcaccc	gcmaacgggcg	cycgcggagg	cgacgmccgc	gcgcgatgg	gtctctcgca	360
tgtccccgcc	aggccacaag	gcacgggtac	cggagtcgtc	gtcgttgaa	atgagagtgc	420
aaccaggatg	atggGacaag	cagaaggctc	ctgctgtcga	tgacgasstc	ccgcgacccg	480
gtcgtcgagc	aacatgaaga	ggctgcggga	gtacggctac	ggcgctcgag	agctggatct	540
ctccctcagg	ctttgatctg	ttctctcttc	tcctccacyn	nnanataaa	ttcgcctcgt	600
tngtcnagat	aattcgatct	ttgtggtcag	tgcaatcctc	tgtttcgctg	gcgtgggtat	660
tcagtgtgtg	atccgtcact	ttcttctctc	tgtagttgtt	gtgcagttat	attcttccat	720
ccgatgatgg	aacctatcgg	caagaactat	tgctggccca	tcctgctatc	caaaggcgct	780
ggatttttgt	gtgctctttt	cggtttttct	ccttgatctc	tctttgtgcg	atctaaattc	840
gcagcttggt	ttttccaaaa	cggcggaac	agttttgccc	caatttcggt	tggaaccttt	900
tcaagtgact	ctaaattggg	c				

(2) INFORMATION FOR SEQ ID NO:3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1576714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3397:

Met	Glu	Gln	Glu	Leu	Ser	Leu	Glu	Leu	Thr	Leu	Leu	His	Pro	Ser	Ala	
1				5					10				15			
Ser	Pro	Pro	Glu	Pro	Pro	Gly	Tyr	Phe	Val	Cys	Met	Tyr	Cys	Asp	Arg	
			20					25					30			
Lys	Phe	Phe	Ser	Ser	Gln	Ala	Leu	Gly	His	Gln	Asn	Ala	His	Lys		
			35					40					45			
Tyr	Glu	Arg	Xaa	Trp	Pro	Ser	Ala	Ala	Gly	Arg						
	50				55											

(2) INFORMATION FOR SEQ ID NO:3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: / Ceres Seq. ID 1576715
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3398:
Met Gly Ser Arg Asp Val Pro Ala Arg Pro Gln Gly Thr Gly 15
1 5 10
Val Val Val Val Glu Asp Glu Ser Ala Thr Arg Met Met Gly Gln Ala
20 25 30
Glu Gly Ser Cys Cys
35

(2) INFORMATION FOR SEQ ID NO:3399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1576716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3399:

Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Val Val 15
1 5 10
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu
20 25 30
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Tyr Asn Ser Pro Arg Xaa
35 40 45
Xaa Arg
50

(2) INFORMATION FOR SEQ ID NO:3400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..831
(D) OTHER INFORMATION: / Ceres Seq. ID 1576730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3400:

tcaagcacct atatagtagt acctcataat ggcaggcaaa aacctaatat cattggggct 60
cattatccctc atgaccatgg gattagccaa tgctgttagg gtggttagat acctagtagc 120
cgatggtagt ggcacaggag agggagaaag ttggtgatat gtgaatggcg ggggatcagg 180
gtctgggtct ggcaccggct caggtgatag ttgctcctat ggtgcacatg caagtctcatg 240
tmagagtggt ggaggggggtg gaactagcca gtacggtggg tctggatatg gttctgggtc 300
agggctcagg tcaggatccta gtacatatag tcaaggaggg tattctggtt atggagaatc 360
ttctagtgtc ggtRggcatc ggtgggggtg gaggtggagg acaagctgca ggccatgga 420
attccaatgc tcaaggatcc ggtagtggaa ctggttctgg ctctagctat gctaacaggt 480
attggtacgg atcaagtga gacaggtgcaa gtgctaattg caatggtggt gccacaggaa 540
atagtcacaaa cgggtggaagt ggtgggtgct caggtgctgg atctgggttt ggcaatgcct 600
accocctaatt tctatatcta agtcaacctat tagttggagc ccaacagtag ttgtcatttc 660
aagtttgaggt attagtttagt ttgtttgtac ctctattaca cttttgctag aactaaataa 720
ataaaggccc caactattct agtaatggca gcagtttagt gtgagggtca gcttgaataa 780
atttgttgta aacatgtcag tctatgaatg aaataataa ttccttttag c

(2) INFORMATION FOR SEQ ID NO:3401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1576731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3401:

```
Met Ala Gly Lys Asn Leu Ile Pro Leu Gly Leu Ile Leu Met Thr
1      5      10      15
Met Gly Leu Ala Asn Ala Val Arg Val Val Arg Tyr Ser Ser Ala Asp
      20      25      30
Gly Thr Gly Thr Gly Gln Gly Glu Gly Gly Tyr Val Asn Gly Gly
      35      40      45
Gly Ser Gly Ser Gly Ser Gly Thr Gly Ser Gly Asp Ser Gly Pro Tyr
      50      55      60
Gly Ala His Ala Ser Xaa Ser Xaa Gly Gly Gly Gly Gly Thr Ser
      65      70      75      80
Gln Tyr Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Ser Gly Ser Gly
      85      90      95
Ser Ser Thr Tyr Ser Gln Gly Gly Tyr Ser Gly Tyr Gly Glu Ser Ser
      100      105      110
Ser Ala Gly Xaa His Arg Trp Gly Trp Arg Trp Arg Thr Ser Cys Arg
      115      120      125
Arg Met Glu Phe Gln Cys Ser Arg Ile Arg
      130      135
```

(2) INFORMATION FOR SEQ ID NO:3402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1576732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3402:

```
Met Ala Gly Asp Gln Gly Leu Gly Leu Ala Pro Asp Gln Val Ile Val
1      5      10      15
Val Leu Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val
      20      25      30
Glu Leu Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln
      35      40      45
Gly Gln Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu
      50      55      60
Asn Leu Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gln
      65      70      75      80
Ala Ala Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr
      85      90      95
Gly Ser Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu
      100      105      110
Ala Gly Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln
      115      120      125
Asn Gly Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn
      130      135      140
Ala Tyr Pro
      145
```

(2) INFORMATION FOR SEQ ID NO:3403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1576733
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3403:
Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val Glu Leu
1 5 10 15
Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln Gly Gln
20 25 30
Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu Asn Leu
35 40 45
Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gln Ala Ala
50 55 60
Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr Gly Ser
65 70 75 80
Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu Ala Gly
85 90 95
Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln Asn Gly
100 105 110
Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn Ala Tyr
115 120 125
Pro

(2) INFORMATION FOR SEQ ID NO:3404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..744

(D) OTHER INFORMATION: / Ceres Seq. ID 1576754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3404:

ctcacgctca	cggccgcgcg	ctccaccgt	cgcgcttcc	tccggttaga	ctagggttagg	60
ctaggctagg	gtgtcgacca	gctcgcggtta	atggtggcct	tcagggttcca	tcagttaccag	120
gwggtggggc	gcgcgctgcc	gaecgcccgcc	gacgagcacc	ccaagatcta	ccgcatgaag	180
ctctgggccca	ccaacgaagt	ccgcgcccaag	agcaagttct	ggtacttctc	gagggaagttg	240
aagaaggttta	agaagagcaa	cggtcaggtc	ctggccatca	acgagatctt	cgagcgtaac	300
ccgacgacga	tcaagaacta	tggcatctgg	Ctgcgctacc	agagcagaac	cggtaccac	360
aacatgtaca	aggagtaccg	cgacacaacc	ctgaacggcg	ctgtagagca	gatgtacaat	420
gagatggctt	ctcgccaccg	cgtgaggtcc	ccctgcattc	agatcatcaa	gaccgccaca	480
gtacacttca	agctgtgcaa	gagggacaac	accaagcagt	ttcacacaag	tgagatcaag	540
ttcccaactg	tgtaccgcga	ggtcaggccg	ccgaccagga	agctgaagac	cacgtttcaag	600
gcttcgaggg	ccaacctgtt	catgtgattt	agctgtggtc	agtgtatgtg	atcgtaagaa	660
tctgtgtttt	aagttttgac	ctgaagaact	gggtgggttg	aagattcaac	tcgttttgaa	720
acgtgcattg	tgaaccattt	gcgc				

(2) INFORMATION FOR SEQ ID NO:3405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1576755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3405:

Met	Val	Ala	Phe	Arg	Phe	His	Gln	Tyr	Gln	Xaa	Val	Gly	Arg	Ala	Leu	
1				5					10					15		
Pro	Thr	Pro	Gly	Asp	Glu	His	Pro	Lys	Ile	Tyr	Arg	Met	Lys	Leu	Trp	
		20					25						30			
Ala	Thr	Asn	Glu	Val	Arg	Ala	Lys	Ser	Lys	Phe	Trp	Tyr	Phe	Leu	Arg	
		35					40					45				
Lys	Leu	Lys	Lys	Val	Lys	Lys	Ser	Asn	Gly	Gln	Val	Leu	Ala	Ile	Asn	
		50				55				60						
Glu	Ile	Phe	Glu	Arg	Asn	Pro	Thr	Thr	Ile	Lys	Asn	Tyr	Gly	Ile	Trp	
65					70				75					80		
Leu	Arg	Tyr	Gln	Ser	Arg	Thr	Gly	Tyr	His	Asn	Met	Tyr	Lys	Glu	Tyr	
				85					90					95		
Arg	Asp	Thr	Thr	Leu	Asn	Gly	Ala	Val	Glu	Gln	Met	Tyr	Asn	Glu	Met	
				100				105						110		
Ala	Ser	Arg	His	Arg	Val	Arg	Ser	Pro	Cys	Ile	Gln	Ile	Ile	Lys	Thr	
		115					120					125				
Ala	Thr	Val	His	Phe	Lys	Leu	Cys	Lys	Arg	Asp	Asn	Thr	Lys	Gln	Phe	
		130				135					140					
His	Asn	Ser	Glu	Ile	Lys	Phe	Pro	Leu	Val	Tyr	Arg	Lys	Val	Arg	Pro	
145					150					155				160		
Pro	Thr	Arg	Lys	Leu	Lys	Thr	Thr	Phe	Lys	Ala	Ser	Arg	Pro	Asn	Leu	
				165					170					175		
Phe	Met															

(2) INFORMATION FOR SEQ ID NO:3406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3406:

Met	Lys	Leu	Trp	Ala	Thr	Asn	Glu	Val	Arg	Ala	Lys	Ser	Lys	Phe	Trp	
1				5					10					15		
Tyr	Phe	Leu	Arg	Lys	Leu	Lys	Lys	Val	Lys	Lys	Ser	Asn	Gly	Gln	Val	
		20					25						30			
Leu	Ala	Ile	Asn	Glu	Ile	Phe	Glu	Arg	Asn	Pro	Thr	Thr	Ile	Lys	Asn	
		35				40						45				
Tyr	Gly	Ile	Trp	Leu	Arg	Tyr	Gln	Ser	Arg	Thr	Gly	Tyr	His	Asn	Met	
50						55					60					
Tyr	Lys	Glu	Tyr	Arg	Asp	Thr	Thr	Leu	Asn	Gly	Ala	Val	Glu	Gln	Met	
65				70					75					80		
Tyr	Asn	Glu	Met	Ala	Ser	Arg	His	Arg	Val	Arg	Ser	Pro	Cys	Ile	Gln	
				85					90				95			
Ile	Ile	Lys	Thr	Ala	Thr	Val	His	Phe	Lys	Leu	Cys	Lys	Arg	Asp	Asn	
		100					105						110			
Thr	Lys	Gln	Phe	His	Asn	Ser	Glu	Ile	Lys	Phe	Pro	Leu	Val	Tyr	Arg	
		115					120					125				
Lys	Val	Arg	Pro	Pro	Thr	Arg	Lys	Leu	Lys	Thr	Thr	Phe	Lys	Ala	Ser	
		130				135						140				
Arg	Pro	Asn	Leu	Phe	Met											
145					150											

(2) INFORMATION FOR SEQ ID NO:3407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..654
(D) OTHER INFORMATION: / Ceres Seq. ID 1576757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3407:

ggacattttc	atcgcgcgca	ttttttttcc	gaccagccga	vcgcccgcgc	cctccggcag	60
gtctttttcc	cgggcaacgac	caccacagcc	agggtcttccc	ggccccgaac	gcgagcaccc	120
agccctcttc	cagggtcttcc	ccggcgacga	gcggtagaaa	gaggggatcc	ttagcacaaat	180
ggaagaagga	gcaccaggcc	cgctcgcaag	cattcccggat	ctctggagaca	cgtaccgcaa	240
cagctccacc	gcgcccgtgg	gcagcagctc	accgtctgtc	gcgaagCtcc	ggaagctgtc	300
gttccggcgg	atgctcatcg	gcgtcaacga	cgcccgctac	ttccacggcc	tggtccactg	360
catcgacaag	cagggaaca	tcattctcca	ggacgcgcta	gagtagccga	gcgcccgcga	420
ctgctcgctc	ccgacggagc	agcgggtgct	ggggctcctc	ctgattcccg	ccgctgccc	480
gtcgtcgtgc	caggctcgatt	gctccgttga	agagaagatg	ctgctctctg	gttttgagtg	540
aatcgtgctt	caaagggaaat	acactacgca	tgtaactaagt	tactggggct	catctctgct	600
atctgaaact	gagagggcat	atgtgtgttt	ccattttttg	aaggattgtt	tatt	

(2) INFORMATION FOR SEQ ID NO:3408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1576758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3408:

Asp	Leu	Ser	Ile	Ala	Arg	Ile	Phe	Phe	Pro	Thr	Ser	Arg	Xaa	Pro	Pro
1			5						10					15	
Pro	Ser	Gly	Arg	Ser	Ser	Ser	Arg	Pro	Arg	Pro	Pro	Thr	Pro	Gly	Leu
			20					25					30		
Pro	Gly	Pro	Glu	Arg	Glu	His	Pro	Ala	Leu	Leu	Gln	Val	Phe	Pro	Gly
			35				40				45				
Asp	Glu	Arg	Val	Glu	Glu	Gly	Ile	Leu	Ser	Thr	Met	Glu	Glu	Gly	Ala
			50			55					60				
Pro	Gly	Pro	Ser	Gln	Ala	Ile	Pro	Asp	Ser	Gly	Asp	Thr	Tyr	Arg	Asn
65				70				75						80	
Ser	Ser	Thr	Ala	Pro	Val	Gly	Ser	Ser	Ser	Pro	Ser	Val	Ala	Lys	Leu
			85					90						95	
Arg	Lys	Leu	Leu	Phe	Arg	Arg	Met	Leu	Ile	Gly	Val	Asn	Asp	Gly	Arg
			100				105						110		
Tyr	Phe	His	Gly	Leu	Phe	His	Cys	Ile	Asp	Lys	Gln	Gly	Asn	Ile	Ile
		115				120					125				
Leu	Gln	Asp	Ala	Val	Glu	Tyr	Arg	Ser	Ala	Arg	His	Cys	Ser	Pro	Pro
		130				135					140				
Thr	Glu	Gln	Arg	Cys	Leu	Gly	Leu	Ile	Leu	Ile	Pro	Ala	Ala	Cys	Arg
145				150						155					160
Ser	Ser	Cys	Gln	Val	Asp	Cys	Ser	Val	Glu	Glu	Lys	Met	Ser	Leu	Leu
			165						170					175	

Cys Phe Glu

(2) INFORMATION FOR SEQ ID NO:3409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1576759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3409:
Met Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly
1 5 10 15
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro
 20 25 30
Ser Val Ala Lys Leu Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly
 35 40 45
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys
 50 55 60
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg
65 70 75 80
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile
 85 90 95
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu
 100 105 110
Lys Met Ser Leu Leu Cys Phe Glu
 115 120

(2) INFORMATION FOR SEQ ID NO:3410:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..555
(D) OTHER INFORMATION: / Ceres Seq. ID 1576763
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3410:
gactccagcgc cgccagtcac gaccacgccg cgctccgcc tggaaccctt tagccgagcg 60
gasaagggaa gaaatgggga agggtagcgg cagcttcggc aagcgccgga acaagacgca 120
cacgctctgc atccgctgcg cgccgccggc tggagcgggc cgctcaagaa ccgcatcta 180
aatcgggcgc ccagccccga gagctccgac gccgagtgac atgagaagcg agcgagcagc 240
agcagcagca gccaccgcaa aggcctcaac acgacgacgt ccgttggtgc gacggcgccc 300
agcgacgCat gcgctgtcgc tcttcgttgc tatccacgta cgtaacgacg ccacgtgtgac 360
ccgcttgccct accgctccgt tctgtgcgac tggatggtgc gtcggcgggc gtcgcgcgca 420
gggcttcgtg tacgtctgtg ataagcacga gggagggcgc gccagcgcgg aacggagggc 480
gagggcgggc ccccaagtgg cggtctttcc aaatgtcaaa aaggacagct gtaacagtga 540
taagaaaaac aagtc

(2) INFORMATION FOR SEQ ID NO:3411:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1576764
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3411:
Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro
1 5 10 15
Phe Ser Arg Ala Xaa Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu
 20 25 30

Arg Gln Ala Pro Glu Gln Asp Ala His Ala Leu His Pro Leu Arg Arg
35 40 45
Pro Ala Trp Ser Gly Arg Val Lys Asn Pro Asp Leu Asn Arg Ala Pro
50 55 60
Ser Pro Glu Ser Ser Asp Ala Glu
65 70

(2) INFORMATION FOR SEQ ID NO:3412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1576765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3412:

Thr Pro Arg Arg Gln Ser Arg Pro Arg Arg Ala Ser Ala Trp Asn Pro
1 5 10 15
Leu Ala Glu Arg Xaa Arg Glu Glu Met Gly Lys Gly Thr Gly Ser Phe
20 25 30
Gly Lys Arg Arg Asn Lys Thr His Thr Leu Cys Ile Arg Cys Gly Gly
35 40 45
Arg Arg Gly Ala Gly Ala Ser Arg Thr Arg Ile
50 55

(2) INFORMATION FOR SEQ ID NO:3413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1576766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3413:

Met Arg Ser Glu Arg Ala Ala Ala Ala Ala Thr Ala Lys Ala Gln
1 5 10 15
Arg Arg Arg Arg Pro Leu Leu Arg Arg Arg Pro Ala Gln His Ala Ala
20 25 30
Val Val Phe Val Arg Ile His Val Arg Thr Thr Ala Gln Leu Thr Arg
35 40 45
Leu Pro Thr Arg Pro Phe Cys Ala Thr Gly Trp Ser Val Gly Gly Arg
50 55 60
Arg Gly Glu Gly Phe Arg Tyr Val Val Asp Lys His Glu Gly Arg Ala
65 70 75 80
Gly Arg Arg Glu Arg Arg Arg Arg Arg Pro Gln Val Ala Val Phe
85 90 95
Pro Asn Val Lys Lys Asp Ser Cys Asn Ser Asp Lys Lys Asn Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:3414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 925 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..925

(D) OTHER INFORMATION: / Ceres Seq. ID 1576795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3414:

gccaggttcac	ctccgcctccc	gtctctccccc	tcccccctccc	gtcctgccat	ggccaccgca	60
gcacgcgcgc	tgttcgcgcgc	acgcccgcgca	cgccgcctgc	tgccgtctcg	ggcctccccc	120
tctctctctt	ccatccgtctc	cgccgcggcaa	cgtgtgtggcg	tcgggtgctg	ccgctgcctg	180
gctcggcgcc	cggattccac	ctattccccg	ctgcgttcgg	gccagggcgg	tgaccgtgca	240
ccgactgaaa	tggcgctctc	gttccctggc	tgcgactacg	agcactggct	catcgtcatg	300
gacaagcccg	ggggcgaggg	cgccaccaag	cagcaaatga	tagattgtta	catccagacc	360
cttgcccagg	tgttagggag	tgaagaggag	gcgaagaaga	ggatatataa	tgtgtcctgc	420
gagcgctatt	tgtgatttcg	atgcgaattt	gacgaggaga	cctCccaaca	aactcgaagg	480
ccttcacagg	gttctttttg	tgtctcctga	ctcttacgtt	gatgctgaga	acaaggatta	540
tgggtgctgag	ttattttgtg	acggtgaaat	cgttcacgga	tctccagaaa	ggcagagaga	600
ggtggagcca	gtgcctcaga	gagctcagga	tcgaccacgg	tacagtgcac	ggaccgcgta	660
tgtgaagcgg	agggagaaacc	aatcttacca	gagatgatgt	tccgtctctt	gaagatgtaa	720
aatgtcacgg	tttccacaag	tgtccaaatg	cggtagctgaa	gatgcagcag	caactcccca	780
ctactcatat	gagaattgca	tccgttctgt	ttgcgcgcga	ttttaagctg	tatatgetta	840
ttatgcattt	gggcttgtac	ctcagctgat	atgaacgatg	tatcctttga	actaacgcac	900
tataattttt	gaaaccgttt	tagcc				

(2) INFORMATION FOR SEQ ID NO:3415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1576796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3415:

Ala	Ser	Ser	Pro	Pro	Pro	Pro	Leu	Leu	Pro	Ser	Pro	Ser	Arg	Pro	Ala
1			5					10						15	
Met	Ala	Thr	Ala	Ala	Arg	Ala	Leu	Val	Ala	Ala	Arg	Pro	Ala	Arg	Pro
			20					25					30		
Leu	Leu	Pro	Ser	Arg	Arg	Leu	Pro	Ser	Ser	Ser	Ser	Ile	Arg	Pro	Ala
			35					40					45		
Arg	Gln	Arg	Ala	Gly	Val	Gly	Cys	Val	Arg	Cys	Met	Ala	Arg	Arg	Pro
			50				55				60				
Asp	Ser	Thr	Tyr	Ser	Pro	Leu	Arg	Ser	Gly	Gln	Gly	Gly	Asp	Arg	Ala
65			70						75				80		
Pro	Thr	Glu	Met	Ala	Pro	Leu	Phe	Pro	Gly	Cys	Asp	Tyr	Glu	His	Trp
			85						90				95		
Leu	Ile	Val	Met	Asp	Lys	Pro	Gly	Gly	Glu	Gly	Ala	Thr	Lys	Gln	Gln
			100					105					110		
Met	Ile	Asp	Cys	Tyr	Ile	Gln	Thr	Leu	Ala	Gln	Val	Val	Gly	Ser	Glu
			115				120					125			
Glu	Glu	Ala	Lys	Lys	Arg	Ile	Tyr	Asn	Val	Ser	Cys	Glu	Arg	Tyr	Phe
			130				135				140				
Gly	Phe	Gly	Cys	Glu	Ile	Asp	Glu	Glu	Thr	Ser	Gln	Gln	Thr	Arg	Arg
145			150						155					160	
Pro	Ser	Arg	Gly	Ser	Phe	Cys	Ala	Ser							
			165												

(2) INFORMATION FOR SEQ ID NO:3416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1576797
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3416:
Pro Val His Leu Arg Leu Arg Ser Ser Pro Pro Pro Val Leu Pro
1 5 10 15
Trp Pro Pro Gln His Ala Pro Ser Ser Pro His Ala Arg His Gly Arg
20 25 30
Cys Cys Arg Leu Gly Ala Ser Arg Pro Pro Leu Pro Ser Val Pro Arg
35 40 45
Gly Asn Val Leu Ala Ser Gly Ala Ser Ala Ala Trp Leu Gly Gly Arg
50 55 60
Ile Pro Pro Ile Pro Arg Cys Val Arg Ala Arg Ala Val Thr Val His
65 70 75 80
Arg Leu Lys Trp Arg Leu Cys Ser Leu Ala Ala Thr Thr Ser Thr Gly
85 90 95
Ser Ser Ser Trp Thr Ser Pro Gly Ala Arg Ala Pro Pro Ser Ser Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3417:

Met Ala Thr Ala Ala Arg Ala Leu Val Ala Ala Arg Pro Ala Arg Pro
1 5 10 15
Leu Leu Pro Ser Arg Arg Leu Pro Ser Ser Ser Ser Ile Arg Pro Ala
20 25 30
Arg Gln Arg Ala Gly Val Gly Cys Val Arg Cys Met Ala Arg Arg Pro
35 40 45
Asp Ser Thr Tyr Ser Pro Leu Arg Ser Gly Gln Gly Gly Asp Arg Ala
50 55 60
Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp
65 70 75 80
Leu Ile Val Met Asp Lys Pro Gly Gly Glu Gly Ala Thr Lys Gln Gln
85 90 95
Met Ile Asp Cys Tyr Ile Gln Thr Leu Ala Gln Val Val Gly Ser Glu
100 105 110
Glu Glu Ala Lys Lys Arg Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe
115 120 125
Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Gln Gln Thr Arg Arg
130 135 140
Pro Ser Arg Gly Ser Phe Cys Ala Ser
145 150

(2) INFORMATION FOR SEQ ID NO:3418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..545

(D) OTHER INFORMATION: / Ceres Seq. ID 1576799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3418:

aatcttccag	cccaaatgtc	catccattg	ctcgtctgt	ccctccgttc	acaacctcct	60
ccacgaccga	acgagcagag	cagacccttc	ccccccacca	gtcccggtgt	ccagcgcgcg	120
cgggcgcgaa	gatgatcata	ccggtgcgct	gcttcaCctg	cggaagggtg	attgggaaca	180
agtgggacct	ctacctcgac	ctcctccagg	ccgactactc	ggaaggggat	gctctggatg	240
ctttggaatt	gttccgctac	tgctgcaggc	gaatgctcat	gacctatgtt	gacctcattg	300
agaagttgct	caactacaac	acactggaga	agactgagac	aagttaagtg	agcaagcata	360
tcattgcttg	aaagcactac	tgtttcgcag	tatcatatat	attgtaggcg	gtatgttggtt	420
tccttctctat	caggagagga	tgttgtGga	gtgtgaactt	gcttttgcct	tcgagcatct	480
aaggactgac	aagggcattg	tgcatctatg	ttacgatgtt	ggagatttta	atcgatataa	540
cggt						

(2) INFORMATION FOR SEQ ID NO:3419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3419:

Ile	Phe	Gln	Pro	Lys	Val	Pro	Ser	His	Cys	Ser	Leu	Cys	Pro	Ser	Val
1				5					10				15		
His	Asn	Leu	Leu	His	Asp	Arg	Thr	Ser	Arg	Ala	Asp	Pro	Ser	Pro	Ser
			20					25					30		
Pro	Ala	Pro	Gly	Ser	Ser	Gly	Gly	Gly	Glu	Asp	Asp	His	Thr	Gly	
			35				40				45				
Ala	Leu	Leu	His	Leu	Arg	Gln	Gly	Asp	Trp	Glu	Gln	Val	Gly	Pro	Leu
			50				55				60				
Pro	Arg	Pro	Pro	Pro	Gly	Arg	Leu	Leu	Gly	Arg	Gly	Cys	Ser	Gly	Cys
					70					75				80	
Phe	Gly	Ile	Val	Pro	Leu	Leu	Leu	Gln	Ala	Asn	Ala	His	Asp	Pro	Cys
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1576801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3420:

Ser	Ser	Pro	Ser	Lys	Phe	His	Pro	Ile	Ala	Arg	Ser	Val	Pro	Pro	Phe
1				5					10				15		
Thr	Thr	Ser	Ser	Thr	Thr	Glu	Arg	Ala	Glu	Gln	Thr	Leu	Pro	Pro	His
				20				25					30		
Gln	Leu	Arg	Val	Pro	Ala	Ala	Ala	Ala	Lys	Met	Ile	Ile	Pro	Val	
				35			40				45				
Arg	Cys	Phe	Thr	Cys	Gly	Lys	Val	Ile	Gly	Asn	Lys	Trp	Asp	Leu	Tyr
				50			55				60				
Leu	Asp	Leu	Leu	Gln	Ala	Asp	Tyr	Ser	Glu	Gly	Asp	Ala	Leu	Asp	Ala
				70					75					80	

Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met Leu Met Thr His Val
85 90 95
Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr Leu Glu Lys Thr Glu
100 105 110
Thr Ser

(2) INFORMATION FOR SEQ ID NO:3421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1576802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3421:

Met Ile Ile Pro Val Arg Cys Phe Thr Cys Gly Lys Val Ile Gly Asn
1 5 10 15
Lys Trp Asp Leu Tyr Leu Asp Leu Leu Gln Ala Asp Tyr Ser Glu Gly
20 25 30
Asp Ala Leu Asp Ala Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met
35 40 45
Leu Met Thr His Val Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr
50 55 60
Leu Glu Lys Thr Glu Thr Ser
65 70

(2) INFORMATION FOR SEQ ID NO:3422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748

(D) OTHER INFORMATION: / Ceres Seq. ID 1576803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3422:

aacttaacca ctactccgca tctactgacg ccgcccgcgc ctctctccgt 60
cggactagtc agagcatcgc tcattggcga gaaccccaag gtgtttcttc acatctctat 120
cggcaagtcc aaggccgggc gggtcgtgat ggagctcttc gccgacaagg tgcccaagac 180
ggccgagaac ttccgctgcc tgtgcacggc cgagaagggc ctgggtccgc cggggaagcc 240
gctgcactac aagggtccgc ccttccacgc cgtcatccgc ggcttcatgt gccaggcgccg 300
gcacttcacc cggggcaacg gcaacggcgc cgagtccttc tacggcgcca ggctgcgcga 360
cgagaacttc aagCtgcgcc acacggggacc cggcgtgctc tccatggcca acgcggggcc 420
cgacaaccaac ggctcccaag tcttcactgc caccgcgcag acgccctggc ttgacggcaa 480
gcacgtcgtc ttccggaagg tcgtcgawgk ctacgcgcgc gtggacaaga tggaggctgt 540
cggttctcag tcaggtgccca cggccgagag cgtacgcctc gaggactgcg gccagcttgc 600
cgacgaactga gggcctcgct gtgtccgatt gtaaccaaataaat gaatgatcaa taaatttctt 660
tctttcattc ttttgtttct gtggagatgg ataccgcgct gtagttaatt aaccaatata 720
aactatggat ggatggggcg gtgatttg

(2) INFORMATION FOR SEQ ID NO:3423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1576804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3423:

Asn	Leu	Thr	Thr	Thr	Pro	His	Leu	Leu	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Pro
1				5						10					15	
Arg	Ser	Leu	Arg	Arg	Thr	Ser	Gln	Ser	Ile	Arg	His	Gly	Glu	Glu	Pro	
				20				25						30		
Gln	Gly	Val	Leu	Arg	His	Pro	His	Arg	Gln	Val	Gln	Gly	Arg	Ala	Gly	
				35				40					45			
Arg	Asp	Gly	Ala	Leu	Arg	Arg	Gln	Gly	Ala	Gln	Asp	Gly	Arg	Glu	Leu	
				50				55			60					
Pro	Leu	Pro	Val	His	Gly	Arg	Glu	Gly	Pro	Gly	Xaa	Arg	Gly	Glu	Ala	
				65				70			75				80	
Ala	Ala	Leu	Gln	Gly	Leu	Gly	Leu	Pro	Pro	Arg	His	Pro	Gly	Leu	His	
				85					90					95		
Val	Pro	Gly	Arg	Arg	Leu	His	Pro	Gly	Gln	Arg	His	Gly	Arg	Arg	Val	
				100				105					110			
His	Leu	Arg	Arg	Gln	Val	Arg	Arg	Arg	Glu	Leu	Gln	Ala	Ala	Pro	His	
				115				120					125			
Gly	Thr	Arg	Arg	Ala	Leu	His	Gly	Gln	Arg	Gly	Ala	Arg	His	Gln	Arg	
				130				135				140				
Leu	Pro	Val	Leu	His	Leu	His	Arg	Ala	Asp	Ala	Leu	Ala				
				145				150			155					

(2) INFORMATION FOR SEQ ID NO:3424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1576805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3425:

Met	Ala	Lys	Asn	Pro	Lys	Val	Phe	Phe	Asp	Ile	Leu	Ile	Gly	Lys	Ser	
1				5						10					15	
Lys	Ala	Gly	Arg	Val	Val	Met	Glu	Leu	Phe	Ala	Asp	Lys	Val	Pro	Lys	
				20				25					30			
Thr	Ala	Glu	Asn	Phe	Arg	Cys	Leu	Cys	Thr	Gly	Glu	Lys	Gly	Leu	Xaa	
				35				40					45			
Ser	Ala	Gly	Lys	Pro	Leu	His	Tyr	Lys	Gly	Ser	Ala	Phe	His	Arg	Val	
				50				55			60					
Ile	Pro	Gly	Phe	Met	Cys	Gln	Gly	Gly	Asp	Phe	Thr	Arg	Gly	Asn	Gly	
				65				70			75				80	
Thr	Gly	Gly	Glu	Ser	Ile	Tyr	Gly	Ala	Arg	Phe	Ala	Asp	Glu	Asn	Phe	
				85				90					95			
Lys	Leu	Arg	His	Thr	Gly	Pro	Gly	Val	Leu	Ser	Met	Ala	Asn	Ala	Gly	
				100				105					110			
Pro	Asp	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Ile	Cys	Thr	Ala	Gln	Thr	Pro	
				115				120					125			
Trp	Leu	Asp	Gly	Lys	His	Val	Val	Phe	Gly	Lys	Val	Val	Xaa	Xaa	Tyr	
				130				135				140				
Ala	Val	Val	Asp	Lys	Met	Glu	Ala	Val	Gly	Ser	Gln	Ser	Gly	Ala	Thr	
				145				150			155				160	
Ala	Glu	Ser	Val	Arg	Ile	Glu	Asp	Cys	Gly	Gln	Leu	Ala	Asp	Asp		
				165				170					175			

(2) INFORMATION FOR SEQ ID NO:3425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1576806
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3425:
Met Glu Leu Phe Ala Asp Lys Val Pro Lys Thr Ala Glu Asn Phe Arg
1 5 10 15
Cys Leu Cys Thr Gly Glu Lys Gly Leu Xaa Ser Ala Gly Lys Pro Leu
20 25 30
His Tyr Lys Gly Ser Ala Phe His Arg Val Ile Pro Gly Phe Met Cys
35 40 45
Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr Gly Gly Glu Ser Ile
50 55 60
Tyr Gly Ala Arg Phe Ala Asp Glu Asn Phe Lys Leu Arg His Thr Gly
65 70 75 80
Pro Gly Val Leu Ser Met Ala Asn Ala Gly Pro Asp Thr Asn Gly Ser
85 90 95
Gln Phe Phe Ile Cys Thr Ala Gln Thr Pro Trp Leu Asp Gly Lys His
100 105 110
Val Val Phe Gly Lys Val Val Xaa Xaa Tyr Ala Val Val Asp Lys Met
115 120 125
Glu Ala Val Gly Ser Gln Ser Gly Ala Thr Ala Glu Ser Val Arg Ile
130 135 140
Glu Asp Cys Gly Gln Leu Ala Asp Asp
145 150

(2) INFORMATION FOR SEQ ID NO:3426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..642
(D) OTHER INFORMATION: / Ceres Seq. ID 1576807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3426:

caattcatcc agacaagtoa tatctagcta tagctctccc ttgagaagca tttagarggag 60
gagccatgtc tgaggagaaag caccaccacc acctgtttca ccaccgcaag ccagaggagg 120
aggcgccctc cggcgagggtc gactacgaga agaaggagaa gcaccacaag cacatggaga 180
agctcggcga gctcggcgcc atcgccgcgc gcgcgtacgc cctgcacgag aagcaacaag 240
ccaagaagga cccagagaaac gagcacgggc accgggtcaa ggaggagggt gccgccctcg 300
ccgccgtggg ctccgcggcg ttccgctttcc acgagcacca cgagaagaag gacgcccaaga 360
agcacgccca caactgatcc gtccgggttg ctgttccatc tgtttcttca gccctcgcttt 420
cgtctaactgt gtccgcggcca ggccttgatt tgggctacgc atatattgat ggacgtagga 480
actgtgttgg tcggtccctcg gcgttcTttg tatcaagatc aaatcaggcc ttgaataagt 540
gtgtgtgcat atactctttt ttttaatttt tatctctttt ttttttgat cgagagatgt 600
cctgaataat gtgaatttac gtgtgtttat ataaacgaat tt

(2) INFORMATION FOR SEQ ID NO:3427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3427:

```
Met Ser Glu Glu Lys His His His His Leu Phe His His Arg Lys Pro
1      5      10      15
Glu Glu Glu Gly Ala Ser Gly Glu Val Asp Tyr Glu Lys Lys Glu Lys
20     25     30
His His Lys His Met Glu Lys Leu Gly Glu Leu Gly Ala Ile Ala Ala
35     40     45
Gly Ala Tyr Ala Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu
50     55     60
Asn Glu His Gly His Arg Val Lys Glu Glu Val Ala Ala Val Ala Ala
65     70     75     80
Val Gly Ser Ala Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp
85     90     95
Ala Lys Lys His Ala His Asn
100
```

(2) INFORMATION FOR SEQ ID NO:3428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1576809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3428:

```
Met Glu Lys Leu Glu Glu Leu Gly Ala Ile Ala Ala Gly Ala Tyr Ala
1      5      10      15
Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu Asn Glu His Gly
20     25     30
His Arg Val Lys Glu Glu Val Ala Ala Val Ala Val Gly Ser Ala
35     40     45
Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp Ala Lys Lys His
50     55     60
Ala His Asn
65
```

(2) INFORMATION FOR SEQ ID NO:3429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1576816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3429:

```
acacaagtca tccgagaagc aagcacaaagc accgcaccga acgagcagcg agcgtgttga      60
ggcaggcagt cagtggcagt gggagtagga gacaaggcta ccgagatgaa gggcctcttg      120
ttgtctgtcc tgcacctggt cgcgtccgct gcatgcctcg ttgccgtNcg cggcgcGggc      180
gagtgCGggg cgagccgcgc ggacaggatg gcgctgaagc ttgcgcctg Cscgtccgcg      240
gcgcagaacc ccagctcggc gccgtccaac ggctgtgtga cggcgtgtga caccatccgg      300
aagcagagcc cccagtgccct ctgcgcgcgtc atgctgttca agaccgcgca gaagtccggg      360
atcaagcccg agtgggccat caccatcccc aagcgtgtga acctgtgtga ccgcccctgc      420
ggctacaagt gcggagatta cactctgccca tgastgcgcg agagctgtctt ggcacatgtg      480
gcatgatccg tgtcggaagt agcacgcagt ccgcaggaag tgacggtgac gtgtcagttg      540
atgtgtgcgt ttgtaataaa cgtcgcggca ctccgcactt gttgtgatta ccatacatgt      600
```

ggaagtccag tatgatatga gtgtctcaca gtcttcaaaa gaaatatggg tcgtatcgta 660
tgtaagtgtc agggttccag agatgtctgc ctgcacccct gaaataaaac ttgtcttctt 720
gg

(2) INFORMATION FOR SEQ ID NO:3430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1576817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3430:

Thr	Ser	His	Pro	Arg	Ser	Lys	His	Lys	His	Arg	Thr	Glu	Arg	Ala	Ala	
1			5					10						15		
Ser	Val	Leu	Arg	Gln	Ala	Val	Ser	Gly	Ser	Gly	Ser	Arg	Arg	Gln	Gly	
			20					25					30			
Tyr	Arg	Asp	Glu	Gly	Pro	Leu	Val	Ala	Arg	Pro	Arg	Pro	Gly	Arg	Val	
			35				40					45				
Arg	Cys	Met	Pro	Arg	Gly	Arg	Xaa	Arg	Arg	Gly	Arg	Val	Arg	Gly	Asp	
			50				55				60					
Ala	Ala	Gly	Gln	Asp	Gly	Ala	Glu	Ala	Gly	Ala	Val	Xaa	Val	Arg	Gly	
			65				70				75				80	
Ala	Glu	Pro	Gln	Leu	Gly	Ala	Val	Gln	Arg	Leu	Leu	His	Gly	Gly	Ala	
			85					90					95			
His	His	Arg	Glu	Ala	Glu	Pro	Pro	Val	Pro	Leu	Arg	Arg	His	Ala	Val	
			100					105					110			
Gln	Asp	Arg	Gln	Glu	Val	Arg	Asp	Gln	Ala	Arg	Gly	Gly	His	His	His	
			115				120					125				
Pro	Gln	Ala	Leu	Gln	Pro	Arg	Arg	Pro	Pro	Arg	Arg	Leu	Gln	Val	Arg	
			130				135					140				
Arg	Leu	His	Ser	Ala	Met	Xaa	Ala	Arg	Glu	Leu	Leu	Glu	His	Met	Cys	
			145				150				155				160	
Met	Ile	Arg	Val	Gly	Val	Ser	Thr	Thr	Ser	Ala	Gly	Ser	Asp	Gly	Asp	
			165					170					175			
Val	Ser	Val	Tyr	Val	Cys	Val	Gly	Asn	Lys	Arg	Arg	Gly	Thr	Pro	His	
			180					185					190			
Leu	Leu															

(2) INFORMATION FOR SEQ ID NO:3431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1576818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3431:

Met	Lys	Gly	Leu	Leu	Leu	Val	Leu	Ala	Leu	Val	Ala	Ser	Ala	Ala	
1			5					10					15		
Cys	Leu	Val	Ala	Xaa	Arg	Gly	Ala	Gly	Glu	Cys	Gly	Ala	Thr	Pro	Pro
			20					25					30		
Asp	Arg	Met	Ala	Leu	Lys	Leu	Ala	Pro	Cys	Xaa	Ser	Ala	Ala	Gln	Asn
			35				40				45				
Pro	Ser	Ser	Ala	Pro	Ser	Asn	Gly	Cys	Cys	Thr	Ala	Val	His	Thr	Ile
			50				55					60			

Gly Lys Gln Ser Pro Gln Cys Leu Cys Ala Val Met Leu Ser Lys Thr
65 70 75 80
Ala Lys Lys Ser Gly Ile Lys Pro Glu Val Ala Ile Thr Ile Pro Lys
85 90 95
Arg Cys Asn Leu Val Asp Arg Pro Val Gly Tyr Lys Cys Gly Asp Tyr
100 105 110
Thr Leu Pro
115

(2) INFORMATION FOR SEQ ID NO:3432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1576819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3432:

Met Pro Arg Gly Arg Xaa Arg Arg Gly Arg Val Arg Gly Asp Ala Ala
1 5 10 15
Gly Gln Asp Gly Ala Glu Ala Gly Ala Val Xaa Val Arg Gly Ala Glu
20 25 30
Pro Gln Leu Gly Ala Val Gln Arg Leu Leu His Gly Gly Ala His His
35 40 45
Arg Glu Ala Glu Pro Pro Val Pro Leu Arg Arg His Ala Val Gln Asp
50 55 60
Arg Gln Glu Val Arg Asp Gln Ala Arg Gly Gly His His His Pro Gln
65 70 75 80
Ala Leu Gln Pro Arg Arg Pro Pro Arg Arg Leu Gln Val Arg Arg Leu
85 90 95
His Ser Ala Met Xaa Ala Arg Glu Leu Leu Glu His Met Cys Met Ile
100 105 110
Arg Val Gly Val Ser Thr Thr Ser Ala Gly Ser Asp Gly Asp Val Ser
115 120 125
Val Tyr Val Cys Val Gly Asn Lys Arg Arg Gly Thr Pro His Leu Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:3433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..702

(D) OTHER INFORMATION: / Ceres Seq. ID 1576842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3433:

ttcagttggc agttgcgaact tgcgagtggc tccaacaagg caacacaatc caccggcacc 60
aaccagcgc ggcgccaccg gcgaccctga ccccttccc cggagagcga tggcgacgga 120
gctgacggcg gcgcactggc cgcgtacgac ggcaccgacc cgtccaagcc catctacgtc 180
tcgctccggg gcaaggtcta cgaagtcacc tccggccgCc ggctttctacg gccNccggcg 240
gcgcctaacgc cgtcttcggc ggcgcggagg Ccagcccgcg cctcggaagc atgtccaagg 300
acgagggcga cgtctccggg gacctctccg ggctcaccga caaggagctc ggcgctcctcg 360
ccgactggga gaccaagtgc caGgggcgaag taccctgcgt tcgcccgact ccgcccgac 420
gctgaactc ggacgtctcg gtgtaaattt actctgtcct gcctcttcgc gtgttcagt 480
ttgtgcttc ttgcttggtt ctagtgtgct tgctaSecca ataactgaa tGggaaggac 540

gtatgtgatg tgcttctgta atagctcogag ctctctagtcc ttgcatacac tgctgtgcta 600
ccacatgaca tgatgtactc gtgtgtgctt tggttgtgtg gtaattccat gaccatgatc 660
agtaatctga ataaaaaata ttggagatgt gcttgcttcc tg

(2) INFORMATION FOR SEQ ID NO:3434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..141
(D) OTHER INFORMATION: / Ceres Seq. ID 1576843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3434:

Phe Ser Trp Gln Leu Arg Leu Ala Ser Gly Ser Asn Lys Ala Thr Gln
1 5 10 15
Ser Thr Gly Thr Asn Pro Ala Arg Arg His Arg Arg Pro Val Pro Pro
20 25 30
Ser Pro Glu Ser Asp Gly Asp Gly Ala Asp Gly Gly Ala Leu Arg Ala
35 40 45
Tyr Asp Gly Thr Asp Pro Ser Lys Pro Ile Tyr Val Ser Val Arg Gly
50 55 60
Lys Val Tyr Asp Val Thr Ser Gly Arg Arg Leu Leu Arg Xaa Pro Ala
65 70 75 80
Ala Pro Thr Pro Ser Ser Arg Ala Ala Arg Pro Ala Ala Pro Ser Ala
85 90 95
Arg Cys Pro Arg Thr Arg Pro Thr Ser Pro Gly Thr Ser Pro Gly Ser
100 105 110
Pro Thr Arg Ser Ser Ala Ser Ser Pro Thr Gly Arg Pro Ser Ser Arg
115 120 125
Ala Lys Tyr Pro Val Val Ala Arg Leu Ala Ala Asp Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:3435:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1576844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3435:

Ser Val Gly Ser Cys Asp Leu Arg Val Ala Pro Thr Arg Gln His Asn
1 5 10 15
Pro Pro Ala Pro Thr Gln Arg Gly Ala Thr Gly Asp Pro Tyr Pro Leu
20 25 30
Pro Arg Arg Ala Met Ala Thr Glu Leu Thr Ala Ala His Cys Ala Arg
35 40 45
Thr Thr Ala Pro Thr Arg Pro Ser Pro Ser Thr Ser Pro Ser Gly Ala
50 55 60
Arg Ser Thr Thr Ser Pro Pro Ala Ala Gly Phe Tyr Gly Xaa Arg Arg
65 70 75 80
Arg Leu Arg Arg Leu Arg Gly Pro Arg Gly Gln Pro Arg Pro Arg Gln
85 90 95
Asp Val Gln Gly Arg Gly Arg Arg Leu Arg Gly Pro Leu Arg Ala His
100 105 110
Arg Gln Gly Ala Arg Arg Pro Arg Arg Leu Gly Asp Gln Val Pro Gly
115 120 125

Pro	Ser	Thr	Pro	Ser	Ser	Pro	Asp	Ser	Pro	Pro	Thr	Pro	Glu	Leu	Gly
	130					135					140				
Ser	Leu	Gly	Val	Asn	Leu	Leu	Cys	Pro	Ala	Ser	Cys	Gly	Val	Gln	Cys
145					150						155			160	
Cys	Ala	Cys	Leu	Leu	Val	Ala	Ser	Cys	Phe	Ala	Xaa	Pro	Ile	Ile	
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:3436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1576845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3436:

Met	Ala	Thr	Glu	Leu	Thr	Ala	Ala	His	Cys	Ala	Arg	Thr	Thr	Ala	Pro
1			5						10					15	
Thr	Arg	Pro	Ser	Pro	Ser	Thr	Ser	Pro	Ser	Gly	Ala	Arg	Ser	Thr	Thr
		20						25					30		
Ser	Pro	Pro	Ala	Ala	Gly	Phe	Tyr	Gly	Xaa	Arg	Arg	Arg	Leu	Arg	Arg
		35					40					45			
Leu	Arg	Gly	Pro	Arg	Gly	Gln	Pro	Arg	Pro	Arg	Gln	Asp	Val	Gln	Gly
		50				55					60				
Arg	Gly	Arg	Arg	Leu	Arg	Gly	Pro	Leu	Arg	Ala	His	Arg	Gln	Gly	Ala
65					70					75				80	
Arg	Arg	Pro	Arg	Arg	Leu	Gly	Asp	Gln	Val	Pro	Gly	Pro	Ser	Thr	Pro
				85					90					95	
Ser	Ser	Pro	Asp	Ser	Pro	Pro	Thr	Pro	Glu	Leu	Gly	Ser	Leu	Gly	Val
			100					105					110		
Asn	Leu	Leu	Cys	Pro	Ala	Ser	Cys	Gly	Val	Gln	Cys	Cys	Ala	Cys	Leu
		115					120					125			
Leu	Val	Ala	Ser	Cys	Phe	Ala	Xaa	Pro	Ile	Ile					
		130					135								

(2) INFORMATION FOR SEQ ID NO:3437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..828

(D) OTHER INFORMATION: / Ceres Seq. ID 1576855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3437:

acggttgatc	caactctctc	tgctctctcg	gcctctgcgg	tgctctctcc	cggtccccag	60
tcccgcccat	gtcgtgcgcc	ctggaggatg	tcagcgtggg	catggaggag	gaggatcagc	120
ggccctcgtaa	ccgggccccg	ctccaccgga	gcgccaccac	caacgcctcc	caggtggcca	180
tggtcgccctc	caatccctgc	cctatcgaga	gcctcgacta	cgagatgata	gagaacgagc	240
tggtcgaccac	gaactggagg	acgaggcgca	aggcggaacca	ggtcgcggtac	gtggtgctca	300
agtggaacctt	ctgCttcgcc	atcggcatcc	tcaccgggat	cgtcgcgcttc	ttcatcaacc	360
tcgcgctgca	gaacgtcgcg	gctctcaagg	accaggccgt	ttccgCccct	catggactcc	420
ggcagctact	ggacggcgctt	ctgggtgttc	gccggctgca	acctggcgct	ctcgtctgtg	480
gctcgtgcca	tcacggcgctt	cttgctgcgc	gcggccggcg	ggtcggaagt	cccgaaggtc	540
aaggcctacc	tcacggcgctt	cgacgcgcgc	aacatctctc	cgctcgggag	cctcgctgtc	600
aaggtgcgcc	gtgtgtgttc	cgttcccatc	ctcctgcctc	gcgcgnygct	ttcgttgtct	660
gcagtgacac	tgctccccctc	accatttctc	ggtgccastg	cgcaaatgga	ttaccatcca	720
cactaatata	atgtaacaa	ggcattcatt	cctccatcca	actgcatgat	cagcagaaaa	780

ggaaagcaac cagcaagtaa ataaacaatc ataattagac ttttctkg

(2) INFORMATION FOR SEQ ID NO:3438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1576856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3438:

Arg	Leu	Val	His	Leu	Leu	Leu	Leu	Leu	Trp	Pro	Leu	Arg	Cys	Leu	Leu
1			5						10					15	
Pro	Val	Pro	Ser	Ser	Pro	Gly	His	Val	Val	Ala	Ala	Gly	Gly	Cys	Gln
			20						25					30	
Gly	His	Gly	Gly	Gly	Gly	Ser	Ala	Ala	Pro	Glu	Pro	Gly	His	Pro	Ala
			35					40				45			
Pro	Glu	Arg	His	His	Gln	Arg	Leu	Pro	Gly	Gly	His	Gly	Arg	Leu	Gln
			50				55				60				
Ser	Leu	Pro	Tyr	Arg	Glu	Pro	Arg	Leu	Arg	Asp	Arg	Glu	Arg	Ala	
			65				70			75				80	
Val	Arg	Pro	Glu	Leu	Glu	Asp	Glu	Ala	Gln	Gly	Gly	Pro	Gly	Ala	Val
				85					90				95		
Arg	Gly	Ala	Gln	Val	Asp	Leu	Leu	Leu	Arg	His	Arg	His	Pro	His	Arg
			100					105					110		
Asp	Arg	Arg	Leu	Leu	His	Gln	Pro	Arg	Arg	Glu	Arg	Arg	Gly	Leu	
			115					120				125			
Gln	Ala	Pro	Gly	Arg	Phe	Arg	Pro	Ser	Trp	Thr	Pro	Pro	Ala	Thr	Gly
			130				135					140			
Arg	Arg	Ser	Gly	Cys	Ser	Pro	Ala	Ala	Thr	Trp	Arg	Ser	Cys	Cys	Trp
			145				150			155				160	
Arg	Arg	Pro	Ser	Arg	Arg	Ser	Cys	Arg	Arg	Pro	Ala	Gly	Arg	Glu	
			165					170					175		
Ser	Arg	Arg	Ser	Arg	Pro	Thr	Ser	Thr	Ala	Ser	Thr	Arg	Pro	Thr	Ser
			180					185					190		
Ser	Arg	Cys	Gly	Pro	Ser	Leu	Ser	Arg	Cys	Ala	Val	Cys	Val	Pro	Phe
			195					200				205			
Pro	Ser	Ser	Cys	Pro	Arg	Xaa	Xaa	Phe	Arg	Leu	Leu	Gln	Cys	Thr	Cys
			210				215					220			
Ser	Pro	His	His	Phe	Leu	Val	Pro	Xaa	Arg	Lys	Trp	Ile	Thr	Ile	His
			225				230			235				240	
Thr	Asn	Ile	Met												

(2) INFORMATION FOR SEQ ID NO:3439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1576857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3439:

Gly	Trp	Ser	Thr	Ser	Ser	Cys	Ser	Ser	Gly	Leu	Cys	Gly	Ala	Ser	Ser
1			5						10					15	
Arg	Ser	Arg	Val	Pro	Ala	Met	Ser	Ser	Pro	Leu	Glu	Asp	Val	Ser	Val
			20					25					30		

```

Gly Met Glu Glu Glu Asp Gln Arg Pro Leu Asn Arg Ala Leu Leu His
      35                      40                      45
Arg Ser Ala Thr Thr Asn Ala Ser Gln Val Ala Met Val Gly Ser Asn
      50                      55                      60
Pro Cys Pro Ile Glu Ser Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu
      65                      70                      75
Phe Asp Gln Asn Trp Arg Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr
      85                      90                      95
Val Val Leu Lys Trp Thr Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly
      100                     105                     110
Ile Val Gly Phe Phe Ile Asn Leu Ala Val Glu Asn Val Ala Gly Phe
      115                     120                     125
Lys His Gln Ala Val Ser Ala Pro His Gly Leu Arg Gln Leu Leu Asp
      130                     135                     140
Gly Val Leu Gly Val Arg Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly
      145                     150                     155
Val Val His His Gly Val Leu Val Ala Gly Gly Arg Arg Val Gly Asn
      165                     170                     175
Pro Gly Gly Gln Gly Leu Pro Gln Arg Arg Arg Ala Gln His Leu
      180                     185                     190
Leu Ala Ala Asp Pro Arg Cys Gln Gly Ala Pro Cys Val Phe Arg Ser
      195                     200                     205
His Pro Pro Ala Leu Ala Xaa Ala Phe Ala Cys Cys Ser Ala His Ala
      210                     215                     220
Pro Leu Thr Ile Ser Trp Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr
      225                     230                     235
Leu Ile

```

(2) INFORMATION FOR SEQ ID NO:3440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3440:

```

Met Ser Ser Pro Leu Glu Asp Val Ser Val Gly Met Glu Glu Glu Asp
1      5      10      15
Gln Arg Pro Leu Asn Arg Ala Leu Leu His Arg Ser Ala Thr Thr Asn
      20      25      30
Ala Ser Gln Val Ala Met Val Gly Ser Asn Pro Cys Pro Ile Glu Ser
      35      40      45
Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu Phe Asp Gln Asn Trp Arg
      50      55      60
Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr Val Val Leu Lys Trp Thr
      65      70      75
Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly Ile Val Gly Phe Phe Ile
      85      90      95
Asn Leu Ala Val Glu Asn Val Ala Gly Phe Lys His Gln Ala Val Ser
      100     105     110
Ala Pro His Gly Leu Arg Gln Leu Leu Asp Gly Val Leu Gly Val Arg
      115     120     125
Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly Val Val His His Gly Val
      130     135     140
Leu Val Ala Gly Gly Arg Arg Val Gly Asn Pro Gly Gly Gln Gly Leu
      145     150     155
Pro Gln Arg Arg Arg Arg Ala Gln His Leu Leu Ala Ala Asp Pro Arg

```

165 170 175
Cys Gln Gly Ala Pro Cys Val Phe Arg Ser His Pro Pro Ala Leu Ala
180 185 190
Xaa Ala Phe Ala Cys Cys Ser Ala His Ala Pro Leu Thr Ile Ser Trp
195 200 205
Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr Leu Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:3441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..955
(D) OTHER INFORMATION: / Ceres Seq. ID 1576876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3441:

aagcggtcaagg gcctctcgat cgctcatcag tcgccagagg agtagttgat cgagggtgagt 60
gaggttgaaa agcaggcggc gaacaaaggc accatcgta tggacggcgg atactacggc 120
ggccgcgatc agcgctacac cngcgggtac tacggcggcg gtggcatcgc gacgccgggg 180
tacgctccgg cggtcccgta cgggatgtcg caggtgaaca tcgadgggcha cgggtgcngg 240
cdggcrtcgc cgccgcagcc gaccgtgaag gtgtactgcc gcgcccaacc caactacgcc 300
atgarcgtcc gckacgggaa ggtrgtgtcg gcgccggcga accccaagga cgagtaccag 360
cactggatca aggacatgcn gtggagcaag agcatcaagg acgagkaagg ttacccgggc 420
ttcgcrctgc tgaacaargc gaccggggag gccatcaagR cactcgctGg gggcagtcgcc 480
acccggtgcg cctgggtgcc tacaaccggc actttttgga cgagtcggtg ctgtggacgg 540
agagcccgca cgctggcaac ggcttccgct gcgtccgcat ggtaacaac atctacctca 600
acttcgacgc cctccacggc gacaagtggc acggcggcgt ccgtgacggc accgacgtcg 660
tgctctggaa gtgtgtgcgag ggccagaacc agcgcgtggaa gatccagccc tactactgaa 720
ccaacgggat atatgaccat cgccgccatc gatcgtgcac atgcatgcac acgtactagc 780
agaataacag ggggtttatc tcccaggcgg tcttttgcac gcattgccagc agttgcatag 840
ataaagcagg agcgagacaa aggggtgttca tgtatattgc acgtgtatca ctgtatgtat 900
gtgccattgt gccttgtaat aatacatata ataataaagt tgctcggagt gtatt

(2) INFORMATION FOR SEQ ID NO:3442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..246
(D) OTHER INFORMATION: / Ceres Seq. ID 1576877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3442:

Met Asp Gly Gly Tyr Tyr Gly Gly Arg Asp Gln Arg Tyr Xaa Xaa Gly
1 5 10 15
Tyr Tyr Gly Gly Gly Gly Ile Ala Thr Pro Gly Tyr Ala Pro Ala Val
20 25 30
Pro Tyr Gly Met Ser Gln Val Asn Ile Xaa Gly Xaa Gly Cys Xaa Xaa
35 40 45
Xaa Leu Pro Pro Gln Pro Thr Val Lys Val Tyr Cys Arg Ala Asn Pro
50 55 60
Asn Tyr Ala Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala
65 70 75 80
Asn Pro Lys Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser
85 90 95
Thr Ser Ile Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn
100 105 110

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1576879
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3444:
Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala Asn Pro Lys
1 5 10 15
Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser Thr Ser Ile
20 25 30
Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn Xaa Ala Thr
35 40 45
Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr Arg Cys Ala
50 55 60
Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys Cys Gly Arg
65 70 75 80
Arg Ala Ala Thr Ser Ser Ala Thr Ala Ser Ala Ala Ser Ala Trp Ser Thr
85 90 95
Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser Gly Thr Ala
100 105 110
Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly Ala Arg Ala
115 120 125
Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro Thr Asp Asp
130 135 140
Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile Arg Thr Ser
145 150 155 160
Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala Cys Met Pro
165 170 175
Ala Val Ala

(2) INFORMATION FOR SEQ ID NO:3445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..727
(D) OTHER INFORMATION: / Ceres Seq. ID 1576888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3445:

cttgctcgct ggcgcgcgc ctcgcacatc gtccctctgt cccacagagc aaccgataat 60
ccgcggcggt tgagatgttg gtttatcagg atctcctatc tggcgacgag ctctgtgcgg 120
attCcaattCA acctacaagg agctcgagaa cGggcgctctc gtgggaggtc gagggaaaagt 180
gggtcaccca aggtcctggt gatgtggaca ttggtgccaa tccatccgcc gaggggtggtg 240
aggacgaaa cgttgatgac acagctgtga aggtggttga tattgttgac acattccgctc 300
tacaggagca acctcctttt gacaagaaat catttgtgtc ttacatcaaa aaatacatca 360
agaatctcac tgctgtgttg gagccagaga aagcggatga gttcaaaaaa ggtgtcgagg 420
gtgcaaccaa gtttctcctt agcaagctga aggacctcca atttttGgt tgggtgagtc 480
atgaaggatg atgcgtctgt ggtattcgcc tattacaagg atggtgccac taatccgaca 540
ttctctatt tctctcatgg tcttaaggag atcaagtgtc aggcgtgcgg cgaattaggt 600
taccatggtt gggtactatc tatgtactat tattatatcc aaaactatag ttgtcctggc 660
tgaattgaac tcaaaagggt ttgtttgaga aaaaattgtc ccaagattgg attgcttgtt 720
aaagccc

(2) INFORMATION FOR SEQ ID NO:3446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1576889
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3446:
Leu Ala Arg Cys Ala Ala Ala Ser Asp Ile Val Pro Ser Ser Pro Arg
1 5 10 15
Ala Thr Asp Asn Pro Pro Ala Leu Arg Cys Trp Phe Ile Arg Ile Ser
20 25 30
Tyr Leu Ala Thr Ser Ser Cys Arg Ile Pro Phe Asn Leu Gln Gly Ala
35 40 45
Arg Glu Arg Ala Ser Cys Gly Arg Ser Arg Glu Ser Gly Ser Pro Lys
50 55 60
Val Leu Leu Met Trp Thr Leu Val Pro Ile His Pro Pro Arg Val Val
65 70 75 80
Arg Thr Lys Ala Leu Met Thr Gln Leu
85

(2) INFORMATION FOR SEQ ID NO:3447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..133
(D) OTHER INFORMATION: / Ceres Seq. ID 1576890
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3447:
Met Leu Val Tyr Gln Asp Leu Leu Ser Gly Asp Glu Leu Leu Ser Asp
1 5 10 15
Ser Ile Gln Pro Thr Arg Ser Ser Arg Thr Gly Val Leu Trp Glu Val
20 25 30
Glu Gly Lys Trp Val Thr Gln Gly Pro Val Asp Val Asp Ile Gly Ala
35 40 45
Asn Pro Ser Ala Glu Gly Gly Glu Asp Glu Ser Val Asp Asp Thr Ala
50 55 60
Val Lys Val Val Asp Ile Val Asp Thr Phe Arg Leu Gln Glu Gln Pro
65 70 75 80
Pro Phe Asp Lys Lys Ser Phe Val Ser Tyr Ile Lys Lys Tyr Ile Lys
85 90 95
Asn Leu Thr Ala Val Leu Glu Pro Glu Lys Ala Asp Glu Phe Lys Lys
100 105 110
Gly Val Glu Gly Ala Thr Lys Phe Leu Leu Ser Lys Leu Lys Asp Leu
115 120 125
Gln Phe Phe Gly Trp
130

(2) INFORMATION FOR SEQ ID NO:3448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1576891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3448:

Met Met Arg Leu Trp Tyr Ser Pro Ile Thr Arg Met Val Pro Leu Ile
1 5 10 15
Arg His Ser Ser Ile Ser Leu Met Val Leu Arg Arg Ser Ser Ala Arg
20 25 30
Arg Ala Ala Lys Leu Val Thr His Val Gly Tyr Tyr Leu Cys Thr Ile
35 40 45
Ile Ile Ser Lys Thr Ile Val Val Leu Ala Glu Leu Asn Ser Lys Gly
50 55 60
Phe Val
65

(2) INFORMATION FOR SEQ ID NO:3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..663

(D) OTHER INFORMATION: / Ceres Seq. ID 1576896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3449:

aaacacgcgc gaagaancca gcccaacctt cagcacccgc atttcccaag ggaaccatcac 60
cagagcggcga gagccttccc ctccgctccc cagtcaccac cgcaccttag ccctcagcaa 120
accttaaccg ctctgtcgcca tgaaggacac ctctgttcaag gccacccggCg ccaagcgcaa 180
gaaggtcggc ggcGccaaagc gcgggtccac ccccttcttc gcgtttttgg ctgagtttag 240
gcgcagctac ctggagaagc acctgagct caagggcgta aaggaggtga gcaaggcgcc 300
tggggagaag tggcgctcta tgtcggatga ggagaaggcg aagtatggca gtagcaagaa 360
cgaggatggc aaagcaagca agaaggagaa cactagctcc aagaaggcca aagctgatat 420
tcgggaggga gatgaagcag aaggttctaa caagtcaaaa tctgaggttg aggatgatga 480
gcaggatggt aatgaggatg aggatgagta aatagtagca tggggaacag cagctttgca 540
tttgagtgtt tgctgcttta cttatctttc tatatgctgt tccttttgat gttatatgct 600
gtaaggaaaa tctgtacatg atggtacctt agggtatggc atgctggagt tcccccttaa 660
ccc

(2) INFORMATION FOR SEQ ID NO:3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1576897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3450:

Lys His Arg Arg Arg Xaa Gln Pro Asn Leu His Ala Pro His Phe Pro
1 5 10 15
Arg Glu Pro Tyr Gln Ser Gly Arg Ala Phe Pro Ser Ala Pro Gln Ser
20 25 30
His Pro His Pro Ser Pro Gln Gln Thr Leu Thr Ala Arg Arg His Glu
35 40 45
Gly His Leu Val Gln Gly His Arg Arg Gln Ala Gln Glu Gly Arg Arg
50 55 60
Arg Gln Ala Arg Ala His Pro Leu Leu Arg Val Phe Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:3451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..123
(D) OTHER INFORMATION: / Ceres Seq. ID 1576898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3451:

Met	Lys	Asp	Thr	Ser	Phe	Lys	Ala	Thr	Gly	Ala	Lys	Arg	Lys	Lys	Val
1				5					10					15	
Gly	Gly	Ala	Lys	Arg	Gly	Leu	Thr	Pro	Phe	Phe	Ala	Phe	Leu	Ala	Glu
			20					25					30		
Phe	Arg	Pro	Gln	Tyr	Leu	Glu	Lys	His	Pro	Glu	Leu	Lys	Gly	Val	Lys
		35				40					45				
Glu	Val	Ser	Lys	Ala	Ala	Gly	Lys	Trp	Arg	Ser	Met	Ser	Asp	Glu	
	50					55				60					
Glu	Lys	Ala	Lys	Tyr	Gly	Ser	Ser	Lys	Lys	Ala	Asp	Gly	Lys	Ala	Ser
65				70					75					80	
Lys	Lys	Glu	Asn	Thr	Ser	Ser	Lys	Lys	Ala	Lys	Ala	Asp	Ile	Arg	Glu
			85						90				95		
Gly	Asp	Glu	Ala	Glu	Gly	Ser	Asn	Lys	Ser	Lys	Ser	Glu	Val	Glu	Asp
			100					105					110		
Asp	Glu	Gln	Asp	Gly	Asn	Glu	Asp	Glu	Asp	Glu					
			115					120							

(2) INFORMATION FOR SEQ ID NO:3452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1576899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3452:

Met	Ser	Asp	Glu	Glu	Lys	Ala	Lys	Tyr	Gly	Ser	Ser	Lys	Lys	Gln	Asp
1				5					10					15	
Gly	Lys	Ala	Ser	Lys	Lys	Glu	Asn	Thr	Ser	Ser	Lys	Lys	Ala	Lys	Ala
			20					25					30		
Asp	Ile	Arg	Glu	Gly	Asp	Glu	Ala	Glu	Gly	Ser	Asn	Lys	Ser	Lys	Ser
		35				40					45				
Glu	Val	Glu	Asp	Asp	Glu	Gln	Asp	Gly	Asn	Glu	Asp	Glu	Asp	Glu	
	50					55				60					

(2) INFORMATION FOR SEQ ID NO:3453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..829
(D) OTHER INFORMATION: / Ceres Seq. ID 1576923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3453:

aaactctttt	cttcaccaga	cgctccagacc	tgctcacggc	ctcccaaat	ccgccgccgc	60
ctgcttccca	gtctcccttg	gcaatctccg	cttgcaaac	ctagccgct	gccatggcat	120
atctagctcc	cgcgaccgcc	gctcttctcc	tccgcacccc	catctacgta	gcgcctctt	180
cccgcgccgc	ttctcttctc	ctgcgcgcgc	tcaaaagccat	cgccagtgtt	gcacatccca	240

```
tctctctctc cctccgcatg gcgcctctcg ccgcgcttct cttcgccgcc acctccccgg 300
cactcgctgt caccctctcc gtctctccgc ccccgctcac tctcttgaca gtcacggtgt 360
cccaagcaga cgcctactca gacgcctccc gactcttoga gaagctgata atcgagactg 420
cctgchtcgA scgctgcggc cgcgcggaac aagcgcgctc gcgcctgtcc acagccggat 480
gtggagagaG ctacgcgcgc ctcttagccg ctcaggttct gttcgtggac gggaaagtgg 540
acgaggcgat cgcagcattc gaggagcttg cgcggggagg ccccgccgac tatcgccctc 600
tgctctgcca gggcgtgctg tacctcgccc ttggaaggga ggcggaatca gagtccatcg 660
tcgagcgatg ccgcgaggtc ggcggcgacg cgctaactgt agatccgtca ctgatgataa 720
gcgcgaccgt ggagacggaa ttcatggggg agaagccgga gccgcggcga gtttgacctg 780
taactctgca gcggatgac tcagaataag gtaacactgg cattttggt
```

(2) INFORMATION FOR SEQ ID NO:3454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1576924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3454:

```
Asn Ser Phe Leu His Gln Thr Ser Arg Pro Ala His Gly Leu Pro Asn
1 5 10 15
Ser Ala Ala Ala Leu Leu Pro Val Ser Pro Gly Asn Leu Arg Leu Ala
20 25 30
Asn Pro Ser Arg Cys His Gly Ile Ser Ser Ser Arg Asp Arg Arg Leu
35 40 45
Phe Pro Pro His Pro His Leu Arg Ser Arg Leu Phe Pro Ala Pro Phe
50 55 60
Leu Ser Pro Cys Arg Arg Gln Ser His Arg Gln Phe Cys Thr Ser His
65 70 75 80
Pro Leu Leu Pro Pro His Gly Arg Leu Arg Arg Arg Ser Leu Arg Arg
85 90 95
His Leu Pro Gly Thr Arg Val His Pro Leu Arg Ser Ser Ala Pro Ala
100 105 110
His Ser Ser Asp Ser His Gly Val Pro Arg Arg Arg His Pro Arg Arg
115 120 125
Leu Pro Thr Leu Arg Glu Ala Asp Asn Arg Asp Cys Leu Xaa Arg Xaa
130 135 140
Arg Arg Pro Arg Gly Arg Ser Ala Leu Ala Pro Val His Ser Arg Met
145 150 155 160
Trp Arg Glu Leu Arg Pro Pro Pro Ser Arg Ser Gly Ser Val Arg Gly
165 170 175
Arg Glu Val Gly Arg Gly Asp Arg Ser Ile Arg Gly Ala Cys Ala Gly
180 185 190
Gly Pro Arg Arg Leu Ser Pro Ser Val Leu Pro Gly Arg Ala Val Pro
195 200 205
Arg Pro Trp Lys Gly Gly Gly Ile Arg Val His Ala Arg Ala Met Pro
210 215 220
Arg Gly Arg Arg Arg Arg Ala Asn Arg Arg Ser Val Thr Asp Asp Asn
225 230 235 240
Ala Asp Arg Gly Asp Gly Ile Arg Trp Gly Glu Ala Gly Ala Gly Glu
245 250 255
Gly Leu Thr Cys Asn Ser Ala Ala Asp Asp Leu Arg Ile Arg
260 265 270
```

(2) INFORMATION FOR SEQ ID NO:3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1576925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3455:

```
Thr Leu Phe Phe Thr Arg Arg Pro Asp Leu Leu Thr Ala Ser Gln Thr
1      5      10      15
Pro Pro Pro Pro Cys Phe Gln Ser Pro Leu Ala Ile Ser Ala Leu Gln
20      25      30
Thr Leu Ala Ala Ala Met Ala Tyr Leu Ala Pro Ala Thr Ala Ala Ser
35      40      45
Ser Leu Arg Thr Pro Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser
50      55      60
Phe Leu Pro Ala Ala Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile
65      70      75
Leu Ser Ser Leu Arg Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala
85      90      95
Thr Ser Pro Ala Leu Ala Cys Thr Pro Ser Val Pro Pro Pro Leu
100     105
Thr Pro Leu Thr Val Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala
115     120
Ser Arg Leu Phe Glu Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg
130     135
Val Gly Arg Ala Asp Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys
145     150
Gly Glu Ser Tyr Ala Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp
165     170
Gly Lys Leu Asp Glu Ala Ile Ala Ala Phe Glu Glu Leu Ala Arg Glu
180     185
Asp Pro Ala Asp Tyr Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu
195     200
Ala Leu Gly Arg Glu Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg
210     215
Glu Val Gly Gly Asp Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr
225     230
Pro Thr Val Glu Thr Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys
245     250     255
Val
```

(2) INFORMATION FOR SEQ ID NO:3456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3456:

```
Met Ala Tyr Leu Ala Pro Ala Thr Ala Ala Ser Ser Leu Arg Thr Pro
1      5      10      15
Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser Phe Leu Pro Ala Ala
20      25      30
Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile Leu Ser Ser Leu Arg
35      40      45
Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala Thr Ser Pro Ala Leu
50      55      60
```

```

Ala Cys Thr Pro Ser Val Pro Pro Pro Pro Leu Thr Pro Leu Thr Val
65              70              75              80
Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala Ser Arg Leu Phe Glu
              85              90              95
Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg Val Gly Arg Ala Asp
              100              105              110
Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys Gly Glu Ser Tyr Ala
              115              120              125
Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp Gly Lys Leu Asp Glu
              130              135              140
Ala Ile Ala Ala Phe Glu Glu Leu Ala Arg Glu Asp Pro Ala Asp Tyr
145              150              155              160
Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu Ala Leu Gly Arg Glu
              165              170              175
Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg Glu Val Gly Gly Asp
              180              185              190
Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr Pro Thr Val Glu Thr
              195              200              205
Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys Val
              210              215              220

```

(2) INFORMATION FOR SEQ ID NO:3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3457:

```

gagtgtctcgc gtacgttctt ccccatcac attogggccat tctccaccgt ccaaccaacc      60
accggcgccgc gcacaaggga agcgaagagg aatcaacgcg atgtctgcga ccacggcgccg      120
ggtgccccttc tggcgggcgcg ccgggatgac ctacatcgcc tactccaaca tctGcgtgctc      180
gctggtacgg aactgcctca aggagccctt caagtccaag gccgcgtccc gcgagaaggt      240
ccattttctcc atctccaagt ggacggatgg caaacaggag aagcccactg tccgcacaga      300
atccgatgaa taaagctctg gtgcctatgt ggcatagtcc ttgctacaga tgatttgaag      360
tgttgttgca agtttccgga acatgctatt tagctggcctt gattttatag tcaatgctga      420
ataataaata ctttttacga caattgtctt ttctgttgtc aattgcactc gccctacctc      480
aatcagtcac gtgaacatca tggaaatgctt cagttttgtg caaactaaat ttgtgtgtct      540
gtccgacaga ttctatgtct ggtcctaaaa aataaaggaa taatgaatgt agtgttttgc      600

```

(2) INFORMATION FOR SEQ ID NO:3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3458:

```

Glu Cys Leu Gly Ser Phe Phe Pro Ile His Ile Arg Pro Phe Ser Thr
1              5              10              15
Val Gln Pro Thr Thr Gly Gly Gly Thr Arg Glu Ala Lys Arg Asn Gln
              20              25              30
Arg Asp Val Cys Asp His Gly Gly Gly Ala Leu Leu Ala Gly Gly Arg
              35              40              45

```


Asp Asp Leu His Arg Leu Leu Gln His Leu Arg Cys Ala Gly Thr Glu
50 55 60
Leu Pro Gln Gly Ala Leu Gln Val Gln Gly Arg Val Pro Arg Glu Gly
65 70 75 80
Pro Phe Leu His Leu Gln Val Asp Gly Trp Gln Thr Gly Glu Ala His
85 90 95
Cys Pro His Arg Ile Arg
100

(2) INFORMATION FOR SEQ ID NO:3459:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3459:

Ser Val Ser Val Ala Ser Ser Pro Phe Thr Phe Gly His Ser Pro Pro
1 5 10 15
Ser Asn Gln Pro Pro Ala Ala Ala Gln Gly Lys Arg Arg Gly Ile Asn
20 25 30
Ala Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly
35 40 45
Met Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn
50 55 60
Cys Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val
65 70 75 80
His Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr
85 90 95
Val Arg Thr Glu Ser Asp Glu
100

(2) INFORMATION FOR SEQ ID NO:3460:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1576938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3460:

Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly Met
1 5 10 15
Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn Cys
20 25 30
Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val His
35 40 45
Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr Val
50 55 60
Arg Thr Glu Ser Asp Glu
65 70

(2) INFORMATION FOR SEQ ID NO:3461:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 815 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..815
(D) OTHER INFORMATION: / Ceres Seq. ID 1576943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3461:

agctctcccc	ctctagcctc	acctgcccta	tacacagcca	ctactgtcga	tcgattgaat	60
ttgaaccac	caggatcagg	attaggatta	cagcatgtcg	gcgtccccgc	agttgtacag	120
gccgcgggaa	gscgcggcctt	ctcgcgcgtcc	tgcgccacgc	agccgctcgt	gttcgcggcg	180
gacgactact	gctgcaggac	gccgacgggc	agcgggatct	gctacctgag	ggagcccaacc	240
acgtgccgcg	ccgcgccccc	gaagccgcgc	ccgcgcgcgc	cccatgtgca	ggaagcgccct	300
cttccaagcg	cgggatcagc	agcttgcgtg	ggcgggcccc	gtccctgtta	tcagcatccg	360
ctcgcagcag	ctggagcgcc	tcttccgcgc	ctgtccgcgc	ccgaccacca	ccaccaccga	420
caagcggcgc	cgctccggct	ccggccccag	ccccagatcc	gccacgaaac	atgggtgctca	480
gctgcagCtg	cgcagcatNg	aattgaattg	ggttagcgta	acgtagcttg	cacgcaccaaa	540
ccaaccactC	ccctttttag	tttttgcgtc	tgcactctgc	tgcttcttgt	tgctgcaaca	600
agcaaacgcg	aagcgggtgc	gcttcttttt	atttatttat	tattttatta	cggagtactt	660
gcttcgcttc	tcaaatattt	gtcatttgat	agttcatctc	aaaaatttga	caaataaaaa	720
agaaacgaga	agcaagcagt	acccacctgt	gtaaatcaaa	tcaaatatgc	aaagtattacc	780

ccatagcaat aaaaatcacc gtgtaaatca gatcg

(2) INFORMATION FOR SEQ ID NO:3462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1576944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3462:

Ser	Ser	Pro	Leu	Ala	Ser	Pro	Ala	Leu	Tyr	Thr	Ala	Thr	Val
1			5				10					15	
Asp	Arg	Leu	Asn	Leu	Asn	Pro	Gly	Ser	Gly	Leu	Gly	Leu	His
		20					25					30	
Val	Gly	Val	Pro	Gly	Val	Gln	Ala	Arg	Gly	Xaa	Pro	Ala	Phe
		35				40				45			Ser
Pro	Ser	Cys	Ala	Thr	Gln	Pro	Leu	Val	Phe	Ala	Gly	Asp	Cys
		50			55				60				
Cys	Arg	Thr	Pro	Thr	Gly	Ser	Gly	Ile	Cys	Tyr	Leu	Arg	Glu
65				70				75					80
Thr	Cys	Pro	Pro	Ala	Pro	Arg	Lys	Pro	Pro	Pro	Pro	Pro	His
				85				90					95
Gln	Glu	Ala	Pro	Leu	Pro	Ser	Gly	Gly	Ser	Ala	Ala	Cys	
			100				105						

(2) INFORMATION FOR SEQ ID NO:3463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..167
(D) OTHER INFORMATION: / Ceres Seq. ID 1576945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3463:

Leu	Ser	Pro	Ser	Ser	Leu	Thr	Cys	Pro	Ile	His	Ser	His	Tyr	Cys	Arg
1				5				10					15		

```

Ser Ile Glu Phe Glu Pro Thr Arg Ile Arg Ile Arg Ile Thr Ala Cys
                20                25                30
Arg Arg Pro Arg Ser Cys Thr Gly Pro Arg Lys Xaa Gly Leu Leu Ala
                35                40                45
Val Leu Arg His Ala Ala Ala Arg Val Arg Arg Arg Leu Leu Leu
                50                55                60
Gln Asp Ala Asp Gly Gln Arg Asp Leu Leu Pro Glu Gly Ala His His
                65                70                75                80
Val Pro Ala Arg Ala Pro Glu Ala Ala Ala Ala Ala Pro Cys Ala
                85                90                95
Gly Ser Ala Ser Ser Lys Arg Arg Ile Ser Ser Leu Leu Arg Arg Ala
                100               105               110
Pro Ser Leu Leu Ser Ala Ser Ala Ser Thr Ser Trp Ser Ala Ser Ser
                115               120               125
Ala Pro Val Arg Arg Arg Pro Pro Pro Pro Pro Thr Ser Gly Ala Ala
                130               135               140
Pro Ala Pro Ala Pro Ala Pro Asp Pro Pro Arg Asn Met Val Leu Ser
                145               150               155               160
Cys Ser Cys Ala Ala Xaa Asn
                165

```

(2) INFORMATION FOR SEQ ID NO:3464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..958
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3464:

```

angtctcagc acccgatccg agtaaccgct gccgatctct cctcgctcatt tcgtcgtcgt      60
ctccatctcg cttttgatcg actcagaaaa ttccccacca aaatctctct cccctgaagt      120
cccgaaagctc gcggaagsgc gagatgtacc atccccacgag aggcggcgctc cgcggcggca      180
gagatcaatt caaatgggac gatgtgaagg ttgacaagca tcggggagaat taccttggtc      240
atagtgttaa ggctccggtt ggtagatggc agaaaaggaaa ggatctttac tggatactc      300
gggataagaa atccgcacacg gaagatgctc ttaaggaaaga aatcaggaga gtgaagggaag      360
aggaggaaca ggctatcgct gaggctcttg gcttagctcc taagcgcaGc aatcgaaact      420
agggtaatcg cttggataag catgaatatg ctgagctgat taagagagga tcaactgcgg      480
aggacttggg agcagggcac gctgaagcag cacaagtgcg gggtotagga ttgtacaagg      540
cccttcggca tgagggtgga tcaagttctt tgagccttga cctcctaatg gaggcctgagc      600
aggctgaacc cctactagca cccaagcagg aggatgattt ggaagataat aggaagggga      660
aaaaggccacg tgaactgacg gagaagagag gggagaagga gcggaaaacga gacaggcatg      720
gtgatggaaa cgagaggagg cgggacaagc acgagaggag gcacgacttg gaggacagat      780
caaaagcggca cggcaaaagc aagcagaaga ggaggcacga ttccgattct gattgataac      840
ggccctgcgc ctgctcctgt atgactactg tatactgcga aatttcaaac ccatggagcc      900
gcttttgttt gatgtatgcc tacgctttaa attatgtttg ccctaagatg gtttaaagg

```

(2) INFORMATION FOR SEQ ID NO:3465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..230
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3465:

Met Tyr His Pro Thr Arg Gly Gly Val Arg Gly Gly Arg Asp Gln Phe

1 5 10 15
Lys Trp Asp Asp Val Lys Val Asp Lys His Arg Glu Asn Tyr Leu Gly
20 25 30
His Ser Val Lys Ala Pro Val Gly Arg Trp Gln Lys Gly Lys Asp Leu
35 40 45
Tyr Trp Tyr Thr Arg Asp Lys Lys Ser Asp Thr Glu Asp Ala Leu Lys
50 55 60
Glu Glu Ile Arg Arg Val Lys Glu Glu Glu Glu Gln Ala Met Arg Glu
65 70 75 80
Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln Gly Asn Arg
85 90 95
Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly Ser Thr Ala
100 105 110
Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val Gln Gly Leu
115 120 125
Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser Ser Leu Ser
130 135 140
Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu Leu Ala Pro
145 150 155 160
Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys Arg Pro Arg
165 170 175
Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg Asp Arg His
180 185 190
Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg Arg His Asp
195 200 205
Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln Lys Arg Arg
210 215 220
His Asp Ser Asp Ser Asp
225 230

(2) INFORMATION FOR SEQ ID NO:3466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1576952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3466:

Met Arg Glu Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln
1 5 10 15
Gly Asn Arg Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly
20 25 30
Ser Thr Ala Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val
35 40 45
Gln Gly Leu Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser
50 55 60
Ser Leu Ser Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu
65 70 75 80
Leu Ala Pro Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys
85 90 95
Arg Pro Arg Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg
100 105 110
Asp Arg His Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg
115 120 125
Arg His Asp Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln
130 135 140
Lys Arg Arg His Asp Ser Asp Ser Asp
145 150

(2) INFORMATION FOR SEQ ID NO:3467:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..618

(D) OTHER INFORMATION: / Ceres Seq. ID 1576959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3467:

gcgcgcaaac	gcaggtgcat	gcgtcgtcgc	caagccccc	ggccagctctg	agtggtgcgtt	60
cgattcgttt	gtgctgcagc	tagggttttag	agggttttctg	ggcgcnagag	Gggadgcggc	120
gcggcgatg	gctgcggcgg	aggaggagat	cgcggtgaag	gagccgctg	atctgatacg	180
cctcagcctc	gacgagcgca	tctacgtcaa	gctccgatcc	gaccgcgagc	tgccgcggcaa	240
gctccatg	tatgatacaac	atttaaacat	gatacttgga	gatgttggaag	aggtcggtgac	300
aaactgttgag	atagatgatg	aaacatatga	agaaattgtg	cgacaccacga	aacgcactat	360
ccccctttctt	ttgtcccgag	gtgatggtgt	catattggtt	tctccacccc	ttcgtacggc	420
atgaagtttg	aagtttagatc	atgctggttg	ttaattatga	taactggtgt	atttgaccac	480
ttgatggcgt	tgcatggagt	gGtatgttat	gggcctagcc	gctaactttt	ctgatgggat	540
gtaggtttaa	catgtgatac	aatcgtgtaa	acaactgctt	gtgcttggat	tatctgtcgg	600
atctcagggg	ttcttccc					

(2) INFORMATION FOR SEQ ID NO:3468:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1576960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3468:

Pro	Gln	Asn	Ala	Gly	Ala	Cys	Val	Val	Ala	Lys	Pro	Gln	Gly	Gln	Ser	
1				5						10				15		
Glu	Cys	Ala	Phe	Asp	Ser	Leu	Val	Leu	Gln	Leu	Gly	Phe	Arg	Gly	Phe	
			20					25					30			
Leu	Gly	Xaa	Glu	Arg	Xaa	Ala	Ala	Ala	Met	Ala	Ala	Ala	Glu	Glu		
			35					40					45			
Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	Ile	Arg	Leu	Ser	Leu	Asp	
			50				55				60					
Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Arg	Glu	Leu	Arg	Gly	Lys	
			65				70				75				80	
Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met	Ile	Leu	Gly	Asp	Val	Glu	
				85					90					95		
Glu	Val	Val	Thr	Thr	Val	Glu	Ile	Asp	Asp	Glu	Thr	Tyr	Glu	Glu	Ile	
				100				105					110			
Val	Arg	Thr	Thr	Lys	Arg	Thr	Ile	Pro	Phe	Leu	Phe	Val	Arg	Gly	Asp	
				115				120					125			
Gly	Val	Ile	Leu	Val	Ser	Pro	Pro	Leu	Arg	Thr	Ala					
			130				135				140					

(2) INFORMATION FOR SEQ ID NO:3469:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1576961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3469:

```
Met Ala Ala Ala Glu Glu Glu Ile Ala Val Lys Glu Pro Leu Asp Leu
1      5      10      15
Ile Arg Leu Ser Leu Asp Glu Arg Ile Tyr Val Lys Leu Arg Ser Asp
20      25      30
Arg Glu Leu Arg Gly Lys Leu His Ala Tyr Asp Gln His Leu Asn Met
35      40      45
Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp
50      55      60
Glu Thr Tyr Glu Glu Ile Val Arg Thr Thr Lys Arg Thr Ile Pro Phe
65      70      75      80
Leu Phe Val Arg Gly Asp Gly Val Ile Leu Val Ser Pro Pro Leu Arg
85      90      95
Thr Ala
```

(2) INFORMATION FOR SEQ ID NO:3470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..960
(D) OTHER INFORMATION: / Ceres Seq. ID 1576970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3470:

```
accaccaccaca ccaagccaagc aggtgctgcg atacattgca cacaacaaca accccagctc 60
tgccccagacc cgcccccaagg agttcccgcga tctccctctg gtctggtcac aggaagtctcg 120
agacctctccc aatggcggtt aagatctacg ttgtgtacta ttccatgtat gggcatgttg 180
gcaaaactagc tgaagagatc aagaaagggt ccttatctgt tgaagggtgt gaggctaaaa 240
tatggcaggt ccttgaatt ctctctgaag aagtgtctgg aaagatgggc gcgcccccta 300
agcccgacgt gccagtcac acaccgcaga acttgacagag gctgacggta tctctcttgg 360
gttcccagaca aggttcggaa tgaatggcagc tcagatgaag gcgttctctg atgcccaccg 420
tgggtctctg agggagcaga gcctcgctgg caaGcctgcc ggcattgtct tcagcactgg 480
aaccacgggt ggtggccaag agactacacc gctgacggcg attaccagat tgaacgacca 540
cggcattggt ttgtgcccc tgggctacac ttcggcgcca agctgttctg catggaccag 600
gtccagggtg gcagccccca agtcgcgcgcg acgttctgncg ccgacggctc gaggtggccc 660
agcgacgttg agctggagca cgccttcac caggggaaat acttcgctgg catcgccaag 720
aagytcaggg gctctgcttg atctgcacat acccctctgt cagatatcat aaacatttta 780
cagattctgt ataccctgtc ccgtcaatag attggtctgt gttctctctg ggtgctctga 840
tgctatgtag ttcatttgga ctgctgccgt atgaattctg atgattgtct tggtagcttg 900
gtttgtaatt tggagttgga ctatcgttgt ttctgccgca taaatttcca tgatttggtc 960
```

(2) INFORMATION FOR SEQ ID NO:3471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1576971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3471:

```
His His His Gln Ala Ser Arg Cys Cys Asp Thr Leu His Thr Thr
1      5      10      15
```

Thr Pro Ala Leu Pro Gln Pro Ala His Arg Ser Ser Arg Ile Ser Leu
20 25 30
Trp Ser Gly His Arg Ser Ser Glu Thr Ser Pro Met Ala Val Lys Ile
35 40 45
Tyr Val Val Tyr Tyr Ser Met Tyr Gly His Val Gly Lys Leu Ala Glu
50 55 60
Glu Ile Lys Lys Gly Ala Leu Ser Val Glu Gly Val Glu Ala Lys Ile
65 70 75 80
Trp Gln Val Pro Glu Ile Leu Ser Glu Glu Val Leu Gly Lys Met Gly
85 90 95
Ala Pro Pro Lys Pro Asp Val Pro Val Ile Thr Pro Gln Asn Leu Gln
100 105 110
Arg Leu Thr Val Ser Ser Leu Gly Ser Arg Gln Gly Ser Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:3472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3472:

Met Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu
1 5 10 15
Trp Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser
20 25 30
Thr Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile
35 40 45
Thr Gln Leu Thr His His Gly Met Val Phe Val Pro Val Gly Tyr Thr
50 55 60
Ser Ala Pro Ser Cys Ser Ala Trp Thr Arg Ser Arg Val Ala Ala Pro
65 70 75 80
Thr Ala Pro Ala Arg Ser Xaa Pro Thr Ala Arg Gly Gly Arg Ala Arg
85 90 95
Trp Ser Trp Ser Thr Pro Ser Thr Arg Gly Asn Thr Ser Arg Ala Ser
100 105 110
Pro Arg Xaa Ser Arg Ala Leu Leu Asp Leu His Ile Pro Leu Cys Gln
115 120 125
Ile Ser
130

(2) INFORMATION FOR SEQ ID NO:3473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3473:

Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu Trp
1 5 10 15
Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser Thr
20 25 30
Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile Thr

35										40										45										
Gln	Leu	Thr	His	His	Gly	Met	Val	Phe	Val	Pro	Val	Gly	Tyr	Thr	Ser															
50						55				60																				
Ala	Pro	Ser	Cys	Ser	Ala	Trp	Thr	Arg	Ser	Arg	Val	Ala	Ala	Pro	Thr															
65					70					75					80															
Ala	Pro	Ala	Arg	Ser	Xaa	Pro	Thr	Ala	Arg	Gly	Gly	Arg	Ala	Arg	Trp															
				85					90					95																
Ser	Trp	Ser	Thr	Pro	Ser	Thr	Arg	Gly	Asn	Thr	Ser	Arg	Ala	Ser	Pro															
			100					105					110																	
Arg	Xaa	Ser	Arg	Ala	Leu	Leu	Asp	Leu	His	Ile	Pro	Leu	Cys	Gln	Ile															
			115				120						125																	

Ser

(2) INFORMATION FOR SEQ ID NO:3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3474:

gtcatcacaa	actcactaca	cgatcggtta	tagcgagcta	acagaagctc	tatcaagtac	60
tgtgtaggcc	atggccggag	cctcgtcttt	cgctcgtgtt	ctccctcgcc	caagcgtcgg	120
cgctacgacg	gtaccacgac	tgaccatcca	caacctctgc	ccccaccggc	tgtggccgct	180
gggtgaccgg	agctcgggct	tccctcccat	ctccaccaac	accgcgccgc	tgggccccaa	240
cgcgctgtc	tccctctcct	tcccgcccaac	cttctggggc	ggcgcggtcg	cgcgcgcgac	300
gggctgcgac	ggcgccgctg	cgggctgctg	gacggggacc	acgcccggcg	ccaccgtcgt	360
gcaggtcaac	gtccacgacg	gggggaacct	ggaccaggcc	acctacagcg	tgtctctcgt	420
cgacggttc	aacgtgccca	tgttggtcag	cccgcagccc	gtcggcgccg	ggcagtgccc	480
ggcgtcggg	tgcgccatca	acctcaactg	cgactgcctt	ccccagaacc	gcaccgcgga	540
ngngnctcy	gtgccggcgc	ccgcccggag	acttcaagaa	ccggtgcccc	ytaccaggga	600
ccacgccac	cgacgtcgag	cccgtagccg	cagagctgcc	gcgccccggg	ggagctcaag	660
gtcatcttct	gccaggcgac	catcgtcaca	tgcggcgccg	aagcagagcg	caccgtctct	720
gcgcagagct	agacagatcg	agccgtccag	ctccattcgc	ctccaggtcc	gtgtaatcct	780
tacagttaatt	gtcatgtctt	cttttgcctc	atgtgttttg	tagctttggc	tgcgacgcgc	840
gtgtactcgg	gtggttttat	tttagaaatc	agcagtg			

(2) INFORMATION FOR SEQ ID NO:3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3475:

Met	Ala	Gly	Ala	Leu	Val	Phe	Val	Ala	Val	Leu	Leu	Ala	Ala	Ser	Val
1				5				10					15		
Gly	Ala	Thr	Thr	Ala	Thr	Thr	Leu	Thr	Ile	His	Asn	Leu	Cys	Pro	His
			20				25						30		
Pro	Val	Trp	Pro	Leu	Val	Thr	Pro	Ser	Ser	Gly	Phe	Pro	Ser	Ile	Ser
			35				40					45			
Thr	Asn	Thr	Ala	Arg	Leu	Gly	Pro	Asn	Ala	Leu	Leu	Ser	Leu	Ser	Phe
			50			55				60					
Pro	Thr	Thr	Phe	Trp	Ala	Gly	Arg	Val	Ala	Ala	Arg	Thr	Gly	Cys	Asp

65	70	75	80
Ala Ala Ala Ser Gly Cys Trp Thr Gly Thr Pro Pro Ala Thr Val	85	90	95
Val Gln Val Thr Val His Asp Gly Gly Asn Leu Asp Gln Ala Thr Tyr	100	105	110
Ser Val Ser Leu Val Asp Gly Phe Asn Val Pro Met Val Val Ser Pro	115	120	125
Gln Ala Val Gly Gly Gly Gln Cys Pro Ala Leu Gly Cys Pro Ile Asn	130	135	140
Leu Asn Cys Asp Cys Pro Pro Gln Asn Arg Thr Ala Xaa Xaa Xaa Xaa	145	150	155
Val Pro Arg Pro Ala Gly Val Leu Gln Glu Pro Val Pro Xaa His Gln	165	170	175
Asp His Ala His Arg Arg Arg Ala Arg Asp Arg Arg Ala Ala Pro	180	185	190
Arg Gly Ser Ser Arg Ser Ser Ser Ala Arg Arg Pro Ser Ser His Ala	195	200	205
Ala Ala Lys Gln Ser Ala Pro Ser Ser Pro Thr Ala Arg Gln Ile Glu	210	215	220
Pro Ser Ser Ser Ile Arg Leu Gln Val Arg	225	230	

(2) INFORMATION FOR SEQ ID NO:3476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..893

(D) OTHER INFORMATION: / Ceres Seq. ID 1576998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3476:

aaaaaccacaa	gcacagcagc	aggtagacgc	ctgcagcaaa	accgcncccc	accgctwccc	60
cgtnmccccc	cccgaccgac	tgctccccct	ccccgcgccc	agcctcaagg	catcgccggc	120
gcgcgaacat	cgcctgaggaa	gccccgaccc	ctgcccggat	ccgatggcca	acagcaacct	180
cccgcgggcg	atcatcaagg	agactcagcg	gctgctcagc	gagccagcac	cggggatcag	240
cgcgctgcgc	tcggaGgaga	acatgcgccta	cttcaacggt	atgatccttG	ggggcgggcg	300
agtcgcctca	tgaaggtgga	gttttttaagc	ttgaactctt	ttacctgag	gaatatccaa	360
tggtgcctcc	aaaggttagg	tctctgacaa	agatctatca	tcccaacatc	gacaagcttg	420
gtaggatatg	cctcgacatt	ctcaaggaca	aatgagagcc	agcacttcag	attcgaaacg	480
ttcttttgag	tatacaggtc	ctactgagtg	cgccaaatcc	agacgacctc	cttcgggata	540
acattgcaaa	gcaactggaaa	gccaatgagc	tagaagctgt	tgaacacagc	aaggagtggg	600
ctgcctgata	tgcgagcggt	gcgatgagaac	gcagtgatgt	tcttgatgta	ataaccatc	660
atacttcagt	cctcatctat	tgccatttgt	ttgataaaaa	ataggctgga	gatatttgcc	720
atggaatgaa	gtctctacat	gactatcaat	ctgaattgtt	tggttgatca	cctgtggctg	780
gttcctctta	ccttggggga	cctttgacaa	atcagtatct	gtggtgaaac	ttgctgatac	840
tgtaatatat	ttgttacttc	atttagaaga	gctcttcaac	tgctcatatt	gtc	

(2) INFORMATION FOR SEQ ID NO:3477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1576999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3477:

Arg Asn Pro Ser Thr Ala Ala Gly Arg Pro Leu Gln Gln Asn Arg Xaa

1	5	10	15
Pro Pro Xaa Pro Arg Xaa Pro Pro Arg Pro Thr Ala Pro Pro Pro	20	25	30
His Gln Pro Gln Gly Ile Ala Gly Ala Ala Thr Ser Leu Arg Lys Pro	35	40	45
Ala Pro Leu Pro Gly Ser Asp Gly Gln Gln Gln Pro Pro Ala Ala Asp	50	55	60
His Gln Gly Asp Ser Ala Ala Ala Gln Arg Ala Ser Thr Gly Asp Gln	65	70	75
Arg Val Ala Leu Gly Gly Glu His Ala Leu Leu Gln Arg Tyr Asp Pro	85	90	95
Trp Gly Arg Arg Ser Arg Pro Met Lys Val Glu Phe Leu Ser Leu Asn	100	105	110
Ser Phe Tyr Leu Arg Asn Ile Gln Trp Leu Pro Gln Arg Leu Gly Leu	115	120	125

(2) INFORMATION FOR SEQ ID NO:3478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1577000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3478:

Met Ala Ala Pro Lys Val Arg Ser Leu Thr Lys Ile Tyr His Pro Asn	1	5	10	15
Ile Asp Lys Leu Gly Arg Ile Cys Leu Asp Ile Leu Lys Asp Lys Trp	20	25	30	
Ser Pro Ala Leu Gln Ile Arg Thr Val Leu Leu Ser Ile Gln Ala Leu	35	40	45	
Leu Ser Ala Pro Asn Pro Asp Asp Pro Leu Ser Asp Asn Ile Ala Lys	50	55	60	
His Trp Lys Ala Asn Glu Val Glu Ala Val Glu Thr Ala Lys Glu Trp	65	70	75	80
Thr Arg Leu Tyr Ala Ser Gly Ala	85			

(2) INFORMATION FOR SEQ ID NO:3479:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..636
(D) OTHER INFORMATION: / Ceres Seq. ID 1577001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3479:

accaccaggc accagcatag atctcgttct cgccactatt attctgcaca gcaacgcattc	60
aagccttcta gaaccattctc gccgcgcgca caccacaacc cgtcgaagcg aaGcaagcaa	120
tggcggagat cggatcgag gccctgcgcg ttgcgcgcgt tctggcgccg gtctccctct	180
cggtgccgcg cgcggccgag gcgcgcgcgc ccagcccgct cNtcgcCgc cgtcgcggck	240
tcgtgcacct tcgcgcgcgc cctcgtgcgc tcgcgcgcgc ccttctcttt cgcgcgcgtc	300
cgccactgag ccgatggggc ctgcgtgcgc caggctacct agcagtactt ccgcgcgtgc	360
tgccgcgcgc gcctagatct atttattgga gtgctatcca gtagtactag tagtagtgag	420
atttcttcgg tctcgtcgtg tcgtcgtcgc attttggtgc gatctggttt ccttggtgca	480

gggggggttt ctataccatg tcgcggtgtc Gggttggtg atctcacc cccttgtaga 540
tagtactctg ctatctcgtc gtgacgtga gtggtgattc tgtctggtg atatttgcta 600
ctgataattg tccatttga gatatgcgtt gctgct

(2) INFORMATION FOR SEQ ID NO:3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1577002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3480:

Thr Thr Arg His Gln His Arg Ser Arg Ser Arg His Tyr Tyr Ser Ala
1 5 10 15
Gln Gln Arg Ile Lys Pro Ser Arg Thr Ile Ser Pro Pro Pro His His
20 25 30
Asn Pro Ser Lys Arg Ser Lys Gln Trp Pro Glu Ser Asp Arg Arg Pro
35 40 45
Ser Pro Leu Pro Pro Phe Trp Arg Pro Ser Pro Ser Arg Trp Pro Pro
50 55 60
Arg Pro Arg Arg Arg Arg Pro Ala Pro Xaa Ser Ala Ala Val Ala Xaa
65 70 75 80
Ser Ser Pro Phe Ala Ala Ala Leu Val Ala Ser Ala Ala Ala Phe Leu
85 90 95
Phe Ala Ala Val Arg His
100

(2) INFORMATION FOR SEQ ID NO:3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1577003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3481:

Pro Pro Gly Thr Ser Ile Asp Leu Val Leu Ala Thr Ile Ile Leu His
1 5 10 15
Ser Asn Ala Ser Ser Leu Leu Glu Pro Ser Arg Arg Arg His Thr Thr
20 25 30
Thr Arg Arg Ser Glu Ala Ser Asn Gly Arg Ser Arg Ile Glu Gly Pro
35 40 45
Arg Arg Cys Arg Arg Ser Gly Gly Arg Leu Pro Leu Gly Gly Arg Arg
50 55 60
Gly Arg Gly Ala Gly Ala Gln Pro Arg Xaa Pro Pro Ser Arg Xaa
65 70 75 80
Arg Arg Pro Ser Pro Arg Pro Ser Ser Pro Pro Pro Pro Ser Ser
85 90 95
Ser Pro Pro Ser Ala Thr Glu Pro Met Gly Pro Arg Ala Cys Arg Leu
100 105 110
Pro Ser Ser Thr Ser Ala Ala Ala Ala Ala Ala
115 120

(2) INFORMATION FOR SEQ ID NO:3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1577004
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3482:
Met Ala Gly Val Gly Ser Lys Ala Leu Ala Val Ala Ala Val Leu Ala
1 5 10 15
Ala Val Ser Leu Ser Val Ala Ala Ala Glu Ala Pro Ala Pro Ser
20 25 30
Pro Val Xaa Arg Arg Arg Arg Gly Xaa Val Ala Leu Arg Arg Gly Pro
35 40 45
Arg Arg Leu Arg Arg Arg Leu Pro Leu Arg Arg Arg Pro Pro Leu Ser
50 55 60
Arg Trp Gly Leu Val Pro Ala Gly Tyr Leu Ala Val Leu Pro Pro Leu
65 70 75 80
Leu Pro Pro Pro Pro Arg Ser Ile Tyr Trp Ser Ala Ile Gln
85 90

(2) INFORMATION FOR SEQ ID NO:3483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..722
(D) OTHER INFORMATION: / Ceres Seq. ID 1577048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3483:

ccggaactcg gtaccatccg cggmcgcagc catccgcttg ttctcttcgg ttccagttctc 60
gagttttccag gatgaaggta atagctgcct atctgcttgc tgttctgggt ggaacacctt 120
ccccgactgc tgatgatgtt aagagcattc tggaaatcagt tgggtgctgaa gctgatgaag 180
aaaaactaga gtctctgctc acagaactca aagacaagga cataacagaa gtgattgcag 240
ctggaaggga aaggttatcc tctgtgcctt caggtgggtg tgcaattgac atgggagctc 300
cagcagctgt agctggcggt gccgcaGcac ctgctGgaag aggcacaaagaa ggaagaaaaa 360
gttgaagaga aggaagagtc tgatgragat atgggtttca gcttgcttga ttaaaacagc 420
actacaggtt tacagtttct tcgcgaatgg ttctcataata ttggccggtt tccacaaaaa 480
aagattgtcA atagctacta cgtacttatg ctattctgca tgtgatgtac gagtgtgcatt 540
cttcaagaat ctttaagtgt aatggtcggt ggtccataaa taatattggt aacaatgtaa 600
attgtatgac ctgtacgtac ttgggtatcg cgacatctca gtgtgcatct tcaaggatca 660
taagttgaat gttatcatta aggtcagttt ggttcagata aatataattg ctagtattag 720
cc

(2) INFORMATION FOR SEQ ID NO:3484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1577049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3484:

Gly Asn Trp Tyr His Pro Pro Xaa Gln Pro Ser Ala Cys Ser Leu Arg
1 5 10 15
Phe Ser Ser Arg Val Ser Arg Met Lys Val Ile Ala Ala Tyr Leu Leu
20 25 30

Ala Val Leu Gly Gly Asn Thr Ser Pro Thr Ala Asp Asp Val Lys Ser
35 40 45
Ile Leu Glu Ser Val Gly Ala Glu Ala Asp Glu Glu Lys Leu Glu Phe
50 55 60
Leu Leu Thr Glu Leu Lys Asp Lys Asp Ile Thr Glu Val Ile Ala Ala
65 70 75 80
Gly Arg Glu Arg Leu Ser Ser Val Pro Ser Gly Gly Ala Ile Asp
85 90 95
Met Gly Ala Pro Ala Ala Val Ala Gly Gly Ala Ala Pro Ala Gly
100 105 110
Arg Gly Lys Glu Gly Arg Lys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:3485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3485:

Met Lys Val Ile Ala Ala Tyr Leu Leu Ala Val Leu Gly Gly Asn Thr
1 5 10 15
Ser Pro Thr Ala Asp Asp Val Lys Ser Ile Leu Glu Ser Val Gly Ala
20 25 30
Glu Ala Asp Glu Glu Lys Leu Glu Phe Leu Leu Thr Glu Leu Lys Asp
35 40 45
Lys Asp Ile Thr Glu Val Ile Ala Ala Gly Arg Glu Arg Leu Ser Ser
50 55 60
Val Pro Ser Gly Gly Gly Ala Ile Asp Met Gly Ala Pro Ala Ala Val
65 70 75 80
Ala Gly Gly Gly Ala Ala Pro Ala Gly Arg Gly Lys Glu Gly Arg Lys
85 90 95
Gly

(2) INFORMATION FOR SEQ ID NO:3486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..831
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3486:

acccctcctc	ttcctctcct	tccctcccaa	cctcggtcac	cagtccatcg	atcctogaat	60
cctcgctcgt	cactgcactg	caaggatcat	acgccatgaa	gtgagcagatg	ctttctcttg	120
gctcgtcttc	ctcctcctcc	ggcaagaaga	ggaagggggtc	aaagaccggc	ggctcctctt	180
ctctcgtctc	caccgcgtcg	tcgtctcctg	cgcacgagtg	cgcatcgccg	tcagcccgta	240
cgacgacgcc	acgcaccgtc	ctccaatccc	agccgtcccg	ccccaaccgg	aaGctccgg	300
cggNtagtag	ccgcgcgcgt	gaacgcggag	gaacctggagg	tggcGctcg	ccgggtggte	360
cgacgcgagg	acgagctggc	cgcggtgctg	gccgaggcgg	aggccNgccG	Ggctcgcgcc	420
cgagcaggcc	cgctccgcGg	agggcggagg	cgaggccgag	ctCgcgcagc	cgctcgcggg	480
gttcgacgcg	gaacgcgcag	gcaggatctc	cgcgaggagg	tcgcgcgcgt	gtcgcgcggc	540
ctcggcgacg	ccgcctgctc	cgtcgaggac	tgcgcgcgca	tgatcgcccg	cgtcgacggc	600
gatggcgacg	gcttcgtctg	cttccacgac	ttctcgcgca	tgatgatgca	ggggcgctga	660

ttctggcgctg gtcgtgcctg gctgggttgt gtcggtctcc gctgttttct tctgttgcaa 720
aatctctcta cctgtatgtg gacctgtttt ttccggtgtca tctactcgta tcatctccgt 780
cgtgcgagat gaatgaaccc aaaagagatc tatatatatt catcttttcc g

(2) INFORMATION FOR SEQ ID NO:3487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1577059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3487:

Pro Ser Ser Ser Ser Pro Ser Leu Pro Thr Ser Val Thr Ser Pro Ser
1 5 10 15
Ile Leu Glu Ser Leu Ala Cys Thr Ala Leu Gln Gly Thr Tyr Ala Met
20 25 30
Lys Leu Ser Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Gly Lys
35 40 45
Lys Arg Lys Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser Thr
50 55 60
Ala Ser Ser Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val Thr
65 70 75 80
Thr Thr Pro Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn Pro
85 90 95
Lys Pro Pro Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro Gly
100 105 110
Gly Gly Ala Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg Gly
115 120 125
Ala Gly Arg Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro Arg
130 135 140
Pro Arg Arg Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg Cys
145 150 155 160
Ser Thr Arg Thr Ala Thr Ala Gly Ser Pro Arg Arg Xaa Pro Arg Arg
165 170 175
Ala Arg Arg Ala Arg Arg Arg Arg Leu Leu Arg Arg Gly Leu Pro Pro
180 185 190
His Asp Arg Pro Arg Arg Arg Arg Trp Arg Arg Leu Arg Leu Leu Pro
195 200 205
Arg Leu Leu Ala His Asp Asp Ala Gly Gly Val Ile Leu Ala Ser Ser
210 215 220
Cys Leu Ala Gly Leu Cys Arg Ser Pro Arg Val Ser Ser Val Ala Lys
225 230 235 240
Ser Leu Tyr Leu Tyr Val Asp Leu Phe Phe Arg Cys His Leu Leu Val
245 250 255
Ser Ser Pro Ser Cys Glu Met Asn Glu Pro Lys Arg Asp Leu Tyr Ile
260 265 270
Phe Ile Phe Ser
275

(2) INFORMATION FOR SEQ ID NO:3488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1577060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3488:

Met	Lys	Leu	Ser	Met	Pro	Phe	Phe	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Lys	Lys	Lys	Lys
1				5				10							15				
Lys	Lys	Arg	Lys	Gly	Ser	Lys	Thr	Gly	Gly	Ser	Ser	Ser	Ser	Phe	Val	Ser			
			20					25						30					
Thr	Ala	Ser	Ser	Ser	Ser	Ser	Asp	Glu	Cys	Ala	Ser	Pro	Ser	Ala	Val				
			35				40					45							
Thr	Thr	Thr	Pro	Arg	Thr	Val	Leu	Gln	Ser	Gln	Pro	Ser	Ala	Pro	Asn				
			50			55				60									
Pro	Lys	Pro	Pro	Ala	Xaa	Ser	Ser	Arg	Arg	Arg	Asp	Ala	Gly	Gly	Pro				
65				70						75				80					
Gly	Gly	Gly	Ala	Ala	Pro	Gly	Gly	Pro	Gln	Arg	Gly	Arg	Ala	Gly	Arg				
			85					90					95						
Gly	Ala	Gly	Arg	Gly	Gly	Gly	Xaa	Pro	Gly	Ser	Arg	Pro	Ser	Arg	Pro				
			100				105					110							
Arg	Pro	Arg	Arg	Arg	Arg	Thr	Arg	Pro	Ser	Ser	Ala	Thr	Arg	Ser	Arg				
			115			120					125								
Cys	Ser	Thr	Arg	Thr	Ala	Thr	Ala	Gly	Ser	Pro	Arg	Arg	Xaa	Pro	Arg				
			130			135				140									
Arg	Ala	Arg	Arg	Ala	Arg	Arg	Arg	Arg	Leu	Leu	Arg	Arg	Gly	Leu	Pro				
145				150					155					160					
Pro	His	Asp	Arg	Pro	Arg	Arg	Arg	Arg	Trp	Arg	Arg	Leu	Arg	Leu	Leu				
			165					170					175						
Pro	Arg	Leu	Leu	Ala	His	Asp	Asp	Ala	Gly	Gly	Val	Ile	Leu	Ala	Ser				
			180			185						190							
Ser	Cys	Leu	Ala	Gly	Leu	Cys	Arg	Ser	Pro	Arg	Val	Ser	Ser	Val	Ala				
			195			200					205								
Lys	Ser	Leu	Tyr	Leu	Tyr	Val	Asp	Leu	Phe	Phe	Arg	Cys	His	Leu	Leu				
			210			215					220								
Val	Ser	Ser	Pro	Ser	Cys	Glu	Met	Asn	Glu	Pro	Lys	Arg	Asp	Leu	Tyr				
225				230						235				240					
Ile	Phe	Ile	Phe	Ser															
				245															

(2) INFORMATION FOR SEQ ID NO:3489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1577061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3489:

Met	Pro	Phe	Phe	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Lys	Lys	Arg	Lys
1				5						10				15	
Gly	Ser	Lys	Thr	Gly	Gly	Ser	Ser	Ser	Phe	Val	Ser	Thr	Ala	Ser	Ser
			20					25					30		
Ser	Ser	Ser	Asp	Glu	Cys	Ala	Ser	Pro	Ser	Ala	Val	Thr	Thr	Thr	Pro
			35			40				45					
Arg	Thr	Val	Leu	Gln	Ser	Gln	Pro	Ser	Ala	Pro	Asn	Pro	Lys	Pro	Pro
			50			55				60					
Ala	Xaa	Ser	Ser	Arg	Arg	Arg	Asp	Ala	Gly	Gly	Pro	Gly	Gly	Gly	Ala
65				70						75				80	
Ala	Pro	Gly	Gly	Pro	Gln	Arg	Gly	Arg	Ala	Gly	Arg	Gly	Ala	Gly	Arg
			85					90				95			
Gly	Gly	Gly	Xaa	Pro	Gly	Ser	Arg	Pro	Ser	Arg	Pro	Arg	Pro	Arg	Arg
			100					105				110			
Arg	Arg	Thr	Arg	Pro	Ser	Ser	Ala	Thr	Arg	Ser	Arg	Cys	Ser	Thr	Arg

				5					10					15	
Asp	Leu	Asp	Asn	Pro	Pro	Pro	Arg	Tyr	Glu	Thr	Gly	Xaa	Gly	His	Gln
			20					25					30		
His	Ser	Gly	Asp	Pro	Gly	Gly	Arg	Pro	Ala	Pro	Leu	Gln	Gly	Ala	Ser

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1577065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3493:

Met	Pro	Gln	Pro	Ser	Ser	Tyr	Ala	Val	Leu	Pro	Arg	Arg	Asp	Gly	Glu	
1			5					10					15			
Leu	Val	Ser	Ala	Glu	Glu	Leu	Leu	Leu	Ser	Ala	Ala	Ala	Gln	Leu	Arg	
			20					25					30			
Pro	Trp	Trp	Thr	Thr	Ala	Cys	Thr	Ala	Pro	Xaa	Phe	Pro	Asp	Ala	Ser	
		35				40					45					
Asn	Leu	Pro	Phe	Leu	Glu	Thr	Leu	Arg	Leu	Arg	Ser	Val	Leu	Cys	Leu	
		50				55					60					
Cys	Pro	Glu	Pro	Tyr	Pro	Glu	Ala	Asn	Leu	Glu	Phe	Leu	Arg	Ala	His	
		65				70					75				80	
Gly	Ile	Lys	Leu	Phe	Gln	Phe	Gly	Ile	Asp	Gly	Ser	Lys	Glu	Pro	Phe	
			85						90					95		
Val	Asn	Ile	Pro	Glu	Asp	Arg	Ile	Arg	Glu	Ala	Leu	Glu	Val	Ile	Leu	
			100					105					110			
Asp	Ala	Ser	Asn	His	Pro	Val	Leu	Ile	His	Cys	Lys	Arg	Gly	Lys	His	
			115					120					125			
Arg	Thr	Gly	Cys	Val	Val	Gly	Cys	Phe	Arg	Lys	Leu	Gln	Arg	Trp	Cys	
		130				135					140					
Leu	Thr	Ser	Ile	Phe	Asp	Glu	Tyr	Gln	Arg	Phe	Ala	Ala	Ala	Lys	Thr	
		145				150				155					160	
Arg	Val	Ser	Asp	Tyr	Gly	Ser	Trp	Ser	Tyr	Leu	Met	Tyr	Arg	Ala		
			165					170						175		

(2) INFORMATION FOR SEQ ID NO:3494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..630

(D) OTHER INFORMATION: / Ceres Seq. ID 1577073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3494:

aaaaattaaag	gaaaaacgggtg	gactagaaac	ttccaaatcg	aacggcacac	aaaaatcaca	60
acccggaagaag	ggaccagcag	cgcaaaaggtg	agcgagcttt	ccttcggaac	tctctcgtgc	120
tcacctcAat	ccgtccgaca	gatccacacg	aatcctctga	ttcagagcag	gggtttggca	180
ttgatccagac	gcctgccatg	gctgatcagt	tcgaggattc	ggcgaacaat	gtgatcattg	240
aggaggtgaa	caagggcctg	aaccaggaa	tggtgtgtct	gcttgtgtgt	gcaagcttcc	300
tgctgatctt	ctttgtgggg	aactatgcgc	tgatgtgtga	tgcgacagaag	acgctccocg	360
caaaagaagaa	gaagccgggtg	tcgaagaaga	agctgaagaa	ggaaaaagctg	aagcaggggg	420
tctctgcgcc	gggagagtaa	acggccatgc	tgccgatcct	cccgtccaga	gtctctattc	480
acatgattat	tagagaaaaa	aattatatat	atataccaga	tggagccgta	gtgtDtgag	540
tAactttgtt	ctgtagatgc	tctgtcttta	atggtacatc	tgtattggag	actttgagac	600
ctgttttcag	caactgatga	atcttagccc				

(2) INFORMATION FOR SEQ ID NO:3495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3495:

Lys	Ile	Lys	Gly	Lys	Arg	Trp	Thr	Arg	Asn	Phe	Gln	Ile	Glu	Arg	His
1				5					10				15		
Thr	Lys	Ile	Thr	Thr	Arg	Lys	Gly	Thr	Ser	Ser	Ala	Lys	Val	Ser	Glu
			20				25						30		
Leu	Ser	Phe	Gly	Thr	Leu	Ser	Cys	Ser	Pro	Gln	Ser	Val	Arg	Gln	Ile
		35				40				45					
His	Thr	Asn	Pro	Leu	Ile	Gln	Ser	Arg	Val	Leu	Ala	Leu	Ile	Arg	Arg
	50				55				60						
Leu	Pro	Trp	Leu	Ile	Ser	Ser	Arg	Ile	Arg	Arg	Thr	Met			
65			70						75						

(2) INFORMATION FOR SEQ ID NO:3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1577075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3496:

Met	Ala	Asp	Gln	Phe	Glu	Asp	Ser	Ala	Asn	Val	Ile	Ile	Glu	Glu	
1				5					10				15		
Val	Asn	Lys	Gly	Leu	Asn	Pro	Gly	Met	Val	Val	Leu	Leu	Val	Val	Ala
			20				25						30		
Ser	Phe	Leu	Leu	Ile	Phe	Phe	Val	Gly	Asn	Tyr	Ala	Leu	Tyr	Val	Tyr
		35				40				45					
Ala	Gln	Lys	Thr	Leu	Pro	Pro	Lys	Lys	Lys	Lys	Pro	Val	Ser	Lys	Lys
	50				55				60						
Lys	Leu	Lys	Lys	Glu	Lys	Leu	Lys	Gln	Gly	Val	Ser	Ala	Pro	Gly	Glu
65			70						75					80	

(2) INFORMATION FOR SEQ ID NO:3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1577076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3497:

Met	Leu	Pro	Ile	Leu	Pro	Ser	Arg	Ala	Pro	Ile	His	Met	Ile	Ile	Arg
1				5					10				15		
Glu	Lys	Asn	Tyr	Ile	Tyr	Ile	Pro	Asp	Gly	Ala	Val	Val	Xaa	Gly	Val
			20				25						30		
Thr	Leu	Phe	Cys	Arg	Cys	Ser	Val	Phe	Asn	Gly	Thr	Ser	Val	Leu	Glu
		35				40				45					
Thr	Leu	Arg	Pro	Cys	Phe	Ser	Asn								
	50				55										

(2) INFORMATION FOR SEQ ID NO:3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..885
(D) OTHER INFORMATION: / Ceres Seq. ID 1577089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3498:

atccgagtc	acccaactaa	tcacgcccaa	tcagaacaga	ctcggctgct	tcaccactcc	60
actcgccgca	ggcgccggcg	gcccgcgagg	ggatcgggag	aagatgttct	tcacacatcgt	120
gctggagcgg	aacatgcagc	tgacccacac	acacttcggg	ccgcacctcc	gcgacaagct	180
cgtttccaag	ctcatcaagg	acgtcgaggg	cacctgcagc	ggcgccgacg	gggttcgtgt	240
ggcgatcacg	gggtggagg	acatcgccaa	ggggtcatc	cggaaggca	cgggatacgt	300
caccttcccc	gycaagtacc	agtcggttgt	ctttagacc	ttcaaggcg	agatccctga	360
agctgtgtc	accatggtga	acaagatggg	cttctttg	gaggtgggc	cggtgcagat	420
cttcgtgtcc	aaccatttga	ttccagacga	tatggagttc	caatcaRgga	gatgtgccga	480
actacacaa	ttctgatgga	toggtgaaaa	ttcaaaaa	gagtgaggtg	cggtgaaga	540
ttattgggta	ctcgtgtcga	tgctacagaa	attttttgca	ttggcacAat	Aaaaggatga	600
tttttcgggt	gktatcacgg	atcctgtgtc	gscagtgtaa	atggcttaag	aagcgagatt	660
gtactccatt	gttctgactt	ctgagtacta	tcgcagacgt	gtgtaatcgc	tggtccggtta	720
aaactgcaat	ggctgtactg	actcggaac	ttgttgagaa	tgatgtgact	aggacctgtg	780
ttagggcctg	tttggttctt	tagtatggcc	ctgattggca	caactgctgt	ttattgaaaa	840
aacagcttat	ctgataagct	ggtgaaaaat	agcttctgct	tgttg		

(2) INFORMATION FOR SEQ ID NO:3499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1577090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3499:

Ser	Glu	Ser	Thr	Gln	Leu	Ile	Thr	Pro	Asn	Gln	Asn	Arg	Leu	Gly	Arg	
1					5				10					15		
Phe	Thr	Thr	Pro	Leu	Ala	Ala	Gly	Ala	Gly	Arg	Arg	Arg	Gly	Asp	Arg	
			20					25					30			
Ser	Lys	Met	Phe	Phe	His	Ile	Val	Leu	Glu	Arg	Asn	Met	Gln	Leu	His	
			35				40					45				
Pro	Arg	His	Phe	Gly	Pro	His	Leu	Arg	Asp	Lys	Leu	Val	Ser	Lys	Leu	
			50			55					60					
Ile	Lys	Asp	Val	Glu	Gly	Thr	Cys	Ser	Gly	Arg	His	Gly	Phe	Val	Val	
65					70					75				80		
Ala	Ile	Thr	Gly	Val	Glu	Asp	Ile	Gly	Lys	Gly	Leu	Ile	Arg	Glu	Gly	
			85						90					95		
Thr	Gly	Tyr	Val	Thr	Phe	Pro	Xaa	Lys	Tyr	Gln	Cys	Val	Val	Phe	Arg	
			100					105					110			
Pro	Phe	Lys	Gly	Glu	Ile	Leu	Glu	Ala	Val	Val	Thr	Met	Val	Asn	Lys	
			115				120					125				
Met	Gly	Phe	Phe	Ala	Glu	Ala	Gly	Pro	Val	Gln	Ile	Phe	Val	Ser	Asn	
			130			135					140					
His	Leu	Ile	Pro	Asp	Asp	Met	Glu	Phe	Gln	Ser	Xaa	Arg	Cys	Ala	Glu	
145					150				155					160		
Leu	His	Asn	Phe													

(2) INFORMATION FOR SEQ ID NO:3500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1577091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3500:

Met	Phe	Phe	His	Ile	Val	Leu	Glu	Arg	Asn	Met	Gln	Leu	His	Pro	Arg
1			5					10						15	
His	Phe	Gly	Pro	His	Leu	Arg	Asp	Lys	Leu	Val	Ser	Lys	Leu	Ile	Lys
		20					25					30			
Asp	Val	Glu	Gly	Thr	Cys	Ser	Gly	Arg	His	Gly	Phe	Val	Val	Ala	Ile
		35					40				45				
Thr	Gly	Val	Glu	Asp	Ile	Gly	Lys	Gly	Leu	Ile	Arg	Glu	Gly	Thr	Gly
		50				55					60				
Tyr	Val	Thr	Phe	Pro	Xaa	Lys	Tyr	Gln	Cys	Val	Val	Phe	Arg	Pro	Phe
65			70				75							80	
Lys	Gly	Glu	Ile	Leu	Glu	Ala	Val	Val	Thr	Met	Val	Asn	Lys	Met	Gly
			85				90					95			
Phe	Phe	Ala	Glu	Ala	Gly	Pro	Val	Gln	Ile	Phe	Val	Ser	Asn	His	Leu
		100					105					110			
Ile	Pro	Asp	Asp	Met	Glu	Phe	Gln	Ser	Xaa	Arg	Cys	Ala	Glu	Leu	His
		115					120					125			
Asn	Phe														

(2) INFORMATION FOR SEQ ID NO:3501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1577092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3501:

Met	Gln	Leu	His	Pro	Arg	His	Phe	Gly	Pro	His	Leu	Arg	Asp	Lys	Leu
1			5					10					15		
Val	Ser	Lys	Leu	Ile	Lys	Asp	Val	Glu	Gly	Thr	Cys	Ser	Gly	Arg	His
		20					25					30			
Gly	Phe	Val	Val	Ala	Ile	Thr	Gly	Val	Glu	Asp	Ile	Gly	Lys	Gly	Leu
		35					40				45				
Ile	Arg	Glu	Gly	Thr	Gly	Tyr	Val	Thr	Phe	Pro	Xaa	Lys	Tyr	Gln	Cys
		50				55					60				
Val	Val	Phe	Arg	Pro	Phe	Lys	Gly	Glu	Ile	Leu	Glu	Ala	Val	Val	Thr
65			70				75							80	
Met	Val	Asn	Lys	Met	Gly	Phe	Phe	Ala	Glu	Ala	Gly	Pro	Val	Gln	Ile
			85				90					95			
Phe	Val	Ser	Asn	His	Leu	Ile	Pro	Asp	Asp	Met	Glu	Phe	Gln	Ser	Xaa
		100					105					110			
Arg	Cys	Ala	Glu	Leu	His	Asn	Phe								
		115				120									

(2) INFORMATION FOR SEQ ID NO:3502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..776

(D) OTHER INFORMATION: / Ceres Seq. ID 1577122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3502:

gggcaactcg	aagaagccgc	gtgcgttatc	ctttgagcag	tttgggcgct	gagcaagtcc	60
agtgagarar	ggagarcgac	gagaggatgg	ctgggatggc	atcgctgcag	ggcgccatGg	120
cgctgctctc	catctccGcg	ctaggcgcg	cgacggcgag	cagcagcagc	ttctggggca	180
acgggctcgc	cacctactcc	gcgcgcgagc	ctggggtaag	gtttatggtc	aagatatgcc	240
caattgaaat	gagacttaag	agatggggagc	gaaagaagtg	taaaccaaac	agtcttctctg	300
tgctgcacaa	gatgcactgt	aggtatcgagg	acacgggtaca	ggttattgca	ggcgtgaga	360
aaggaaaggt	tggagaagtc	acacgccttt	tcaagcacaa	cagcagcggtg	atcgtgaaggt	420
acctgaactt	gaagtccaag	cacaagaaag	gcacagacga	tgaaccgggt	gaaatcgta	480
tgattgaagg	ccccattcat	agctcaaatg	tgatgctcta	ctctaaggag	aagagtggtg	540
taagcagggt	tggccacaaa	ttcctggagg	acgggaccaa	ggctccgatac	ctggtcaga	600
ccgggtgaagt	aatgcacagt	gttgagaagt	gggtaaaggt	ttttaaggaa	ggaaattcgg	660
agtaacagtt	ttagcatgaa	aacctgcaca	atgctctgaa	cgctrmtgcg	tcttgcatgt	720
tgaattgagc	ctgtttatcc	ctctatgttg	ttatttacgc	cagtttttcc	ccctgt	

(2) INFORMATION FOR SEQ ID NO:3503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1577123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3503:

Met	Ala	Gly	Met	Ala	Ser	Leu	Gln	Gly	Ala	Met	Ala	Ser	Leu	Ser	Ile	
1			5					10						15		
Ser	Ala	Leu	Gly	Ala	Ala	Thr	Ala	Ser	Ser	Ser	Phe	Trp	Gly	Asn		
		20					25					30				
Arg	Leu	Ala	Thr	Tyr	Ser	Ala	Pro	Gln	Pro	Gly	Val	Arg	Phe	Met	Val	
		35					40				45					
Lys	Ile	Cys	Pro	Ile	Glu	Met	Arg	Leu	Lys	Arg	Trp	Glu	Arg	Lys	Lys	
		50				55					60					
Cys	Lys	Pro	Asn	Ser	Leu	Pro	Val	Leu	His	Lys	Met	His	Val	Arg	Ile	
		65			70				75					80		
Gly	Asp	Thr	Val	Gln	Val	Ile	Ala	Gly	Arg	Glu	Lys	Gly	Lys	Val	Gly	
			85					90					95			
Glu	Val	Thr	Arg	Leu	Phe	Lys	His	Asn	Ser	Thr	Val	Ile	Val	Lys	Asp	
			100					105				110				
Leu	Asn	Leu	Lys	Ser	Lys	His	Lys	Lys	Gly	Thr	Asp	Asp	Glu	Pro	Gly	
			115				120					125				
Glu	Ile	Val	Met	Ile	Glu	Gly	Pro	Ile	His	Ser	Ser	Asn	Val	Met	Leu	
			130			135					140					
Tyr	Ser	Lys	Glu	Lys	Ser	Val	Val	Ser	Arg	Val	Gly	His	Lys	Phe	Leu	
			145			150				155				160		
Glu	Asp	Gly	Thr	Lys	Val	Arg	Tyr	Leu	Val	Lys	Thr	Gly	Glu	Val	Ile	
			165					170				175				
Asp	Ser	Val	Glu	Lys	Trp	Val	Lys	Val	Phe	Lys	Glu	Gly	Asn	Ser	Glu	
			180				185						190			

(2) INFORMATION FOR SEQ ID NO:3504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1577124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3504:

```
Met Ala Ser Leu Gln Gly Ala Met Ala Ser Leu Ser Ile Ser Ala Leu
1      5      10      15
Gly Ala Ala Thr Ala Ser Ser Ser Ser Phe Trp Gly Asn Arg Leu Ala
20     25
Thr Tyr Ser Ala Pro Gln Pro Gly Val Arg Phe Met Val Lys Ile Cys
35     40     45
Pro Ile Glu Met Arg Leu Lys Arg Trp Glu Arg Lys Lys Cys Lys Pro
50     55     60
Asn Ser Leu Pro Val Leu His Lys Met His Val Arg Ile Gly Asp Thr
65     70     75     80
Val Gln Val Ile Ala Gly Arg Glu Lys Gly Lys Val Gly Glu Val Thr
85     90     95
Arg Leu Phe Lys His Asn Ser Thr Val Ile Val Lys Asp Leu Asn Leu
100    105    110
Lys Ser Lys His Lys Lys Gly Thr Asp Asp Glu Pro Gly Glu Ile Val
115    120    125
Met Ile Glu Gly Pro Ile His Ser Ser Asn Val Met Leu Tyr Ser Lys
130    135    140
Glu Lys Ser Val Val Ser Arg Val Gly His Lys Phe Leu Glu Asp Gly
145    150    155    160
Thr Lys Val Arg Tyr Leu Val Lys Thr Gly Glu Val Ile Asp Ser Val
165    170    175
Glu Lys Trp Val Lys Val Phe Lys Glu Gly Asn Ser Glu
180    185
```

(2) INFORMATION FOR SEQ ID NO:3505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1577125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3505:

```
Met Ala Ser Leu Ser Ile Ser Ala Leu Gly Ala Ala Thr Ala Ser Ser
1      5      10      15
Ser Ser Phe Trp Gly Asn Arg Leu Ala Thr Tyr Ser Ala Pro Gln Pro
20     25     30
Gly Val Arg Phe Met Val Lys Ile Cys Pro Ile Glu Met Arg Leu Lys
35     40     45
Arg Trp Glu Arg Lys Lys Cys Lys Pro Asn Ser Leu Pro Val Leu His
50     55     60
Lys Met His Val Arg Ile Gly Asp Thr Val Gln Val Ile Ala Gly Arg
65     70     75     80
Glu Lys Gly Lys Val Gly Glu Val Thr Arg Leu Phe Lys His Asn Ser
85     90     95
Thr Val Ile Val Lys Asp Leu Asn Leu Lys Ser Lys His Lys Lys Gly
100    105    110
Thr Asp Asp Glu Pro Gly Glu Ile Val Met Ile Glu Gly Pro Ile His
115    120    125
Ser Ser Asn Val Met Leu Tyr Ser Lys Glu Lys Ser Val Val Ser Arg
130    135    140
Val Gly His Lys Phe Leu Glu Asp Gly Thr Lys Val Arg Tyr Leu Val
```

145 150 155 160
Lys Thr Gly Glu Val Ile Asp Ser Val Glu Lys Trp Val Lys Val Phe
165 170 175
Lys Glu Gly Asn Ser Glu
180

(2) INFORMATION FOR SEQ ID NO:3506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..814

(D) OTHER INFORMATION: / Ceres Seq. ID 1577130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3506:

agtgtaaacc	agccccacct	cctccccgtc	tcctctccct	ccccatgcgc	tgttttgttc	60
tgtattgggt	tgtgcgcggt	ggacaggacg	cctcctgcgc	cgaccgttcc	gttcgtgttt	120
gtgcctgcct	gtgccttcgg	ttgttctctc	gagcgacggc	gagtcggcga	ccgaggggga	180
ccacagacgc	attagctggg	tgaactcttt	caaaaggggc	aggtgcgcta	gtttgaatgg	240
ctgtacaaaa	gcttcaggcc	ttttggaacc	accctgcgtg	ccccaaaaac	attcattttc	300
ggcgcccaac	attcaaatgg	ggatatcgca	ttgccaacat	agcgcacttt	gcaaaagccgc	360
ctgaaaagat	attttaccct	cagcaagtgt	ctgtgtcatg	cactggaatc	atttggtcac	420
ggtaacagct	ggttatcaca	cogaaaaact	ggaacctttt	cagtgttaac	gttgcaatgg	480
cgggtacagg	ctgtgtacag	ctttcacgga	agattagsga	agattacntt	gtctgggtgg	540
aaggatgNct	gNctccacaa	ctgNcaagaa	tagataatga	caacacacaa	agaataaactg	600
attgagaagt	cgncggcct	agggatctta	ctcttgattt	ttctgggnca	ggncaggatg	660
atgtctcgat	ccaggacggg	tcatgtttgt	tttctgttgc	ttctgaaatc	atgagncagg	720
ttaatgtgaa	aattctctgc	caaaaaaaga	agcccatgaa	gtaatatatt	gtgcattttt	780
gtgggaaaaa	agtcatgncc	aggacatgat	tcgt			

(2) INFORMATION FOR SEQ ID NO:3507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1577131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3507:

Ser	Val	Asn	Gln	Pro	Thr	Leu	Leu	Pro	Val	Ser	Ser	Pro	Ser	Pro	Cys
1		5						10					15		
Ala	Val	Leu	Phe	Cys	Ile	Gly	Leu	Cys	Ala	Gly	Asp	Arg	Thr	Pro	Pro
		20						25					30		
Ala	Pro	Thr	Val	Pro	Phe	Val	Phe	Val	Pro	Ala	Cys	Ala	Phe	Gly	Cys
		35						40					45		
Ser	Ser	Glu	Arg	Arg	Arg	Val	Gly	Asp	Arg	Gly	Gly	Pro	Gln	Thr	His
		50				55						60			

(2) INFORMATION FOR SEQ ID NO:3508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1577132
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3508:
Met Ala Ala Thr Lys Leu Gln Ala Phe Trp Asn His Pro Ala Gly Pro
1 5 10 15
Lys Thr Ile His Phe Trp Ala Pro Thr Phe Lys Trp Gly Ile Ser Ile
20 25 30
Ala Asn Ile Ala Asp Phe Ala Lys Pro Pro Glu Lys Ile Ser Tyr Pro
35 40 45
Gln Gln Val Ala Val Ala Cys Thr Gly Ile Ile Trp Ser Arg Tyr Ser
50 55 60
Leu Val Ile Thr Pro Lys Asn Trp Asn Leu Phe Ser Val Asn Val Ala
65 70 75 80
Met Ala Gly Thr Gly Leu Tyr Gln Leu Ser Arg Lys Ile Xaa Gln Asp
85 90 95
Tyr Xaa Val Trp
100

(2) INFORMATION FOR SEQ ID NO:3509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..764
(D) OTHER INFORMATION: / Ceres Seq. ID 1577133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3509:

gaaataccgc cgcgtacagc ctactgctgg acatctaagg gccacactga aaaaaccctt 60
gcgcgcgtga gctgagtccc ctcccttct ctcgtcgccct ccgcctccgc cttcagttta 120
gcctccaagg agggggcgcc cgcggggtat tctgtccgtc gttgaggata gagagtcact 180
tgacacgggg gagcggagat gaagccgggt gtggggatcg tgggtgcgaa caagatgcag 240
aagtcgggtg tgggtgcatt ggaccgcctc ttccacaacC Aaaggtatac Aaaccgctac 300
gtcaagcgca chctCccaag ttcattggcac acgacgatga caacacctgc aacattggcg 360
aCccgggtta ggctggatcc Tttctaggcc cttgagcaga cacaagcact ggggtgttgc 420
tgaattcttc cgcagagcta aggtgtacgt tccaccagct gcaacacgct ccagtgaacg 480
tggtagcaaa tctcaacaag ctggtgtgtc taccaaatga tccatctgaa gttactcaga 540
acaagatgca gtcacggctt gtttttctt cgctgtatgt ttgtttcctt gtggaatggt 600
gttgccatgt ttacgatggg agaaaaaata gcaagcagcc agcatctttg ctaataact 660
gttgtttctt tgtgtgttcc ttogtttaac ggtactagcc attaaggatg tagttaccag 720
attcaacaag accaatggat tcatattgta ttggttcaact tccg

(2) INFORMATION FOR SEQ ID NO:3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1577134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3510:

Met Lys Pro Val Val Gly Ile Val Val Ser Asn Lys Met Gln Lys Ser
1 5 10 15
Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln Arg Tyr Thr Asn
20 25 30
Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His Thr Thr Met Thr
35 40 45

Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp Pro Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3511:

Met Gln Lys Ser Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln
1 5 10 15
Arg Tyr Thr Asn Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His
20 25 30
Thr Thr Met Thr Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp
35 40 45
Pro Phe
50

(2) INFORMATION FOR SEQ ID NO:3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3512:

Met Ile His Leu Lys Leu Leu Arg Thr Arg Cys Ser His Gly Leu Phe
1 5 10 15
Phe Phe Arg Cys Met Phe Val Ser Leu Trp Asn Val Val Ala Met Phe
20 25 30
Ser Met Gly Glu Lys Ile Ala Ser Ser Gln His Leu Cys Leu Ile Thr
35 40 45
Val Val Leu Leu Trp Cys Pro Ser Phe Asn Gly Thr Ser His
50 55 60

(2) INFORMATION FOR SEQ ID NO:3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3513:

tgcataatag	tcggcggtt	aattcaattt	gctagcttct	cctaacgata	cgccgggtggt	60
ttctaattca	atgcgtttat	acgtgtagct	ggagaagctg	gcgcagatgc	tgcaagagcc	120
gccgcagggc	aagtactacg	gcggcaatgc	ggacgacgtg	cgctcgggcg	gcgtcgggcg	180
cacgaaggag	gaggaggagt	Cccacagacg	cctgcgccgg	ggccgcgcct	tactcgctcg	240
agtgcgctgg	cggtggcagg	ttcatcgccg	actctcttgg	ggacgacgac	gtgggagcag	300
ccctcttccg	gccgcgctcg	tctccgcagc	cgacgcgtgg	cttactcaac	tcgtcggggc	360
cgccggagca	ccagccggtt	cagttccact	cggcgtactg	ctggcgctgc	tcgtcgggcg	420

(2) INFORMATION FOR SEQ ID NO:3514:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1577138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3514:

[illegible]

(2) INFORMATION FOR SEO ID NO:3515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

{A} NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3515:

Met	Arg	Thr	Thr	Cys	Ala	Arg	Ala	Ala	Ser	Ala	Ala	Arg	Arg	Arg	Arg
1				5					10					15	
Arg	Ser	Pro	Thr	Asp	Ala	Cys	Ala	Gly	Ala	Ala	Leu	Tyr	Ser	Ser	Glu
			20					25					30		
Cys	Ala	Gly	Gly	Gly	Arg	Phe	Ile	Ala	His	Phe	Leu	Ala	Asp	Asp	
		35					40					45			
Val	Gly	Ala	Ala	Leu	Phe	Arg	Pro	Pro	Ser	Ser	Pro	Gln	Pro	Thr	Ala
	50					55					60				
Gly	Leu	Leu	Thr	Ser	Ser	Gly	Pro	Pro	Glu	His	Gln	Pro	Phe	Gln	Phe
65					70					75				80	
His	Ser	Gly	Tyr	Cys	Trp	Pro	Ser	Ser	Ser	Ala	Glu	Gln	Thr	Cys	Ser
				85					90					95	

Gly Ser Gln Trp Trp Glu Phe Glu Ser Leu Ser Glu
100 105

(2) INFORMATION FOR SEQ ID NO:3516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3516:

aaagaattag tgggagtgca aactgaagtt gtgtatgaga aatgcccaac cgaagctatg	60
attgaaactg gggggttttc ctatgcggtg gtggtgtgtg gagaggttcc atatgccgaa	120
ttgacaggag atagaactga ccttagtatt ccgtttaatg gctctgacct tatcatccgt	180
gttgcaagta aaatccctac cctagtgtat gttatatctg gaaggccatt aattattgag	240
tcacaagttt tggaaaaagat agaagctcta gtcgctgcct ggctgctggg aagtgagggc	300
atgggaatta ccgattgcct ctttggagat catgattttg tgggcacatt gcctgtgaca	360
tggtgtaagt ctgttgatca attgcctata gatgctggag actctaacta tgaccgccta	420
ttccctgttg gatattggct aaaaatgttt cgaagcgata atgattcaac ataactttat	480
tatttattgg gtacatttga atctttgtga tgttaaatac tctgtattta ttgctatttg	540
gGaaacttaa atgaaataat atattgttgt	

(2) INFORMATION FOR SEQ ID NO:3517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3517:

Lys Glu Leu Val Gly Val Gln Thr Glu Val Val Tyr Glu Lys Cys Pro	
1 5 10 15	
Thr Glu Ala Met Ile Glu Thr Gly Gly Phe Ser Tyr Ala Val Val Val	
20 25 30	
Val Gly Glu Val Pro Tyr Ala Glu Leu Thr Gly Asp Arg Thr Asp Leu	
35 40 45	
Ser Ile Pro Phe Asn Gly Ser Asp Leu Ile Ile Arg Val Ala Ser Lys	
50 55 60	
Ile Pro Thr Leu Val Ile Val Ile Ser Gly Arg Pro Leu Ile Ile Glu	
65 70 75 80	
Ser Gln Val Leu Glu Lys Ile Glu Ala Leu Val Ala Ala Trp Leu Pro	
85 90 95	
Gly Ser Glu Gly Met Gly Ile Thr Asp Cys Leu Phe Gly Asp His Asp	
100 105 110	
Phe Val Gly Thr Leu Pro Val Thr Trp Cys Lys Ser Val Asp Gln Leu	
115 120 125	
Pro Ile Asp Ala Gly Asp Ser Asn Tyr Asp Pro Leu Phe Pro Val Gly	
130 135 140	
Tyr Gly Leu Lys Met Phe Arg Ser Asp Asn Asp Ser Thr	
145 150 155	

(2) INFORMATION FOR SEQ ID NO:3518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1577148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3518:

```
Met Ile Glu Thr Gly Gly Phe Ser Tyr Ala Val Val Val Gly Glu
1      5      10      15
Val Pro Tyr Ala Glu Leu Thr Gly Asp Arg Thr Asp Leu Ser Ile Pro
20      25      30
Phe Asn Gly Ser Asp Leu Ile Ile Arg Val Ala Ser Lys Ile Pro Thr
35      40      45
Leu Val Ile Val Ile Ser Gly Arg Pro Leu Ile Ile Glu Ser Gln Val
50      55      60
Leu Glu Lys Ile Glu Ala Leu Val Ala Ala Trp Leu Pro Gly Ser Glu
65      70      75      80
Gly Met Gly Ile Thr Asp Cys Leu Phe Gly Asp His Asp Phe Val Gly
85      90      95
Thr Leu Pro Val Thr Trp Cys Lys Ser Val Asp Gln Leu Pro Ile Asp
100      105      110
Ala Gly Asp Ser Asn Tyr Asp Pro Leu Phe Pro Val Gly Tyr Gly Leu
115      120      125
Lys Met Phe Arg Ser Asp Asn Asp Ser Thr
130      135
```

(2) INFORMATION FOR SEQ ID NO:3519:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1047
(D) OTHER INFORMATION: / Ceres Seq. ID 1577163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3519:

```
agccacaccc ggacacccca cacaggcacg aggcacaccg ccacgcgagc ggcgaaaactg
cgggagccaa tcagaaaccta cagcgatgca atgatcgccg tcgcatcgct cttccctctg 120
cgcgcccaac cggtctccgtt cggtctgggg acactgccac cgccgtctac gcggcgccasa 180
cgctccctccg ccaccccgccg gctctggcgc tcggtggagg cctcgaagga gagccgggga 240
agatactgga tcgcgcggcc acgcgcgttc agatcctcgg cctcgacgcc gcgcgcggct 300
atcccgccgc cgaactcaag gccgcttttc gcgcgcgggt taaggaattc catctgatg 360
tttcaagaga cccagaaaaa cgagatttaa taatgaggcg agtgatcgag gccatcaga 420
tgttatctgg caaccaagaa atgatgtttt aaaggaacaa tgttgaccoc tttgatgaac 480
ctgagtgtga agctcgtgac atatttgtca atgaacttct atgcattggc actggatgtc 540
ctattctctg tgttaaaagg gcaCctcatg tattttcatt ttcagatgat actggtacag 600
ctcgtgcaat actccaaggt aatggagaag atgatcttgt tcagctcgct gttgggcagt 660
gtccaagaaa gtgcatabac tatgtgacgc cttgccaaac cactattttg gaggatgttc 720
ttgtagtgtg gtttgatggt ccttaacgatc ttgctgaagc agcagttctg gattccctoc 780
tttcaaaagc gaagtctcag aataacaggt ataagaagcc ccaaagagga gcaaatcat 840
cctccgatta tgttgattgg atgtgatctg atcccgagac acaaagagga tgccagattc 900
agccgaaggc agttcggtag atttatgctg gtttgctat tctccttggt cagttgcccg 960
atagtttata aaatggaata cgtttacgtg gacagactgc tttgtttgtg gtatacggtt 1020
```

(2) INFORMATION FOR SEQ ID NO:3520:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1577164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3520:

```
Pro His Pro Asp Thr Pro His Arg His Glu Ala Thr Ser His Ala Ser
1      5      10      15
Gly Glu Thr Ala Gly Ala Asn Gln Asn Leu Gln Arg Cys Asn Asp Arg
20      25
Arg Arg Ile Val Leu Pro Leu Ala Arg Pro Arg Gly Ser Val Arg Leu
35      40      45
Gly Asp Thr Ala Thr Ala Val Tyr Ala Ala Xaa Thr Ser Leu Arg His
50      55      60
Pro Arg Val Ser Ala Leu Gly Gly Gly Leu Glu Gly Glu Pro Gly Lys
65      70      75      80
Ile Leu Asp Pro Arg Ala Thr Pro Phe Gln Ile Leu Gly Leu Asp Ala
85      90      95
Ala Ala Gly Tyr Ser Ser Ala Ala Glu Leu Lys Ala Ala Phe Arg Ala Arg
100      105      110
Val Lys Glu Phe His Pro Asp Val Cys Lys Asp Pro Glu Asn Ala Asp
115      120      125
Leu Ile Met Arg Arg Val Ile Glu Ala Tyr Gln Met Leu Ser Gly Asn
130      135      140
Gln Glu Met Met Phe Glu Arg Asn Asn Val Asp Pro Phe Asp Glu Pro
145      150      155      160
Glu Cys Glu Ala Arg Asp Ile Phe Val Asn Glu Leu Leu Cys Ile Gly
165      170      175
Thr Gly Cys Pro Tyr Ser Cys Val Lys Arg Ala Pro His Val Phe Ser
180      185      190
Phe Ser Asp Asp Thr Gly Thr Ala Arg Ala Ile Ser Gln Gly Asn Gly
195      200      205
Glu Asp Asp Leu Val Gln Leu Ala Val Gly Gln Cys Pro Arg Lys Cys
210      215      220
Ile Tyr Tyr Val Thr Pro Cys Gln His Thr Ile Leu Glu Asp Val Leu
225      230      235      240
Ala Ser Val Leu Met Val Pro Tyr Asp Leu Ala Glu Ala Ala Val Leu
245      250      255
Asp Ser Leu Leu Ser Lys Ala Lys Phe Glu Asn Asn Arg Tyr Lys Lys
260      265      270
Pro Gln Arg Gly Ala Lys Ser Ser Ser Asp Tyr Val Asp Trp Met
275      280      285
```

(2) INFORMATION FOR SEQ ID NO:3521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1577165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3521:

```
Met Arg Arg Val Ile Glu Ala Tyr Gln Met Leu Ser Gly Asn Gln Glu
1      5      10      15
Met Met Phe Glu Arg Asn Asn Val Asp Pro Phe Asp Glu Pro Glu Cys
20      25      30
Glu Ala Arg Asp Ile Phe Val Asn Glu Leu Leu Cys Ile Gly Thr Gly
35      40      45
Cys Pro Tyr Ser Cys Val Lys Arg Ala Pro His Val Phe Ser Phe Ser
```

50	55	60
Asp Asp Thr Gly Thr Ala Arg Ala Ile Ser Gln Gly Asn Gly Glu Asp		
65	70	75
Asp Leu Val Gln Leu Ala Val Gly Gln Cys Pro Arg Lys Cys Ile Tyr		80
	85	90
Tyr Val Thr Pro Cys Gln His Thr Ile Leu Glu Asp Val Leu Ala Ser		95
	100	105
Val Leu Met Val Pro Tyr Asp Leu Ala Glu Ala Val Leu Asp Ser		110
	115	120
Leu Leu Ser Lys Ala Lys Phe Glu Asn Asn Arg Tyr Lys Lys Pro Gln		125
	130	135
Arg Gly Ala Lys Ser Ser Ser Asp Tyr Val Asp Trp Met		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:3522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3522:

Met Leu Ser Gly Asn Gln Glu Met Met Phe Glu Arg Asn Asn Val Asp	
1	5
Pro Phe Asp Glu Pro Glu Cys Glu Ala Arg Asp Ile Phe Val Asn Glu	10
	15
	20
Leu Leu Cys Ile Gly Thr Gly Cys Pro Tyr Ser Cys Val Lys Arg Ala	25
	30
	35
Pro His Val Phe Ser Phe Ser Asp Asp Thr Gly Thr Ala Arg Ala Ile	40
	45
	50
Ser Gln Gly Asn Gly Glu Asp Asp Leu Val Gln Leu Ala Val Gly Gln	55
	60
	65
Cys Pro Arg Lys Cys Ile Tyr Tyr Val Thr Pro Cys Gln His Thr Ile	70
	75
	80
	85
Leu Glu Asp Val Leu Ala Ser Val Leu Met Val Pro Tyr Asp Leu Ala	90
	95
	100
Glu Ala Ala Val Leu Asp Ser Leu Leu Ser Lys Ala Lys Phe Glu Asn	105
	110
	115
Asn Arg Tyr Lys Lys Pro Gln Arg Gly Ala Lys Ser Ser Ser Asp Tyr	120
	125
	130
	135
Val Asp Trp Met	140
145	

(2) INFORMATION FOR SEQ ID NO:3523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..832
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3523:

attttcgtca cccctgacgc tcgacgcctc tctctctctc cdccccacc cgtccatcgc	60
ccctccctcc ggtctgcgt cccacagcct caccctgcgc cccccgccga ttccgctcgc	120
ctttgtgtgg aaggaacgat ggagcagacc ttcatcatga tcaagcccca cggcgtccag	180
cggggcctga tcggggacat catcagtcgc ttcgagaaga aagggttcta cctcaagggg	240

atgaagtcca	tgaactgtga	gaggtccttc	gcgcagCCag	cactacgtcg	acctttccga	300
caagccttcc	ttYCCCCcg	gttggtggag	tacatcattt	cgggccccgt	ggtggcgatg	360
gtgtgggagg	ggaaggacgt	cgtgttgact	ggccgcaGga	tcattggggc	caccaggcct	420
tgggaggcag	cccccggtac	cattcgtggg	gactacgcgc	tggaaagtgcg	caggaatgtc	480
atccatggaa	gcgactccgt	ggagaacggg	aagaaggaga	tcgctctctg	gttcctgaa	540
ggtgtggcac	agtggaaag	caaccttcac	ccctggatct	acgaggcttg	agcagttgag	600
cttggatgcc	ttgctgtct	catggaaacc	agagttttgt	ttgagtatta	tctgttggt	660
ctgggtgaag	agtcataagt	tagcgctctg	tgtgttacac	cagagttaag	tctgcctgaa	720
cttatgtggc	atttgtttga	gtttctgcct	tctgtccctg	ttttctaatg	taccgtggtt	780
gtgaaccggt	caatgtgac	tgaataaaaa	cattgcgtgc	caagtttgtg	tc	

(2) INFORMATION FOR SEQ ID NO:3524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1577168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3524:

Ile	Phe	Val	Thr	Pro	Asp	Ala	Arg	Arg	Leu	Ser	Ser	Ser	Xaa	Pro	Pro
1				5					10					15	
Pro	Val	His	Arg	Pro	Ser	Leu	Arg	Ser	Ala	Leu	Pro	Gln	Pro	His	Pro
				20					25				30		
Cys	Ala	Pro	Ala	Asp	Ser	Arg	Arg	Pro	Leu	Leu	Glu	Gly	Thr	Met	Glu
				35					40				45		
Gln	Thr	Phe	Ile	Met	Ile	Lys	Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile
				50					55				60		
Gly	Asp	Ile	Ile	Ser	Arg	Phe	Glu	Lys	Lys	Gly	Phe	Tyr	Leu	Lys	Gly
				65					70				75		80
Met	Lys	Phe	Met	Asn	Val	Glu	Arg	Ser	Phe	Ala	Gln	Pro	Ala	Leu	Arg
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:3525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3525:

Met	Val	Trp	Glu	Gly	Lys	Asp	Val	Val	Leu	Thr	Gly	Arg	Arg	Ile	Ile
1				5					10					15	
Gly	Ala	Thr	Arg	Pro	Trp	Glu	Ala	Ala	Pro	Gly	Thr	Ile	Arg	Gly	Asp
				20					25				30		
Tyr	Ala	Val	Glu	Val	Gly	Arg	Asn	Val	Ile	His	Gly	Ser	Asp	Ser	Val
				35					40				45		
Glu	Asn	Gly	Lys	Lys	Glu	Ile	Ala	Leu	Trp	Phe	Pro	Glu	Gly	Val	Ala
				50					55				60		
Gln	Trp	Lys	Ser	Asn	Leu	His	Pro	Trp	Ile	Tyr	Glu	Ala			
				65					70				75		

(2) INFORMATION FOR SEQ ID NO:3526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1577170

(2) INFORMATION FOR SEO ID NO:3527:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..866

(D) OTHER INFORMATION: / Ceres Seq. ID 1577175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3527:

(2) INFORMATION FOR SEO ID NO:3528:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

FEATURE:

(A) NAME/KEY: peptid

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1577176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3528:

1 Phe Ser Pro Pro Gly Ser Trp Val Ser Ser Pro Pro Phe Ala Ser Gln
5 10 15
Gly Gln Gln Gly Thr Pro Pro Arg Thr Ala Ala Pro Ala Pro Ala Pro

20	25	30
Ala Leu Cys Cys His Gly Val Val	Leu Arg Arg Ala His Arg Tyr Val	
35	40	45
Arg Leu His Arg Ser Pro Val Leu	Pro Pro Ala Pro Arg Arg Gly His	
50	55	60
His Gly His Asp His Asp Pro Glu Arg	Ser Arg Ala Pro Gly Arg Gly	
65	70	75
Leu Pro Gly Pro Gly Gly Pro Xaa Arg	Pro Asp Ala Asp Pro Ala Ala	
85	90	95
Xaa Val Arg Ala Arg Ala Arg Pro Cys	Arg Gly Gly Gly Gly Ala Arg	
100	105	110
Val Gly Pro Cys Gln Gly Asp Pro Pro	Arg Gly Asp Gly Gly Ser Arg	
115	120	125
Arg Gly Gly Arg Gly Ala Ala Arg Arg	Arg Arg Ala Pro Arg Pro Arg	
130	135	140
Xaa Asp Asp Val Ala Arg Leu Asn Val Lys		
145	150	

(2) INFORMATION FOR SEQ ID NO:3529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3529:

Ser Leu Leu Leu Leu Ala Pro Gly Ser His Leu Leu Pro Ser Leu Arg Lys	
1	5
Ala Asn Lys Glu Leu His His Ala Arg Pro His Pro His Pro His Pro	
20	25
Leu Ser Ala Ala Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe	
35	40
Gly Phe Thr Ala Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr	
50	55
Thr Ala Thr Thr Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala	
65	70
Ser Leu Val Pro Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa	
85	90
Ala Phe Ala Arg Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val	
100	105
Ser Gly Leu Ala Lys Ala Thr Leu Leu Ala Gly Thr Val Ala Leu Val	
115	120
Ala Ala Ala Val Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa	
130	135
Pro Thr Thr Ser Arg Ala	
145	150

(2) INFORMATION FOR SEQ ID NO:3530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3530:

Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe Gly Phe Thr Ala
1 5 10 15
Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr Thr Ala Thr Thr
20 25 30
Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala Ser Leu Val Pro
35 40 45
Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa Ala Phe Ala Arg
50 55 60
Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val Ser Gly Leu Ala
65 70 75 80
Lys Ala Thr Leu Leu Ala Gly Thr Val Ala Leu Val Ala Ala Val
85 90 95
Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa Pro Thr Thr Ser
100 105 110
Arg Ala

(2) INFORMATION FOR SEQ ID NO:3531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1577198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3531:

gccttcaacc atggttagag ttctccttgg agtttttttc cctcttgcca cagcaccccc 60
caccacacac cacccaagcc cccaactgca gtgcccatcc ggcagacagg tcgatggcgg 120
cggaagcagc ggcagcghng gaaggagaag atgcggacgc tagtcagcag cgacttcaag 180
aagttcgatg ttgaggagtc tgtggcgagg gaatcgctga ttatcctgaa cctgatggcg 240
gactgcgacg acagtgacat ccggtctctc aacgtcaacg ccaatatcct cgacaaggtc 300
atcgcgtaact gcaggaaqca cgccctyggcg ccgcgcscga NTtggcggtg atgcggaGcc 360
aagtgctgcg agtaacaagg cctcagcgga cgaatctcaag tcctttgatg ctgagttcgt 420
cgatgttgac ctggtcaacc ttttggagct cattaagctg gcagactacc tggagatcaa 480
tgggctgctg gacctgacct gccaggccgt cgcggacatg atcaagggga agactccaga 540
ggagatacgc gagacattcg acatcgagaa tgacttcaca cctgagggaag aggctaaagt 600
gaggagggag aatcagtggtg cctttgaatg aagaagctgc aggctagctc taacaaaaca 660
atagcaatat catataacca ggccagagat gaagtgcctg ttcaggatgt tatgatgcga 720
aggtttgggt ggtcgtgagc agactatatt gctgttccag tattttggct ggtttgggtc 780
cc

(2) INFORMATION FOR SEQ ID NO:3532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1577199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3532:

Pro Ser Thr Ile Val Arg Val Ser Leu Val Val Phe Phe Pro Leu Val
1 5 10 15
Thr Ala Pro Pro Thr His Thr His Pro Arg Pro Gln Leu Gln Cys Pro
20 25 30
Ser Gly Arg Gln Val Asp Gly Gly Gly Ser Ser Gly Ser Xaa Gly Arg
35 40 45
Arg Arg Cys Gly Arg

50

(2) INFORMATION FOR SEQ ID NO:3533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3533:

```
Met Arg Thr Leu Val Ser Ser Asp Phe Lys Lys Phe Asp Val Glu Glu
1           5           10           15
Ser Val Ala Arg Glu Ser Leu Ile Ile Leu Asn Leu Met Ala Asp Cys
          20           25           30
Asp Asp Ser Asp Ile Pro Val Phe Asn Val Asn Ala Asn Ile Leu Asp
          35           40           45
Lys Val Ile Ala Tyr Cys Arg Lys His Ala Xaa Ala Pro Arg Xaa Xaa
          50           55           60
Trp Arg
65
```

(2) INFORMATION FOR SEQ ID NO:3534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3534:

```
Met Arg Ser Gln Val Leu Arg Val Thr Arg Pro Gln Arg Thr Ile Ser
1           5           10           15
Ser Pro Leu Met Leu Ser Ser Ser Met Leu Thr Trp Ser Pro Ser Trp
          20           25           30
Ser Ser Leu Arg Leu Gln Thr Thr Trp Arg Ser Met Gly Cys Trp Thr
          35           40           45
```

(2) INFORMATION FOR SEQ ID NO:3535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..870
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3535:

```
caatgtcggc tgcggccact agatttttcc tgacgcgggt tctgtctcca ctccccctcc      60
tctccccag gtggcggcag cggcggcggg gtacgatttg tgcacagagg gcttttgcaa      120
tggcgcttc ggggttcrgc ggcggcgagg cgccaaaacc ctaccgcgc cgcgaatccc      180
gcacgacccc aaccatgacc gtgctgagcc gccctacccc gggcacggcc cagtgtctcg      240
ggcgggaaga gaccgcgcgt gcggtcgcgt acacgaagcc ggggcgcggc ctgatcaagg      300
tgaacgcgct cccgattgar ctgatccgac cggagatgct ccgcctcaag gccttcgagc      360
```

ccatctctgct	ggcggggggc	gtcccggttc	aaggacatcg	acatgcggat	cgcgcctccr	420
ggcggcgggg	agacgtcgca	gatctacgcc	atccgccAag	vccgtcgsc	aggggctcgt	480
cgctactac	cagaagtac	tcgacgaggc	cgcyaaag	gagatcaagg	acatctttac	540
ccgctacgat	cgcaccctcc	tcgtcgctga	cccccgcg	tgcgagccga	agaagtctcg	600
cggacgtggt	gcccgcgcga	ggttccagaa	gtcgtaacct	tgagcggctg	cctgtcccat	660
ctcgattttt	cgatcggtt	tgggtgttct	tcgttttatt	tcctatcaat	ggatctgctt	720
atctgggtct	atatctagct	gctgctttac	cataatgttt	agactttaat	gcctagcctg	780
aaacctgtgt	tgcaatgtga	aattaatgtg	agagattatg	aagactattt	tggctagtcc	840
ctctattatg	atttttcat	ttccmgtatt				

(2) INFORMATION FOR SEQ ID NO:3536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1577207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3536:

Met	Ser	Arg	Ala	Ala	Thr	Arg	Phe	Phe	Leu	Thr	Arg	Cys	Leu	Leu	Pro
1			5					10					15		
Leu	Pro	Leu	Leu	Ser	Pro	Arg	Trp	Arg	Gln	Arg	Arg	Arg	Gly	Ser	Ile
			20					25					30		
Cys	Ala	Thr	Arg	Ala	Phe	Ala	Met	Ala	Ala	Ser	Gly	Phe	Xaa	Gly	Gly
			35				40					45			
Glu	Ala	Pro	Lys	Pro	Tyr	Arg	Arg	Arg	Glu	Ser	Arg	Thr	Thr	Pro	Thr
			50				55				60				
Met	Thr	Val	Leu	Ser	Arg	Pro	Thr	Pro	Gly	Thr	Ala	Gln	Cys	Phe	Gly
65					70					75				80	
Arg	Lys	Lys	Thr	Ala	Val	Ala	Val	Ala	Tyr	Thr	Lys	Pro	Gly	Arg	Gly
			85						90					95	
Leu	Ile	Lys	Val	Asn	Gly	Val	Pro	Ile	Xaa	Leu	Ile	Arg	Pro	Glu	Met
			100					105					110		
Leu	Arg	Leu	Lys	Ala	Phe	Glu	Pro	Ile	Leu	Leu	Ala	Gly	Ala	Val	Pro
			115				120					125			
Val	Gln	Gly	His	Arg	His	Ala	Asp	Pro	Arg	Xaa	Arg	Arg	Arg	Glu	Asp
			130				135					140			
Val	Ala	Asp	Leu	Arg	His	Pro	Pro	Xaa	Pro	Ser	Xaa	Arg	Gly	Ser	Ser
145					150					155				160	
Pro	Thr	Thr	Arg	Ser	Thr	Ser	Thr	Arg	Pro	Xaa	Arg	Arg	Arg	Ser	Arg
			165						170					175	
Thr	Ser	Leu	Pro	Ala	Thr	Ile	Ala	Pro	Ser	Ser	Ser	Leu	Thr	Pro	Gly
			180					185					190		
Ala	Ala	Ser	Arg	Arg	Ser	Ser	Ala	Asp	Val	Val	Pro	Ala	Pro	Gly	Ser
			195				200				205				
Arg	Ser	Arg	Thr	Val	Glu	Arg	Leu	Pro	Ala	Pro	Ser	Arg	Phe	Phe	Arg
			210				215				220				
Ser	Leu	Trp	Val	Phe	Phe	Ala	Leu	Phe	Pro	Ile	Asn	Gly	Ser	Ala	Tyr
225					230				235					240	
Leu	Val	Leu	Tyr	Leu	Ala	Ala	Leu	Pro							
			245				250								

(2) INFORMATION FOR SEQ ID NO:3537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..211
(D) OTHER INFORMATION: / Ceres Seq. ID 1577209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3537:

Met Ala Ala Ser Gly Phe Xaa Gly Gly Glu Ala Pro Lys Pro Tyr Arg
1 5 10 15
Arg Arg Glu Ser Arg Thr Thr Pro Thr Met Thr Val Leu Ser Arg Pro
20 25 30
Thr Pro Gly Thr Ala Gln Cys Phe Gly Arg Lys Lys Thr Ala Val Ala
35 40 45
Val Ala Tyr Thr Lys Pro Gly Arg Gly Leu Ile Lys Val Asn Gly Val
50 55 60
Pro Ile Xaa Leu Ile Arg Pro Glu Met Leu Arg Leu Lys Ala Phe Glu
65 70 75 80
Pro Ile Leu Leu Ala Gly Ala Val Pro Val Gln Gly His Arg His Ala
85 90 95
Asp Pro Arg Xaa Arg Arg Arg Glu Asp Val Ala Asp Leu Arg His Pro
100 105 110
Pro Xaa Pro Ser Xaa Arg Gly Ser Ser Pro Thr Thr Arg Ser Thr Ser
115 120 125
Thr Arg Pro Xaa Arg Arg Arg Ser Arg Thr Ser Leu Pro Ala Thr Ile
130 135 140
Ala Pro Ser Ser Ser Leu Thr Pro Gly Ala Ala Ser Arg Arg Ser Ser
145 150 155 160
Ala Asp Val Val Pro Ala Pro Gly Ser Arg Ser Arg Thr Val Glu Arg
165 170 175
Leu Pro Ala Pro Ser Arg Phe Phe Arg Ser Leu Trp Val Phe Phe Ala
180 185 190
Leu Phe Pro Ile Asn Gly Ser Ala Tyr Leu Val Leu Tyr Leu Ala Ala
195 200 205
Ala Leu Pro
210

(2) INFORMATION FOR SEQ ID NO:3538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3538:

atgtcttacc ggagtagcgc aactccgcaa gcaaatcttc ctatctccaa gctccaatc 60
tgtgaacctgt gaaccccaat cgaatgacgc cgacggsagc ctctctctcc cggtccccc 120
attcgctctct atctccgatg tgcgcgcgct ccagctcccc ccgcgcggcg gccaccggcc 180
tcgccccctgc tggaaaggct tggagtcgcg ctccgtacag acgcggatgg tctcttcttt 240
cgttggggagc agaacaacgc gcagaaacgt tatatgtgct tcctgttgcg gaggttggagc 300
tcgccgaagca ctggtcattg ctgtagtcgc ctgtgttggt ttccgccccca agggctctagc 360
agaggtagccc aggaatttgg ggaagacttt gcgtgctttc caaccaacca ttagagagat 420
acaggatgta tcaaggaggt tcaggagcac tcttgaacga gaaatcgga ttgatgaggt 480
ttcccagtcg acgaattata caccacacac catgaataac aaccaacaac ctgctgccga 540
ctcaaatatc aagcctgcac ctgcacotta caccagcgat gaacttgta aagtAactga 600
agaacaaatt gctgcacacg ctgctgcaga gagTtatcgt cagttgtgtgc ggtgtgtccg 660
cttaaacatt atttgtggtt ggttggtact ttgtgtgtgt ttattttttt ggacctcgtg 720
atagtcggtc ggttcaatgt tatcgcggtc actggcaaac cttaagtgat acggtattct 780
tcttttcggt

(2) INFORMATION FOR SEQ ID NO:3539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1577253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3539:

Cys	Ser	Thr	Gly	Val	Ala	Gln	Leu	Arg	Lys	Gln	Ile	Leu	Leu	Ser	Pro	
1				5					10					15		
Ser	Leu	Gln	Ser	Val	Asn	Gly	Glu	Pro	Gln	Ser	Asn	Asp	Ala	Asp	Xaa	
			20					25					30			
Ser	Leu	Leu	Leu	Pro	Ala	Pro	Pro	Phe	Val	Ser	Ile	Ser	Asp	Val	Arg	
			35					40				45				
Arg	Leu	Gln	Leu	Pro	Pro	Arg	Gly	Gly	His	Arg	Pro	Arg	Pro	Cys	Trp	
			50			55					60					
Lys	Gly	Leu	Glu	Cys	Gly	Ser	Val	Gln	Thr	Arg	Met	Val	Ser	Ser	Phe	
65				70					75						80	
Val	Gly	Ser	Arg	Thr	Arg	Arg	Arg	Asn	Val	Ile	Cys	Ala	Ser	Leu	Phe	
				85					90				95			
Gly	Val	Gly	Ala	Pro	Glu	Ala	Leu	Val	Ile	Gly	Val	Val	Ala	Leu	Leu	
			100					105					110			
Val	Phe	Gly	Pro	Lys	Gly	Leu	Ala	Glu	Val	Ala	Arg	Asn	Leu	Gly	Lys	
			115					120				125				
Thr	Leu	Arg	Ala	Phe	Gln	Pro	Thr	Ile	Arg	Glu	Ile	Gln	Asp	Val	Ser	
			130			135					140					
Arg	Glu	Phe	Arg	Ser	Thr	Leu	Glu	Arg	Glu	Ile	Gly	Ile	Asp	Glu	Val	
			145		150				155				160			
Ser	Gln	Ser	Thr	Asn	Tyr	Thr	Pro	Thr	Thr	Met	Asn	Asn	Asn	Gln	Gln	
				165				170					175			
Pro	Ala	Ala	Asp	Ser	Asn	Ile	Lys	Pro	Ala	Pro	Ala	Pro	Tyr	Thr	Ser	
			180				185					190				
Asp	Glu	Leu	Val	Lys	Val	Thr	Glu	Glu	Gln	Ile	Ala	Ala	Ser	Ala	Ala	
			195				200				205					
Ala	Glu	Ser	Tyr	Arg	Gln	Leu	Val	Arg	Cys	Val	Arg	Leu	Asn	Phe	Ile	
			210			215					220					
Cys	Gly	Trp	Leu	Val	Leu	Leu	Trp	Trp	Leu	Phe	Phe	Trp	Thr	Ser		
225				230					235							

(2) INFORMATION FOR SEQ ID NO:3540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1577254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3540:

Met	Val	Ser	Ser	Phe	Val	Gly	Ser	Arg	Thr	Arg	Arg	Asn	Val	Ile		
1				5					10				15			
Cys	Ala	Ser	Leu	Phe	Gly	Val	Gly	Ala	Pro	Glu	Ala	Leu	Val	Ile	Gly	
			20					25				30				
Val	Val	Ala	Leu	Leu	Val	Phe	Gly	Pro	Lys	Gly	Leu	Ala	Glu	Val	Ala	
			35			40					45					
Arg	Asn	Leu	Gly	Lys	Thr	Leu	Arg	Ala	Phe	Gln	Pro	Thr	Ile	Arg	Glu	
			50			55					60					
Ile	Gln	Asp	Val	Ser	Arg	Glu	Phe	Arg	Ser	Thr	Leu	Glu	Arg	Glu	Ile	
65				70					75					80		

Gly Ile Asp Glu Val Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met
85 90 95
Asn Asn Asn Gln Gln Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro
100 105 110
Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Ile
115 120 125
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val
130 135 140
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Leu Trp Trp Leu Phe
145 150 155 160
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:3541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..859

(D) OTHER INFORMATION: / Ceres Seq. ID 1577263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3541:

agcttctgtct	cgtagactgt	cgacagattc	cgctccaacg	cgacactgca	gtcccgcacg	60
ccctcgccca	cgctgcctt	tcaaaaagct	ggaggattct	cgagarggag	aagcgcgctt	120
ggcagctcgc	ttccatccgc	ccccacgaat	gtccgacgar	gccaggcgcg	ggcccgcggg	180
cgccgcgacg	ggcagtgctc	cgggcctcct	ccgaggaccg	caagCCgggt	ggcgctgggt	240
ccccggcggc	ggttgccgac	aagatccagc	tcaagagcgc	cgatatgaag	gaggagatgc	300
ggcaggagcg	cttcgaaatt	gcccgcacgc	cggttcgataa	gcacagcatg	gagaaggaca	360
tcgctgagta	cataaagaag	gagttcgaca	agaaccacgc	cccaaCctgc	gcaactgcac	420
gtcggccgca	acttcggttc	atacgtgacg	cacgagacaa	actactttgt	atatttctac	480
atcgactcta	aagctgtctt	gctattcaag	tctgggtgat	tgctcgacgc	cgacgcaatc	540
adccttgca	gcctacgttc	cattgctccc	atgtatgcac	cgaccccttc	ccccaggccc	600
cagggtgcgc	tgcaaccaag	ctggaagccg	gtaattctaa	tgagcctgca	tggtgatgta	660
tatcagcaac	ggattattct	tcgtatgccc	attagtgtga	gatcagattg	catcttacct	720
atgtctgata	tatctagcta	ggttaggtgt	tgtagtgaca	ttgtcttgtt	gcaatatgat	780
tgccggacaa	ctgggtgaac	tgctctctgt	ctgtttgtga	ttatctcaat	agaagcgtcc	840
ttgtctatgc	gtaatactc					

(2) INFORMATION FOR SEQ ID NO:3542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3542:

Val	Leu	Ser	Ala	Arg	Leu	Ser	Thr	Asp	Ser	Ala	Pro	Thr	Arg	Thr	Cys
1				5				10					15		
Ser	Pro	Ala	Arg	Pro	Arg	Pro	Pro	Ser	Pro	Phe	Lys	Lys	Leu	Glu	Asp
			20					25					30		
Ser	Arg	Xaa	Gly	Glu	Ala	Arg	Leu	Ala	Ala	Pro	Phe	His	Pro	Pro	Pro
			35					40				45			
Arg	Met	Ser	Asp	Xaa	Ala	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Ala	
			50				55			60					
Xaa	Ala	Pro	Gly	Leu	Leu	Arg	Gly	Pro	Gln	Ala	Gly	Gly	Arg	Trp	Val
65				70				75					80		

Pro Gly Gly Gly Cys Ala Gln Asp	Pro Ala Gln Glu Arg Arg Tyr Glu
85	90
Gly Gly Asp Ala Ala Gly Arg Leu Arg Asn Cys Pro His Arg Val Arg	
100	110

(2) INFORMATION FOR SEQ ID NO:3543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3543:

Ser Cys Leu Leu Asp Cys Arg Gln Ile	Pro Leu Gln Arg Ala Pro Ala
5	10
Val Pro His Ala Leu Ala His Arg Arg Leu Ser Lys Ser Trp Arg Ile	
20	30
Leu Glu Xaa Glu Lys Arg Ala Trp Gln Leu Arg Ser Ile Arg Pro His	
35	45
Glu Cys Pro Thr Xaa Pro Gly Ala Gly Pro Arg Ala Pro Arg Arg Arg	
50	60
Xaa Leu Arg Ala Ser Ser Glu Asp Arg Lys Pro Val Gly Ala Gly Ser	
65	75
Pro Ala Ala Val Ala His Lys Ile Gln Leu Lys Ser Ala Asp Met Lys	
85	95
Glu Glu Met Arg Gln Asp Ala Phe Glu Ile Ala Arg Ile Ala Phe Asp	
100	110
Lys His Ser Met Glu Lys Asp Ile Ala Glu Tyr Ile Lys Lys Glu Phe	
115	125
Asp Lys Asn His Gly Pro Thr Leu Ala Leu His Arg Arg Pro Gln Leu	
130	140
Arg Phe Ile Arg Asp Ala Arg Asp Lys Leu Leu Cys Ile Phe Leu His	
145	155
Arg Leu	160

(2) INFORMATION FOR SEQ ID NO:3544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..521

(D) OTHER INFORMATION: / Ceres Seq. ID 1577296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3544:

taagattatt gatgttatcg agaagggaga gaaacagccc aacatcacta ttggcatttt	60
ggctcccggt gtcacgtgtg tcgttacctg tctctgcaa ctcctgtttg gtggcaagaa	120
accagtgcca cctgtgaaac ctgcagctga ggcgaagaag cccaaggccg cggagacgca	180
cggctgctga agcagtggtg acaaggatga gaaagaggat gaaaaggagg agacaggccc	240
acgtcggagg acccgaagg agNacataga cctgtttttg acgtgtttta gctcttctgg	300
cgtctgctta ttttgagaac ttctaattat tgtgagtgtg taataggagc ttatgtcacc	360
ctctgcgctt ccccgcgtgc tgatttggtt ttaattggta gaccaggacc cttcacgagc	420
gtagaattta gttctgtgtg gtcatttatg tgctgtgcct gacgggtgttc aatcagatag	480
agggtgatggt ttttttggtg gatcaaatca aggaatatatt c	

(2) INFORMATION FOR SEQ ID NO:3545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3545:

```
Lys Ile Ile Asp Val Ile Glu Lys Gly Glu Lys Gln Pro Asn Ile Thr
1           5           10           15
Ile Gly Ile Leu Val Ser Val Val Ile Val Phe Val Thr Val Leu Cys
20           25           30
Lys Leu Leu Phe Gly Gly Lys Lys Pro Val Ala Pro Val Lys Pro Ala
35           40           45
Ala Glu Ala Lys Lys Pro Lys Ala Ala Glu Thr Asp Gly Ala Gly Ser
50           55           60
Ser Gly Asp Lys Asp Glu Lys Glu Asp Glu Lys Glu Glu Thr Gly Pro
65           70           75           80
Arg Arg Arg Thr Arg Xaa Xaa Ile Asp Leu Phe Leu Thr Cys Phe
85           90           95
Ser Ser Ser Gly Val Cys Leu Phe
100
```

(2) INFORMATION FOR SEQ ID NO:3546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..811
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3546:

```
aggaagaag gaaccaccacca aagcttcaaa aaaagaaaaa gagctgcaca ctggctcactg      60
gaaaacgaag gcaaacacctta atcgctactc caccgcagcg cccactacac cgatcgggct      120
ccgatggact tcgcgggastg gaggccctcg agggcctccg gtggccatcg cactcgtggc      180
cgcgactacc ccccgccgcc cgctccctcg tcgtccccac ctcgctctc tcctcgccgc      240
tcgacgaccc caccgcccgc gacctctccc cgctgctacc ctacgcgcgc ctcgctgcgc      300
ctctcccgccg ttgtggcgcc cgctcaacc cgttctgcgc cgtgcaccac ggctccgcgc      360
gctggtctcg cgcctctctg Ggcgcgcgcg ccaaccgctt ccccgcccta ctggcccccgc      420
acgcgctccc cgccgaactc ttccccacc actccagcgt cgagtacttg ctgccccccg      480
accgccgctga gcccgggggga cggggggcac ctgcgctcgt gttcgtgatc gatcgggcca      540
cggcgccoga ggagctcaacc gtgctcaagg acgaggtgcg cagggtcatg cagggggtgc      600
ctgaggggat cagggtggcg ctgcgtactt tcgctgcgtc tgtgtgggtg cagcatcttg      660
gatttgaggg ttgcgctcgc gtgtgtgtgc ttaatggcga gcgtgagctc gagtctgaca      720
aggtttgtga atttgttaata taatccttag gacaccgaat ttgtaatttg gttctgcgcc      780
aatctatgtg acatgatcag cattotagtt c
```

(2) INFORMATION FOR SEQ ID NO:3547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3547:

Gly	Arg	Lys	Glu	Pro	Thr	Lys	Ala	Ser	Lys	Lys	Glu	Lys	Glu	Leu	His
1			5						10					15	
Thr	Gly	His	Trp	Lys	Thr	Lys	Ala	Asn	Pro	Asn	Arg	Tyr	Ser	Thr	Ala
			20					25					30		
Ala	Pro	Thr	Thr	Pro	Ile	Gly	Leu	Arg	Trp	Thr	Ser	Arg	Xaa	Gly	Gly
			35				40					45			
Arg	Gly	Gly	Pro	Pro	Val	Ala	Met	Ala	Leu	Val	Ala	Ala	Asp	Tyr	Pro
			50			55					60				
Arg	Arg	Arg	Val	Pro	Arg	Arg	Ala	His	Leu	Arg	Pro	Leu	Leu	Ala	Ala
65					70				75					80	
Ala	Ala	Pro	His	Gly	Ala	Gly	Pro	Pro	Pro	Ala	Ala	Thr	Leu	Arg	Ala
				85					90					95	
Ala	Pro	Leu	Arg	Leu	Pro	Gly	Leu	Trp	Arg	Arg	Ala	Gln	Pro	Val	Leu
			100				105						110		
Ala	Arg	Ala	Pro	Arg	Leu	Arg	Ala	Leu	Val	Leu	Arg	Leu	Leu	Trp	Arg
			115				120					125			
Arg	Arg	Gln	Pro	Val	Pro	Pro	Pro	Thr	Gly	Pro	Arg	Arg	Ala	Pro	Arg
			130				135				140				
Arg	Thr	Leu	Pro	His	Pro	Leu	Gln	Arg	Arg	Val	Leu	Ala	Ala	Pro	Gly
145					150					155					160
Pro	Arg														

(2) INFORMATION FOR SEQ ID NO:3548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1577304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3548:

Glu	Glu	Arg	Asn	Pro	Pro	Lys	Leu	Gln	Lys	Lys	Lys	Ser	Cys	Thr
1			5						10				15	
Leu	Val	Thr	Gly	Lys	Arg	Arg	Gln	Thr	Leu	Ile	Ala	Thr	Pro	Gln
			20				25					30		
Arg	Pro	Leu	His	Arg	Ser	Gly	Ser	Asp	Gly	Leu	Arg	Gly	Xaa	Ala
			35				40					45		
Val	Glu	Gly	Leu	Arg	Trp	Pro	Trp	His	Ser	Trp	Pro	Pro	Thr	Pro
			50			55					60			
Ala	Ala	Ala	Ser	Leu	Val	Val	Pro	Thr	Ser	Val	Leu	Cys	Ser	Pro
65					70				75				80	
Gln	His	Pro	Thr	Ala	Pro	Asp	Leu	Leu	Pro	Leu	Leu	Pro	Tyr	Ala
				85					90				95	
Leu	Arg	Cys	Ala	Ser	Pro	Gly	Cys	Gly	Ala	Ala	Leu	Asn	Pro	Phe
			100				105					110		
Arg	Val	His	His	Gly	Ser	Ala	Arg	Trp	Ser	Cys	Ala	Phe	Cys	Gly
			115				120					125		
Ala	Ala	Asn	Pro	Phe	Pro	Arg	Leu	Leu	Ala	Pro	Asp	Ala	Leu	Pro
130						135				140				
Glu	Leu	Phe	Pro	Thr	His	Ser	Ser	Val	Glu	Tyr	Leu	Leu	Pro	Asp
145					150				155					160
Pro	Ala	Glu	Pro	Gly	Gly	Pro	Gly	Pro	Pro	Ala	Leu	Val	Phe	Val
			165						170				175	
Asp	Ala	Ala	Thr	Ala	Ala	Glu	Glu	Leu	Thr	Val	Leu	Lys	Asp	Glu
			180					185					190	

Arg Arg Leu Met Gln Gly Leu Pro Glu Gly Ile Arg Val Ala Leu Val
195 200 205
Thr Phe Ala Ala Ser Val Trp Val His Asp Leu Gly Phe Glu Gly Cys
210 215 220
Ala Arg Val Val Val Leu Asn Gly Glu Arg Glu Leu Glu Ser Asp Lys
225 230 235 240
Val Cys Glu Phe Val Ile
245

(2) INFORMATION FOR SEQ ID NO:3549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3549:

Met Asp Phe Ala Xaa Trp Arg Pro Trp Arg Ala Ser Gly Gly His Gly
1 5 10 15
Thr Arg Gly Arg Arg Leu Pro Pro Pro Pro Arg Pro Ser Ser Cys Pro
20 25 30
Pro Pro Ser Ser Ala Arg Arg Cys Ser Thr Pro Arg Arg Arg Thr Ser
35 40 45
Ser Arg Cys Tyr Pro Thr Arg Arg Ser Ala Ala Pro Pro Arg Val Val
50 55 60
Ala Pro Arg Ser Thr Arg Ser Arg Ala Cys Thr Thr Ala Pro Arg Ala
65 70 75 80
Gly Pro Ala Pro Ser Val Ala Pro Pro Pro Thr Arg Ser Pro Ala Tyr
85 90 95
Trp Pro Pro Thr Arg Ser Pro Pro Asn Ser Ser Pro Pro Thr Pro Ala
100 105 110
Ser Ser Thr Cys Cys Pro Arg Thr Pro Leu Ser Pro Gly Asp Arg Gly
115 120 125
His Leu Arg Ser Cys Ser
130

(2) INFORMATION FOR SEQ ID NO:3550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 887 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..887

(D) OTHER INFORMATION: / Ceres Seq. ID 1577310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3550:

acctgacggg ctcgcatcgc acccgccacc cccaccgcac gcaccctctc gtccctctctg 60
cgccgacccg gctctctctc cccaacacaa tctctcttcc cccatccagt ctccgctctcg 120
cgccgacgct gagggacagc gagaagagac agacacagat cgcgcgcgga gatgctgctcg 180
gactcgtcgt cgtggcgcg cgccctgggt cagatctcgc cctacacctt ctccgcaatc 240
ggatcgccgc tctccatcgc cgtctccgtc ctccggcgcg catgggggtat ctccatcacg 300
gggagcagcc tcactcgggc cgccatcaag gcgcccagga tcactcttaa gaacctcatc 360
agtgtcatct tctgtgaggg tctcgcaatt tatggcgtaa ttgtggcatt catcctccag 420
acaaagcttg aaagtgtgcc aacatctcaa atgtatgata cggagctctct tcgagctggc 480
tatgcaatct ttgcacatgc cttatcgttt ggctttgcta atcttgtttg cggggtatcg 540
Ggtggggata attggaagca Gctgcgcact gtctgatgct cagaactcat cactctctgt 600
aaagattttg gtgattgaga tcttcggcag cgctctggga ctgttcggtg tcattgtggg 660

catcattatg tcattctcaag cgacatggcc agcaaaaagct tgattttcac catttgtagc 720
tctgtaaatt attcagatgg agtgtatoga aatgtgcatg tggcttaact gcattttcat 780
gttcctttta tgtggcgctct tttttggcag aacacgaaat gcggcgcsyt accgcaccgg 840
attgtagagt tgcatttctt actgcccggag tactccatgt gtgttgg

(2) INFORMATION FOR SEQ ID NO:3551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1577311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3551:

Pro Asp Gly Leu Ala Ser His Pro Pro Pro Pro His Ala Pro Ser
1 5 10 15
Arg Pro Leu Cys Ala Asp Pro Ala Leu Leu Pro Gln His Asn Pro Pro
20 25 30
Ser Pro Ile Gln Ser Arg Gly Arg Gly His Ala Glu Gly Gln Arg Glu
35 40 45
Glu Thr Asp Thr Asp Arg Ala Arg Cys Arg Arg Thr Arg Arg Arg
50 55 60
Gly Arg Ala Pro Trp Cys Arg Ser Arg Pro Thr Pro Ser Pro Gln Ser
65 70 75 80
Val Ser Pro Ser Pro Ser Ala Ser Pro Ser Ser Ala Arg His Gly Val
85 90 95
Ser Ser Ser Arg Gly Ala Ala Ser Ser Gly Pro Pro Ser Arg Arg Pro
100 105 110
Gly Ser Leu Leu Arg Thr Ser Ser Val Ser Ser Val Arg Leu Ser
115 120 125
Gln Phe Met Ala
130

(2) INFORMATION FOR SEQ ID NO:3552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1577312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3552:

Leu Thr Gly Ser His Arg Thr Arg His Pro His Arg Thr His Pro Leu
1 5 10 15
Val Leu Ser Ala Pro Thr Arg Leu Phe Ser Pro Asn Thr Ile Leu Leu
20 25 30
Pro Arg Ser Ser Leu Ala Val Ala Ala Thr Leu Arg Asp Ser Glu Lys
35 40 45
Arg Gln Thr Gln Ile Ala Arg Gly Asp Val Val Gly Leu Val Val Val
50 55 60
Gly Ala Arg Pro Gly Ala Asp Leu Ala Leu His Leu Leu Arg Asn Arg
65 70 75 80
Tyr Arg Arg Leu His Arg Arg Leu Arg Pro Arg Arg Gly Met Gly Tyr
85 90 95
Leu His His Gly Glu Gln Pro His Arg Gly Arg His Gln Gly Ala Gln
100 105 110
Asp His Phe

115

(2) INFORMATION FOR SEQ ID NO:3553:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3553:

```
Met Ser Ser Asp Ser Ser Ser Trp Ala Arg Ala Leu Val Gln Ile Ser
1      5      10      15
Pro Tyr Thr Phe Ser Ala Ile Gly Ile Ala Val Ser Ile Gly Val Ser
20      25      30
Val Leu Gly Ala Ala Trp Gly Ile Phe Ile Thr Gly Ser Ser Leu Ile
35      40      45
Gly Ala Ala Ile Lys Ala Pro Arg Ile Thr Ser Lys Asn Leu Ile Ser
50      55      60
Val Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Val Ile Val Ala Ile
65      70      75      80
Ile Leu Gln Thr Lys Leu Glu Ser Val Pro Thr Ser Gln Met Tyr Asp
85      90      95
Pro Glu Ser Leu Arg Ala Gly Tyr Ala Ile Phe Ala Ser Gly Leu Ile
100     105     110
Val Gly Phe Ala Asn Leu Val Cys Gly Val Cys Gly Gly Asp Asn Trp
115     120     125
Lys Gln Leu Arg Thr Val
130
```

(2) INFORMATION FOR SEQ ID NO:3554:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1577318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3554:

```
atccgaaacc agagcggaaga atcgccatca cagcaagcta cgcgcactga aatcctccaa 60
tccacaggagc acagctctac ttccgcagtt cgcactcgca cgcaccaagc cgctagcaac 120
gaagcagaaaa tgtcgtctggt gagggcgasa cgcgtgttoga cccattctcc gtggacctct 180
tcgacccggtt cgacagcatg ttccgtctca tcgtgccgtc gtctgtctgc tcggggtccg 240
agaccgcgcgc cttcgccagc gccgcgatcg actggaagga gacgcccag ggcacagtg 300
tcaaggtccga cctcccgcgc gtgaagaaag aggaagtgcaa ggtggaagtg gagcagcgga 360
acgtgctgtct catcagcggg cagcgcaGca gggagaagga ggacaagggc gacaagtggc 420
accgcgtgga gcgcagcagc ggccagtctg tgcggcgctt ccgcctgccg gagaacgcca 480
agacggagga ggtgagggcc gcgctggaga acggcgctgt cacggtcaac gtgcccgaag 540
ccgaggtcaa gaagcccgag gtgaagagca tccagatctc cggctgaaga agacatggag 600
gggaggtgaa tggntcgcgt cgcgttcgcg tcgcgcgcgc ggaatcttggg ttccagcgac 660
gcgactcgtg tgtgtgtgct gtgtggttgc tctgctttgg tatgtttggt gtgtacgtgt 720
gcgtgttcagt gtttctcgtt cctcgtctgt actttgcgct gttcggtaga cttcctggct 780
cagtatgttg ttgtgtgcga gtgaataaat aaawacaaac cagctgtagt atattcacct 840
actactatcg tgtttcaaaa agaagaaga acgctt
```

(2) INFORMATION FOR SEQ ID NO:3555:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1577319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3555:
Ile Arg Asn Gln Ser Glu Glu Ser Pro Ser Gln Gln Ala Thr Arg Thr
1 5 10 15
Glu Ile Leu Gln Ser Thr Gly His Ser Ser Thr Ser Ala Val Arg Thr
20 25 30
Arg Thr His Gln Ala Ala Ser Asn Glu Ala Glu Met Ser Leu Val Arg
35 40 45
Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr Ser Ser Thr Arg Ser
50 55 60
Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg Arg Arg Ala Pro
65 70 75 80
Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser Thr Gly Arg Arg Arg Pro
85 90 95
Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala
100 105

(2) INFORMATION FOR SEQ ID NO:3556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..64
(D) OTHER INFORMATION: / Ceres Seq. ID 1577320
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3556:

Met Ser Leu Val Arg Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr
1 5 10 15
Ser Ser Thr Arg Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg
20 25 30
Arg Arg Arg Ala Pro Arg Pro Pro Ser Pro Ala Pro Ala Ser Thr
35 40 45
Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:3557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1577321
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3557:

Met Phe Arg Ser Ile Val Pro Ser Ser Ser Ser Gly Ser Glu Thr
1 5 10 15
Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro Glu Ala
20 25 30

His Val Phe Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu Val Lys
35 40 45
Val Glu Val Glu Asp Gly Asn Val Leu Leu Ile Ser Gly Gln Arg Ser
50 55 60
Arg Glu Lys Glu Asp Lys Gly Asp Lys Trp His Arg Val Glu Arg Ser
65 70 75 80
Ser Gly Gln Phe Val Arg Arg Phe Arg Leu Pro Glu Asn Ala Lys Thr
85 90 95
Glu Glu Val Arg Ala Ala Leu Glu Asn Gly Val Leu Thr Val Thr Val
100 105 110
Pro Lys Ala Glu Val Lys Lys Pro Glu Val Lys Ser Ile Gln Ile Ser
115 120 125
Gly

(2) INFORMATION FOR SEQ ID NO:3558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3558:

acggccaatc	aggagtcCaa	aggccCacat	gtatcMagag	cacgtccgtc	gccccctgga	60
ccacgcagcc	Cggcagccca	gagccggaga	gcccagtgaa	acagagccgg	tgaacgcagc	120
ccagtcagtg	acccccccga	tcccgaactcc	ggcgatctcc	ccaaccccat	ggcctccgccc	180
ggcgaggccc	ccagcacgct	cctccgcttc	ctctacttcc	tccggccggg	agtaatctgc	240
accaaggcca	tcaacacctc	tccgactcac	gagcacaaaga	aggagtcac	cgccgccttc	300
gccgcgcgcg	aatcggCgtG	tggtgtctgc	cgcggcgccc	gagcccgcctc	ctgcaacccg	360
cgcgcggaag	ccCgtgattgt	ggacgagggc	ctgtctctcg	cggttagggt	tctcggaatg	420
ttgtctctcca	taggggagat	agatatcttc	tttgtttct	gatgtttcag	ctacgtgtat	480
gtgtctctttt	ggcttgaatc	aatcagtaat	aatacttctc	tctctgtct		

(2) INFORMATION FOR SEQ ID NO:3559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3559:

Arg Pro Ile Arg Ser Pro Lys Ala His Met Tyr Xaa Glu His Val Arg
1 5 10 15
Arg Pro Leu Asp His Ala Ala Arg Gln Pro Arg Ala Gly Glu Pro Ser
20 25 30
Glu Thr Glu Pro Val Asn Ala Ala Gln Ser Val Thr Pro Pro Ile Pro
35 40 45
Thr Pro Ala Ile Ser Pro Thr Pro Trp Pro Pro Ala Arg Pro Pro
50 55 60
Ala Arg Ser Ser Ala Ser Thr Ser Ser Ala Pro Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1577348
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3560:
Met Tyr Xaa Glu His Val Arg Arg Pro Leu Asp His Ala Ala Arg Gln
1 5 10 15
Pro Arg Ala Gly Glu Pro Ser Glu Thr Glu Pro Val Asn Ala Ala Gln
20 25 30
Ser Val Thr Pro Pro Ile Pro Thr Pro Ala Ile Ser Pro Thr Pro Trp
35 40 45
Pro Pro Pro Ala Arg Pro Pro Ala Arg Ser Ser Ala Ser Ser Thr Ser
50 55 60
Ser Ala Pro Glu
65

(2) INFORMATION FOR SEQ ID NO:3561:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1577349
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3561:
Met Ala Ser Ala Gly Glu Ala Pro Ser Thr Leu Leu Arg Phe Leu Tyr
1 5 10 15
Phe Val Gly Ala Gly Val Ile Cys Thr Lys Ala Ile Asn Thr Tyr Arg
20 25 30
Asp Tyr Glu His Lys Lys Glu Ser Thr Ala Ala Leu Ala Ala Glu
35 40 45
Ser Ala Cys Gly Cys Cys Arg Gly Gly Arg Ala Arg Ser Cys Asn Arg
50 55 60
Arg Arg Glu Ala Leu Ile Val Asp Glu Gly Leu Ser Ser Ala Val Arg
65 70 75 80
Val Leu Gly Met Leu Leu Ser Ile Gly Glu Ile Asp Ile Phe Phe Cys
85 90 95
Phe

(2) INFORMATION FOR SEQ ID NO:3562:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 737 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..737
(D) OTHER INFORMATION: / Ceres Seq. ID 1577353
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3562:
aaaaaatttaa aatctctccg gaaatcagag acgcgaatcc ctgcgcccg gccccgaaac 60
ctccgagttc tctcgccaat tcgatccgcc tcacgcgcgc cgcgcgctcc ccggtcggcc 120
ttgaactgct cgtgcacgt ggcggttcgc agcgcggaaat ctaccttggt ttgagagatc 180
cggggaaacc cttgttcccg gtcgttcccg ctccaattct ctgcggactg gcaatgtgaa 240
cgtttctcat cggagggcga cgaatctacgg ggcggttggt ggcgggggttk aggggaatgga 300

gcacgtgttc ggaggggaagt ttaagcttgg gaagaagatc gggagcggat Cctttcggcg 360
agctctatct cggcgccaac atacagagcg gcgaggaggt ggctatcaag ttggtatgag 420
ataaatctgat actgttctgt caccattttt ctctgycgtg gaggttatag cctggcattc 480
ggcatgagtt tgttccatat gcaaacatat catggtcaac cattctagca acggtttctg 540
gaagaatttg tgtgtagatt atgggatgac agaaaaatgga tgatgttctg catgtaattg 600
ctttaaaaaa gactggcatg gtcccagact atatttttac atgagtaata acaagatttt 660
caaacctttt ctgtgttgta catgcgaatt aacctgtgga tccagtteta attccaatca 720
tgggtttgtt aaccttc

(2) INFORMATION FOR SEQ ID NO:3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1577354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3563:

Lys	Lys	Leu	Lys	Ser	Ser	Arg	Lys	Ser	Glu	Thr	Arg	Ile	Pro	Arg	Pro
1		5						10						15	
Arg	Pro	Arg	Asn	Leu	Arg	Val	Leu	Ser	Pro	Ile	Arg	Ser	Ala	Ser	Pro
		20					25						30		
Pro	Pro	Pro	Val	Arg	Arg	Ser	Ala	Leu	Thr	Ala	Pro	Ser	His	Val	Ala
		35					40					45			
Val	Arg	Ser	Ala	Glu	Ser	Thr	Leu	Cys							
		50				55									

(2) INFORMATION FOR SEQ ID NO:3564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1577355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3564:

Lys	Ile	Lys	Ile	Leu	Pro	Glu	Ile	Arg	Asp	Ala	Asn	Pro	Ser	Pro	Gln
1		5						10						15	
Ala	Pro	Lys	Pro	Pro	Ser	Ser	Leu	Ala	Asn	Ser	Ile	Arg	Leu	Thr	Ala
		20					25						30		
Ala	Ala	Arg	Pro	Pro	Val	Gly	Leu	Asp	Cys	Ser	Val	Ala	Arg	Gly	Gly
		35					40				45				
Ser	Gln	Arg	Gly	Ile	Tyr	Leu	Val	Leu	Arg	Asp	Pro	Gly	Lys	Pro	Leu
		50				55					60				
Phe	Pro	Val	Val	Pro	Ala	Arg	Ile	Phe	Cys	Gly	Leu	Ala	Met		
		65				70					75				

(2) INFORMATION FOR SEQ ID NO:3565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1577356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3565:

Met	Glu	His	Val	Phe	Gly	Gly	Lys	Phe	Lys	Leu	Gly	Lys	Lys	Ile	Gly
1			5				10			15					
Ser	Gly	Ser	Phe	Arg	Arg	Ala	Leu	Ser	Arg	Arg	Gln	His	Thr	Glu	Arg
			20				25						30		
Arg	Gly	Gly	Gly	Tyr	Gln	Val	Gly	Met	Arg						
			35				40								

(2) INFORMATION FOR SEQ ID NO:3566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3566:

cgggccacct	cgagctgcgc	aaccgcgacc	ccgacgacaa	cccgtgtgtg	acgttcaact	60
actttctgcg	ccccgaggac	ctccgcgcgt	gcgtggccgg	cttgtcggtc	atcgagcgcg	120
tcataccttc	ccaggccttc	aagaacttca	cgtaccocga	ctctccatg	gagacgctgc	180
tcaacatgtc	gacgggggttc	cccgctcaacc	tgtgcctccg	gcacgacaa	gactccaagt	240
cgcttgagat	gtttctgcaa	gacaccgtca	tgaccatctg	gcactaccac	gggtgctgcc	300
aggtcgccag	ggctcgtcgc	gctgaatacc	gagtgctcgg	catcgacCcg	ctgcgcgtca	360
ttgacggctc	cactttcaac	gcctgcgccg	gaaccaaccc	gcaggcaacc	gtcatgatgc	420
tcggcaggta	tatggggagt	agaatcacaa	acgaagggtt	ggcagctgaa	ggattagagg	480
gaacaaaact	gtgatgatcc	tataatccaa	gacagtaggc	gaggcgtaTt	taagaatctc	540
tattgaacta	tgtaatgctg	gattcaatat	tggtgtgtgt	attctgatat	tgataggttg	600
cacatattgt	cggagttgta	tcattgttgt	tggtgttact	atgtggacta	ttatgagtga	660
aatctgc						

(2) INFORMATION FOR SEQ ID NO:3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3567:

Gly	His	Leu	Glu	Leu	Arg	Asn	Arg	Asp	Pro	Asp	Asp	Asn	Pro	Leu	Val
1			5					10					15		
Thr	Phe	Asn	Tyr	Phe	Ser	His	Pro	Glu	Asp	Leu	Arg	Arg	Cys	Val	Ala
			20					25					30		
Gly	Leu	Ser	Val	Ile	Glu	Arg	Val	Ile	His	Ser	Gln	Ala	Phe	Lys	Asn
			35				40					45			
Phe	Thr	Tyr	Pro	Asp	Phe	Ser	Met	Glu	Thr	Leu	Leu	Asn	Met	Ser	Thr
			50				55				60				
Gly	Phe	Pro	Val	Asn	Leu	Leu	Pro	Arg	His	Asp	Asn	Asp	Ser	Thr	Ser
			65				70			75				80	
Leu	Glu	Met	Phe	Cys	Lys	Asp	Thr	Val	Met	Thr	Ile	Trp	His	Tyr	His
			85					90					95		
Gly	Gly	Cys	Gln	Val	Gly	Arg	Val	Asp	Ala	Glu	Tyr	Arg	Val	Leu	
			100				105						110		
Gly	Ile	Asp	Ala	Leu	Arg	Val	Ile	Asp	Gly	Ser	Thr	Phe	Asn	Ala	Ser
			115				120					125			
Pro	Gly	Thr	Asn	Pro	Gln	Ala	Thr	Val	Met	Met	Leu	Gly	Arg	Tyr	Met
			130				135								

Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly Leu Glu Gly
145 150 155 160
Thr Lys Pro

(2) INFORMATION FOR SEQ ID NO:3568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3568:

Met Glu Thr Leu Leu Asn Met Ser Thr Gly Phe Pro Val Asn Leu Leu
1 5 10 15
Pro Arg His Asp Asn Asp Ser Thr Ser Leu Glu Met Phe Cys Lys Asp
20 25 30
Thr Val Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Arg
35 40 45
Val Val Asp Ala Glu Tyr Arg Val Leu Gly Ile Asp Ala Leu Arg Val
50 55 60
Ile Asp Gly Ser Thr Phe Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala
65 70 75 80
Thr Val Met Met Leu Gly Arg Tyr Met Gly Val Arg Ile Thr Asn Glu
85 90 95
Arg Leu Ala Ala Glu Gly Leu Glu Gly Thr Lys Pro
100 105

(2) INFORMATION FOR SEQ ID NO:3569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3569:

Met Ser Thr Gly Phe Pro Val Asn Leu Leu Pro Arg His Asp Asn Asp
1 5 10 15
Ser Thr Ser Leu Glu Met Phe Cys Lys Asp Thr Val Met Thr Ile Trp
20 25 30
His Tyr His Gly Gly Cys Gln Val Gly Arg Val Val Asp Ala Glu Tyr
35 40 45
Arg Val Leu Gly Ile Asp Ala Leu Arg Val Ile Asp Gly Ser Thr Phe
50 55 60
Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala Thr Val Met Met Leu Gly
65 70 75 80
Arg Tyr Met Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly
85 90 95
Leu Glu Gly Thr Lys Pro
100

(2) INFORMATION FOR SEQ ID NO:3570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..722
(D) OTHER INFORMATION: / Ceres Seq. ID 1577378
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3570:
gctctcatcc ggcctcttcgc ggggctcaac ctcagcgta cccagctggt cgcgctctcg 60
ggctcgcaact ccatcggcga ggcccgctgc ttctccatcg tcttcgcgct ctacaaccag 120
ctctggatccg gccgcccga cccgcacatg gacacgcgct accgcgcgtc gctcgacgca 180
ctctgccccca agggcggcga cgaggaggct acgggaggcc tggacgcac ccacgcgcatc 240
ttcgacaacc agtacttcga gcgacctcgt Gcgctccgcg gcttcctcaa ctccgaccag 300
acgctcttct ctgacaacac caggaccctg cgggtcgctc agcggtctca caaggaccag 360
gacgcttct ctagggcctt catcgagggg atgataaaga tgggggagct ccaaaacccc 420
aggaaggggg agatacggcg caactgNtcg cgttgctaac aactcgccgt ggcaaccaag 480
gacggggagt gcgtccggac agtcgacatc tgagctcccg tgatgaggtt ggtgtttcag 540
aagaaatcga gccctgatat ggtactaata tgttgacatg cattgttgtt tttttggtcg 600
tgtgtgaagt ttgcacctac ctatggctgt ggtgcncrrg tgcgctcatt gctgacgtgg 660
ggaaataatt agacattgtg ccttagctcc aataacgttc aatatattta tcctttatat 720
cg

(2) INFORMATION FOR SEQ ID NO:3571:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1577379
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3571:
Ala Leu Ile Arg Leu Phe Ala Gly Leu Asn Leu Ser Val Thr Asp Leu
1 5 10 15
Val Ala Leu Ser Gly Ser His Ser Ile Gly Glu Ala Arg Cys Phe Ser
20 25 30
Ile Val Phe Arg Leu Tyr Asn Gln Ser Gly Ser Gly Arg Pro Asp Pro
35 40 45
His Met Asp Thr Ala Tyr Arg Arg Ser Leu Asp Ala Leu Cys Pro Lys
50 55 60
Gly Gly Asp Glu Glu Val Thr Gly Gly Leu Asp Ala Thr Pro Arg Ile
65 70 75 80
Phe Asp Asn Gln Tyr Phe Glu Asp Leu Xaa Ala Leu Arg Gly Phe Leu
85 90 95
Asn Ser Asp Gln Thr Leu Phe Ser Asp Asn Thr Arg Thr Arg Arg Val
100 105 110
Val Glu Arg Leu Ser Lys Asp Gln Asp Ala Phe Phe Arg Ala Phe Ile
115 120 125
Glu Gly Met Ile Lys Met Gly Glu Leu Gln Asn Pro Arg Lys Gly Glu
130 135 140
Ile Arg Arg Asn Xaa Ser Arg Cys
145 150

(2) INFORMATION FOR SEQ ID NO:3572:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1577380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3572:

Leu Ser Ser Gly Ser Ser Arg Gly Ser Thr Ser Ala Ser Pro Thr Trp
1 5 10 15
Ser Arg Ser Arg Ala Arg Thr Pro Ser Ala Arg Pro Ala Ala Ser Pro
20 25 30
Ser Ser Ser Ala Ser Thr Thr Ser Leu Asp Pro Ala Ala Pro Thr Arg
35 40 45
Thr Trp Thr Pro Pro Thr Ala Ala Arg Ser Thr His Ser Ala Pro Arg
50 55 60
Ala Ala Thr Arg Arg Ser Arg Glu Ala Trp Thr Pro Pro His Ala Ser
65 70 75 80
Ser Thr Thr Ser Thr Ser Arg Thr Ser Xaa Arg Ser Ala Ala Ser Ser
85 90 95
Thr Pro Thr Arg Arg Ser Ser Leu Thr Thr Pro Gly Pro Val Gly Ser
100 105 110
Ser Ser Gly Ser Ala Arg Thr Arg Thr Pro Ser Ser Gly Pro Ser Ser
115 120 125

Arg Gly
130

(2) INFORMATION FOR SEQ ID NO:3573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1577381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3573:

Ser His Pro Ala Leu Arg Gly Ala Gln Pro Gln Arg His Arg Pro Gly
1 5 10 15
Arg Ala Leu Gly Leu Ala Leu His Arg Gly Pro Leu Leu His
20 25 30
Arg Leu Pro Pro Leu Gln Pro Val Trp Ile Arg Pro Pro Arg Pro Ala
35 40 45
His Gly His Arg Leu Pro Pro Leu Ala Arg Arg Thr Leu Pro Gln Gly
50 55 60
Arg Arg Arg Gly Gly His Gly Arg Pro Gly Arg His Pro Thr His Leu
65 70 75 80
Arg Gln Pro Val Leu Arg Gly Pro Arg Xaa Ala Pro Arg Leu Pro Gln
85 90 95
Leu Arg Pro Asp Ala Leu Leu
100

(2) INFORMATION FOR SEQ ID NO:3574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..761

(D) OTHER INFORMATION: / Ceres Seq. ID 1577382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3574:

cattctctcgt gcagggtggt gaggttaatg ttaagggtgaa aagtcaggc acacataaca 60
tgcaacaataa tgatttctat gctaagaga agttggtcaa atcaatgcgt gattgtgatac 120

cttcgtcttt	gogccattgg	attgtaagag	ttgttttctt	gttttatatt	ttttttgtta	180
ttctaccat	tgaattgggc	attcaatacc	tgtycattat	ctttatgctt	atgcaatcca	240
ataatgatgg	aaaataactg	acttggtctg	tctcttgagt	tgtggcaacC	ggaagttcca	300
ggccccattg	cagcacYtac	actgcgctaa	tggaccttca	ggactattct	gagaatggaa	360
ctgtaaccgt	ggatatatga	gtgatactta	aaggaaactga	tggagaggca	tatagagatg	420
ccacggggcac	aacacagttG	coatgagggg	cgcagggaag	atgctgttgc	agccgcagag	480
gaagctgcac	tcagcaaagc	ttgcgcgatg	tctcggtttg	gcctgtatct	gtaccaccag	540
gatgaatctc	attacgaactg	ccactttocat	tgaggctcaa	tctgcaaaag	agttgatcat	600
aagtgtgaac	atgcgtttgga	tatgcccccta	gaaaattcgt	atctagaatc	aatttttgtgt	660
ctttgcgtag	tatcatactc	ataacacaaa	gaagtgaacc	tatgtagatg	ctatttgaaa	720
ccddkttatt	aatattataa	ttcttattaa	tattattgta	t		

(2) INFORMATION FOR SEQ ID NO:3575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3575:

Phe	Leu	Val	Gln	Val	Val	Glu	Val	Asn	Val	Lys	Val	Glu	Ser	Ala	Gly
1		5								10				15	
Thr	His	Asn	Met	His	Asn	Asn	Asp	Phe	Tyr	Ala	Lys	Glu	Lys	Leu	Leu
		20					25						30		
Lys	Ser	Met	Arg	Asp	Cys	Asp	Pro	Ser	Ser	Leu	Arg	His	Trp	Ile	Val
		35					40					45			
Arg	Val	Val	Phe	Leu	Phe	Tyr	Ile	Phe	Phe	Val	Ile	Pro	Thr	Ile	Glu
		50				55				60					
Leu	Gly	Ile	Gln	Tyr	Leu	Xaa	Ile	Ile	Phe	Met	Leu	Met	Gln	Ser	Asn
					70					75					80
Asn	Asp	Gly	Lys												

(2) INFORMATION FOR SEQ ID NO:3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3576:

Met	His	Asn	Asn	Asp	Phe	Tyr	Ala	Lys	Glu	Lys	Leu	Lys	Ser	Met	
1		5								10				15	
Arg	Asp	Cys	Asp	Pro	Ser	Ser	Leu	Arg	His	Trp	Ile	Val	Arg	Val	Val
		20					25						30		
Phe	Leu	Phe	Tyr	Ile	Phe	Phe	Val	Ile	Pro	Thr	Ile	Glu	Leu	Gly	Ile
		35					40					45			
Gln	Tyr	Leu	Xaa	Ile	Ile	Phe	Met	Leu	Met	Gln	Ser	Asn	Asn	Asp	Gly
		50				55					60				
Lys															
65															

(2) INFORMATION FOR SEQ ID NO:3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1577385
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3577:
Met Arg Gly Ala Gly Lys Met Leu Leu Gln Pro Gln Arg Lys Leu His
1 5 10 15
Ser Ala Lys Leu Ala His Gly Ser Val Leu Ala Cys Ile Cys Thr Thr
20 25 30
Arg Met Asn Leu Ile Thr Thr Thr Ser Ile Glu Ala Gln Ser Ala
35 40 45
Lys Glu Leu Ile Ile Ser Cys Asn Met Arg Trp Ile Cys Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:3578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..780
(D) OTHER INFORMATION: / Ceres Seq. ID 1577401
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3578:
gagctcgctg cgcgcgtctt caatgctccc cggcgcgcct cccgctataa agcacctgcc 60
ttggcacctc tctctctctc cgaccacaca ccacgcctcc acacacaaga agagagccga 120
gagctagcta cctagcgcgc gatggcgatg tccgcttcca agatgatggc ggtagccgcc 180
gctnccctg ctagccctg tcttggccgc gtcgacgcgc naggcgagga acatcaagac 240
gacgacgacg acgacggaga agaaggacga tgcgggtggt bagccgcaga ccttccccgc 300
cttcgacgac ctcggcggcg gNcgctCcc ccggcgctcc gtagcctccc cggcacctcg 360
tcggcgccga gcagcattcc agcgttcagc atcgccggca gcggcagcag cctccccggc 420
gggtggttct tgcccggcag cagcggcagc atcgccgaga tgcccctctt cagcggcgcc 480
tcccccgctc tcagcggctt cggcgccatg cccgggtccc ncggcccgcc cctcgctccc 540
ctcgtccccg tgcacggcag caagccctga aaatccgtcc gtccgcggag ccgggaagtc 600
tgtcgggcca acttgtgccc tagtaactct ttgctgcat tgtattggag agttggatc 660
cggtttcgtg ttggtgtttg tttgttatta taggcgcctc atctaccgag acatgtgat 720
ttgttgctgg taaataatcaa tcggttgtat tcatgctgct gctgtgtgct ttaatttgct 780

(2) INFORMATION FOR SEQ ID NO:3579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1577402
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3579:
Met Ala Met Ser Ala Ser Lys Met Met Ala Val Ala Ala Ala Xaa Pro
1 5 10 15
Ala Ser Pro Gly Pro Gly Arg Val Asp Arg Xaa Gly Glu Glu His Gln
20 25 30
Asp Asp Asp Asp Asp Asp Gly Glu Glu Gly Arg Cys Gly Gly Xaa Ala
35 40 45
Ala Asp Leu Pro Ala Leu Arg Xaa Pro Arg Arg Arg Xaa Arg Pro Pro

50 55 60
Ala Ser Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro
65 70 75 80
Ala Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe
85 90 95
Leu Pro Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly
100 105 110
Gly Ser Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala
115 120 125
Ala Gly Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3580:

Met Ser Ala Ser Lys Met Met Ala Val Ala Ala Ala Xaa Pro Ala Ser
1 5 10 15
Pro Gly Pro Gly Arg Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp
20 25 30
Asp Asp Asp Asp Gly Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp
35 40 45
Leu Pro Ala Leu Arg Xaa Pro Arg Arg Arg Xaa Arg Pro Ala Ser
50 55 60
Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe
65 70 75 80
Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro
85 90 95
Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser
100 105 110
Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly
115 120 125
Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1577404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3581:

Met Met Ala Val Ala Ala Xaa Pro Ala Ser Pro Gly Pro Gly Arg
1 5 10 15
Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp Asp Asp Asp Gly
20 25 30
Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp Leu Pro Ala Leu Arg
35 40 45
Xaa Pro Arg Arg Arg Xaa Arg Pro Pro Ala Ser Gly Gly Leu Pro Gly
50 55 60

Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe Ser Met Pro Gly Ser
65 70 75 80
Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro Gly Ser Ser Gly Ser
85 90 95
Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser Pro Ala Phe Ser Gly
100 105 110
Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly Ser Val Ser Val Val
115 120 125
Pro Val His Gly Ser Lys Pro
130 135

(2) INFORMATION FOR SEQ ID NO:3582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 837 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..837

(D) OTHER INFORMATION: / Ceres Seq. ID 1577405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3582:

accctctcca	cttcggttcc	cggatcccg	ttccagctcc	gatccaaccc	agcatctgtta	60
ccgcgcgcgc	gagcacgtcc	ggcgccggtg	cggcaggcga	aatccgagag	cactctctmcc	120
ccgctacgccc	gcaccgcgca	tggccgcagc	tagccgcaga	tagagagagg	cgcaggcgag	180
ggcgtgcaga	tccagatccg	gtggcgcgga	aggacttgat	cgccccacc	accatggccg	240
gcccgtgtgt	ggcgctcttc	ctgctggaca	tgaaggccgc	cggtctctgct	tggcgcgact	300
accgcgcgca	tgtctccgcg	ctccaggccg	agcgcttctt	caccaagctc	ctcgacaagg	360
agggcgattc	ggaagtgcac	tcgcctgtgg	tctacgacga	cgctggcgctc	acttaccatgt	420
tcattccagca	caacaatgtc	ttctctctca	ccgcgcgctg	ccagaactgt	aacggcgcc	480
agcatctctc	tctctctcca	ccgtgttaata	gatgtgttta	agcactactt	cgaggagctg	540
gaggaggagt	cgctcaagaga	taacttgcgt	gttggtgatg	agttgctcga	tgagatgatg	600
gattttgggt	accacacaata	cacggaggcg	aagatattga	gtgagttcat	caagacagat	660
gcatacacga	tggagggtcac	acagcgtcca	cccatggccg	tgacaaaatgc	tgtgtcatgg	720
aggagcgagg	ggatcccggtta	caagaagaat	gaagtcttct	tggatgtagt	ggagagtggt	780
aaacattctag	ttaacacgcaa	tggccagatt	gtgagatcag	atgtgggttg	ggcactg	

(2) INFORMATION FOR SEQ ID NO:3583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1577406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3583:

Pro	Leu	His	Phe	Arg	Phe	Arg	Ile	Pro	Phe	Pro	Ala	Pro	Ile	Gln	Pro
1		5						10					15		
Ser	Ile	Cys	Thr	Ala	Pro	Xaa	Ser	Thr	Ser	Gly	Ala	Gly	Ala	Ala	Gly
			20				25						30		
Glu	Ile	Arg	Glu	His	Ser	Xaa	Pro	Ala	Thr	Pro	His	Arg	Pro	Trp	Pro
		35				40					45				
Gln	Leu	Ala	Ala	Asp	Arg	Glu	Arg	Arg	Arg	Gly	Arg	Ala	Asp	Pro	
	50				55					60					
Asp	Pro	Val	Gly	Gly	Lys	Asp	Leu	Ile	Ala	Pro	Thr	Thr	Met	Ala	Gly
65			70						75				80		
Pro	Val	Ser	Ala	Leu	Phe	Leu	Leu	Asp	Met	Lys	Gly	Arg	Val	Leu	Val
			85					90					95		
Trp	Arg	Asp	Tyr	Arg	Gly	Asp	Val	Ser	Ala	Leu	Gln	Ala	Glu	Arg	Phe

100 105 110
Phe Thr Lys Leu Leu Asp Lys Glu Gly Asp Ser Glu Val His Ser Pro
115 120 125
Val Val Tyr Asp Asp Ala Gly Val Thr Tyr Met Phe Ile Gln His Asn
130 135 140
Asn Val Phe Leu Leu Thr Ala Ala Arg Gln Asn Cys Asn Ala Ala Gln
145 150 155 160
His Pro Pro Leu Pro Pro Cys Asn Arg Cys Val
165 170

(2) INFORMATION FOR SEQ ID NO:3584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3584:

Met Ser Pro Arg Ser Arg Pro Ser Ala Ser Ser Pro Ser Ser Ser Thr
1 5 10 15
Arg Arg Ala Ile Arg Lys Cys Thr Arg Leu Trp Ser Thr Thr Thr Leu
20 25 30
Ala Ser Leu Thr Cys Ser Ser Ser Thr Thr Met Ser Ser Ser Ser Pro
35 40 45
Pro Leu Ala Arg Thr Val Thr Arg Pro Ser Ile Leu Leu Phe Leu His
50 55 60
Arg Val Ile Asp Val Phe Lys His Tyr Phe Glu Glu Leu Glu Glu Glu
65 70 75 80
Ser Leu Arg Asp Asn Phe Val Val Val Tyr Glu Leu Leu Asp Glu Met
85 90 95
Met Asp Phe Gly Tyr Pro Gln Tyr Thr Glu Ala Lys Ile Leu Ser Glu
100 105 110
Phe Ile Lys Thr Asp Ala Tyr Arg Met Glu Val Thr Gln Arg Pro Pro
115 120 125
Met Ala Val Thr Asn Ala Val Ser Trp Arg Ser Glu Gly Ile Arg Tyr
130 135 140
Lys Lys Asn Glu Val Phe Leu Asp Val Val Glu Ser Val Asn Ile Leu
145 150 155 160
Val Asn Ser Asn Gly Gln Ile Val Arg Ser Asp Val Val Gly Ala Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:3585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3585:

Met Ser Ser Ser Ser Pro Pro Leu Ala Arg Thr Val Thr Arg Pro Ser
1 5 10 15
Ile Leu Leu Phe Leu His Arg Val Ile Asp Val Phe Lys His Tyr Phe
20 25 30

Met	Gly	Arg	Ala	Thr	Val	Thr	Arg	Thr	Thr	Met	Gly	Lys	Ala	Val	Thr
1			5						10				15		
Arg	Arg	Met	Met	Xaa	Arg	Trp	Met	Gly	Arg	Arg	Arg	Xaa	Arg	Gln	
		20					25					30			
Gly	Leu	Trp	Arg	Ser	Pro	Thr	Glu	Asp	Asp	Asp	Asp	Gly	Asp	Gly	Xaa
		35					40					45			
Ala	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Gly	Asp	Asp	Asp	Asp	Asp	Asp	Asp
50						55					60				

Glu Asp Ser Asp Asp Glu Glu Glu Val Asp Gly Glu Asp Asp Gln Glu
65 70 75 80
Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln Pro Leu Gly Arg Ala Glu
85 90 95
Asp Glu Glu His Ser Ser Asp Phe Glu Pro Glu Glu Asn Gly Glu Gly
100 105 110
Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp Asp Gly Glu Asp Ser
115 120 125
Val Lys Ala Gln Thr Ser Thr Lys Arg Lys Arg Ser Gly Asp Glu Glu
130 135 140
Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp Gly Asp Asp Asp Asp
145 150 155 160
Gly Arg Pro Pro Ser Lys Arg
165

(2) INFORMATION FOR SEQ ID NO:3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3588:

Met Gly Lys Ala Val Thr Arg Arg Met Met Xaa Arg Trp Met Gly
1 5 10 15
Arg Arg Arg Xaa Arg Gln Gly Leu Trp Arg Ser Pro Thr Glu Asp Asp
20 25 30
Asp Asp Gly Asp Gly Xaa Ala Asp Asp Asp Asp Asp Asp Gly Asp
35 40 45
Asp Asp Asp Asp Asp Asp Glu Asp Ser Asp Asp Glu Glu Val Asp
50 55 60
Gly Glu Asp Asp Gln Glu Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln
65 70 75 80
Pro Leu Gly Arg Ala Glu Asp Glu Glu His Ser Ser Asp Phe Glu Pro
85 90 95
Glu Glu Asn Gly Glu Gly Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp
100 105 110
Asp Asp Gly Glu Asp Ser Val Lys Ala Gln Thr Ser Thr Lys Arg Lys
115 120 125
Arg Ser Gly Asp Glu Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp
130 135 140
Gly Asp Asp Asp Asp Asp Gly Arg Pro Pro Ser Lys Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3589:

Met Met Met Xaa Arg Trp Met Gly Arg Arg Arg Xaa Arg Gln Gly Leu
1 5 10 15
Trp Arg Ser Pro Thr Glu Asp Asp Asp Gly Asp Gly Xaa Ala Asp

Thr	Gly	Gln	Leu	Pro	Thr	Lys	Pro	Ser	Val	Leu	Phe	Ser	Pro	Val	Asn
1				5					10					15	
Arg	Lys	Phe	Val	Phe	Pro	Ala	His	Leu	Ser	Leu	Gly	His	Leu	Cys	Lys
			20					25					30		
Gly	Ala	His	Gly	Ser	Arg	Glu	Gly	Gln	Gly	Asp	His	Arg	Val	Leu	Pro
		35				40						45			
Gly	Arg	Pro	Ser	Ser	Pro	Lys	Gly	Gln	Gly	Asp	Arg	Arg	Leu	Pro	Pro
		50				55					60				
Arg	Arg	Arg	Leu	Gln	Gln	Asn	Leu	Leu	Pro	Phe	Leu	His	Pro	Ser	Gln

(2) INFORMATION FOR SEO ID NO:3592:

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Ala | Pro | His | Lys | Thr | Val | Ser | Ser | Leu | Phe | Pro | Cys | Lys | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Ile | Arg | Leu | Pro | Cys | Pro | Ser | Ile | Ala | Trp | Thr | Pro | Leu | Gln | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Thr | Trp | Leu | Ser | Arg | Arg | Pro | Arg | Arg | Ser | Ser | Arg | Pro | Pro | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |

(2) INFORMATION FOR SEO ID NO:3593:

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Glu | Lys | Ala | Lys | Glu | Ile | Ile | Ala | Ser | Ser | Pro | Val | Asp |
| 1 | | | 5 | | | | 10 | | | | | | 15 | | |
| Leu | Ala | Leu | Arg | Lys | Ala | Lys | Glu | Thr | Val | Ala | Ser | His | Pro | Val | Val |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Val | Phe | Ser | Lys | Thr | Tyr | Cys | Pro | Phe | Cys | Thr | Arg | Val | Lys | Gln | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Ala | Lys | Leu | Gly | Ala | Ser | Tyr | Lys | Ala | Ile | Glu | Xaa | Gly | Cys | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |

(2) INFORMATION FOR SEO ID NO:3594:

- | | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| tgagtatacar | gaggcactac | agtggaggat | gcgggagcca | aatttgggtg | caaagctctt | 60 |
| ccttggtggt | gttgagatgc | agaagacaga | tgaggagatt | gcgactgcac | tgaacaacat | 120 |
| gacattatgc | ctctgagtat | ttctgaagct | cgcctgagat | cttgaggagc | ctctgcgtgga | 180 |
| gtgtttttac | actcacaact | atccagaaga | gatacaatgc | tatttatcac | actctgagaa | 240 |

ggtcagtgct	tcatttaaga	agatccttca	tcttgcaactg	gagcattttg	tggcactctgt	300
ggtaccacgc	attcgctccag	tccttgacac	tggtgctact	gtcagttatg	agttggatga	360
tactgaactt	ggggaaaatg	agggtgaacga	tccatgggtg	cagaagctta	tacttacagt	420
waacagtaat	gttgctctggc	tcacgccagt	tatgacatta	aacaactacg	attcctttgt	480
gcacttgatc	attgacttca	ttgtcaagag	gctcgaggtg	attatgatgc	agaagaggtt	540
cagccagctc	ggcgggctcc	agctcgataa	ggaggtccgc	tctctgatca	accatttctc	600
agagatgtCc	cagagaccag	tcagagacaa	gttctctagg	ctttcgcaga	tgctgacctc	660
tttgaaactc	gagcgggtat	cggagatatt	ggatttctgg	ggtgacaatg	ctggccatct	720
gagctggctg	ttgacacctg	cagaggtgcg	gagagtgtta	ggacttagga	ttgacttcag	780
gcctgaagct	attgctgctt	tgaggctctg	aatcggtgat	ttatttgatc	ttgttaattc	840
attatcatgt	atatatagca	acgagatgcc	ttagaaattt	ttgttgtaat	gacgaaagac	900
ctgcattgta	gaagaaatct	gcg				

(2) INFORMATION FOR SEQ ID NO:3595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1577489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3595:

Gl	Tyr	Xaa	Glu	Ala	Leu	Gln	Trp	Arg	Met	Arg	Glu	Pro	Asn	Leu	Gly
1			5					10					15		
Ala	Lys	Leu	Phe	Leu	Gly	Gly	Val	Gly	Val	Gln	Lys	Thr	Gly	Glu	Glu
			20					25					30		
Ile	Ala	Thr	Ala	Leu	Asn	Asn	Ile	Asp	Ile	Ser	Ser	Glu	Tyr	Val	Leu
			35					40					45		
Lys	Leu	Arg	His	Glu	Ile	Glu	Glu	Leu	Cys	Val	Glu	Val	Phe	His	Thr
			50					55					60		
Pro	Ala	Asp	Arg	Glu	Lys	Ile	Lys	Ser	Cys	Leu	Ser	Glu	Leu	Gly	Glu
65								70					75		80
Val	Ser	Ala	Ser	Phe	Lys	Lys	Ile	Leu	His	Ser	Ala	Leu	Glu	His	Leu
								85					90		
Val	Ala	Ser	Val	Val	Pro	Arg	Ile	Arg	Pro	Val	Leu	Asp	Thr	Val	Ala
								105					110		
Thr	Val	Ser	Tyr	Glu	Leu	Asp	Asp	Thr	Glu	Tyr	Gly	Glu	Asn	Glu	Val
								120					125		
Asn	Asp	Pro	Trp	Val	Gln	Lys	Leu	Ile	Leu	Thr	Xaa	Asn	Ser	Asn	Val
								135				140			
Ala	Trp	Leu	Gln	Pro	Val	Met	Thr	Leu	Asn	Asn	Tyr	Asp	Ser	Phe	Val
145								150				155		160	
His	Leu	Ile	Ile	Asp	Phe	Ile	Val	Lys	Arg	Leu	Glu	Val	Ile	Met	Met
								165					175		
Gln	Lys	Arg	Phe	Ser	Gln	Leu	Gly	Gly	Leu	Gln	Leu	Asp	Lys	Glu	Val
								185					190		
Arg	Ser	Leu	Ile	Asn	His	Phe	Ser	Glu	Met	Ser	Gln	Arg	Pro	Val	Arg
								200				205			
Asp	Lys	Phe	Ser	Arg	Leu	Ser	Gln	Met	Ser	Thr	Ile	Leu	Asn	Phe	Glu
								215				220			
Arg	Val	Ser	Glu	Ile	Leu	Asp	Phe	Trp	Gly	Asp	Asn	Ala	Gly	His	Leu
225								230				235		240	
Thr	Trp	Leu	Leu	Thr	Pro	Ala	Glu	Val	Arg	Arg	Val	Leu	Gly	Leu	Arg
								245					250		
Ile	Asp	Phe	Arg	Pro	Glu	Ala	Ile	Ala	Ala	Leu	Arg	Leu			
								265							

(2) INFORMATION FOR SEQ ID NO:3596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

acacaaagcct	ccrcccccct	cctgcacac	ctcgccgcgcg	cgcacgcacg	cacgaaccag	60
caagcagatg	cgctgctaca	cctctcgtgtg	cgcgarccrc	ggcgggscga	ngtgagccgc	120
caagcagac	tcgcgcgaga	tggagcgctc	cgcgcacac	cctcagcagc	gtgcgcgcgc	180
ectcgtcgcc	gCgcctccg	cGgcgcactc	cgcgtccgcg	gtccagtcgt	ccttctCcca	240
tggtcacccc	caGctccgcc	gtctctccag	tatgctcggt	tggtggcgcg	atgatggtta	300
ctgAnqcaq	caGccqccqg	tgccqccAv	naccCdkcg	aktNgcctc	cagccccaag	360

ctcccaaGgg aggagaagaa ggaagaggag aaggaagaga ggcagcagca catgggattc 420
tccctgttcc actagagtta agctgcgtgt gcatgggttc ggttcGggtc gtgtcgcgcg 480
aaacgtgaag agctcaagcg gcctttttgt tccagtccca catgtgagag ctttgatacg 540
ttgtctggaa tgaaaaaaatt tcccttgac accctgtctg caccgagga ggagttagcg 600
tggggaaaaa actgtagaac ctgtgggatg caaaatctat ctagtctagt ttgggatcg 660
gttacgaatt tgtcttcaac aaatagtgtg gatgagacga gtggaaaaa tgggtggtgt 720
tgatttcaga aacgaatggc gatatgacat gtgttggtgc

(2) INFORMATION FOR SEQ ID NO:3598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3598:

Thr Lys Ala Ser Xaa Pro Phe Pro Asp Thr Leu Ala Ala Ala His Ala
1 5 10 15
Arg Thr Asn Gln Arg Arg Asp Gly Arg Leu His Leu Arg Val Pro Xaa
20 25 30
Xaa Arg Arg Xaa Xaa Val Asp Arg Gln Ala Ala Leu Arg Arg Asp Gly
35 40 45
Gly Leu Arg Arg His Pro Leu Arg Ala Ala Ala Pro Pro Arg Arg Arg
50 55 60
Arg Leu Arg Gly Arg Leu Arg Val Arg Arg Pro Val Val Leu Leu Pro
65 70 75 80
Trp Ser Pro Pro Ala Pro Pro Ser Ser Arg
85 90

(2) INFORMATION FOR SEQ ID NO:3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3599:

Pro Lys Pro Xaa Pro Pro Ser Leu Thr Pro Ser Pro Pro Arg Thr His
1 5 10 15
Ala Arg Thr Ser Glu Glu Met Gly Val Tyr Thr Phe Val Cys Arg Xaa
20 25 30
Xaa Gly Xaa Ala Xaa Trp Thr Ala Lys Gln His Ser Gly Glu Met Glu
35 40 45
Ala Ser Ala Ala Thr Pro Tyr Glu Leu Gln Arg Arg Leu Val Ala Ala
50 55 60
Ala Ser Ala Ala Asp Ser Ala Ser Gly Val Gln Ser Ser Phe Ser His
65 70 75 80
Gly His Pro Gln Leu Arg Arg Leu Pro Gly Asp Arg Arg Trp Trp Arg
85 90 95
Asp Asp Gly

(2) INFORMATION FOR SEQ ID NO:3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1577516
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3600:

Met	Val	Thr	Pro	Ser	Ser	Ala	Val	Phe	Gln	Val	Ile	Val	Gly	Gly	Gly
1			5						10				15		
Ala	Met	Met	Val	Ser	Gly	Xaa	Gly	Ala	Arg	Arg	Cys	Gly	Arg	Xaa	Pro
			20					25					30		
Xaa	Arg	Xaa	Xaa	Ala	Ala	Ala	Glu	Ala	Pro	Lys	Gly	Gly	Glu	Glu	Gly
			35					40					45		
Arg	Gly	Glu	Gly	Arg	Glu	Arg	Arg	Arg	His	Gly	Ile	Leu	Pro	Val	Arg
			50					55				60			
Leu	Glu	Leu	Ser	Cys	Val	Cys	Met	Val	Ala	Val	Arg	Val	Val	Ser	Arg
			65		70				75					80	
Glu	Thr														

- (2) INFORMATION FOR SEQ ID NO:3601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1006
(D) OTHER INFORMATION: / Ceres Seq. ID 1577517
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3601:

ctagggttta	catcccttat	aaaatctcgt	cttcaccccc	tgccctccctc	agtcgcactt	60
ctctcggcgg	cggcaactcg	acggccaacc	gcgcacccct	gcgcgcgcag	ccatggtgca	120
tgtaaacttc	taccgcaact	atgggaagac	tttcaagaag	ccaaggcggc	cgtatgagaa	180
ggagcgcccta	gatgctgagc	tgaagctggt	tggtgagtat	ggcctgcggt	gcaagcgcga	240
gctgtggcgc	gtgcagtatg	ccctgagccg	tatcaggaat	gcagccaggg	agctgctcac	300
ctctgatgag	aagaacccac	gccgtatctt	tgagggcgag	gcgctctccc	gcgcgatgaa	360
cagatatggt	cttcttggtg	agggacagaa	caagcttgat	tacgtgcttg	ctctcaactg	420
tgagaacttc	ctccagcgcc	gcctccagac	catcgtcttc	aagaatggca	tggccaagtc	480
catccacatc	gctcgtgtcc	tgatcaggca	gcgcCacatc	agggtgggaa	ggcagctcgt	540
caacatcccc	tcgttcatgt	tcagggtcga	atcagagaag	cacatcgact	tctccctcac	600
cagccctctg	gggtggtggtc	ctgcgcggaag	ggtgaagcgg	aagaaccaga	agaaggccctc	660
agggggcggc	gacgctgagg	aggacgagga	gtaaaggggg	gggggggcag	taggattctg	720
ggaacggcaat	tggtttaaat	gtgaggtgga	cactttagtt	gttggtgcctg	agtggtgttg	780
tggtgtaaat	aatacaaat	ctactgtggt	agacaatttt	gcacccccac	tactgacact	840
cgtgttttaa	tttaaacatt	ggcatcgtgt	ctggacacga	tgaattgtat	tctggtttgg	900
gtggctattt	gtatggtttg	tctttaggcc	aatgtttaag	actgaaacaa	attggttagcc	960
aactttaacta	tcttatgctc	tgctggtctg	tttggtgatt	tttttt		

- (2) INFORMATION FOR SEQ ID NO:3602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..193
(D) OTHER INFORMATION: / Ceres Seq. ID 1577518
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3602:

Met Val His Val Asn Phe Tyr Arg Asn Tyr Gly Lys Thr Phe Lys Lys
1 5 10 15
Pro Arg Arg Pro Tyr Glu Lys Glu Arg Leu Asp Ala Glu Leu Lys Leu
20 25 30
Val Gly Glu Tyr Gly Leu Arg Cys Lys Arg Glu Leu Trp Arg Val Gln
35 40 45
Tyr Ala Leu Ser Arg Ile Arg Asn Ala Ala Arg Glu Leu Leu Thr Leu
50 55 60
Asp Glu Lys Asn Pro Arg Arg Ile Phe Glu Gly Glu Ala Leu Leu Arg
65 70 75 80
Arg Met Asn Arg Tyr Gly Leu Leu Gly Glu Gly Gln Asn Lys Leu Asp
85 90 95
Tyr Val Leu Ala Leu Thr Val Glu Asn Phe Leu Gln Arg Arg Leu Gln
100 105 110
Thr Ile Val Phe Lys Asn Gly Met Ala Lys Ser Ile His His Ala Arg
115 120 125
Val Leu Ile Arg Gln Arg His Ile Arg Val Gly Arg Gln Leu Val Asn
130 135 140
Ile Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe
145 150 155 160
Ser Leu Thr Ser Pro Leu Gly Gly Gly Pro Ala Gly Arg Val Lys Arg
165 170 175
Lys Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Glu Glu Asp Glu
180 185 190
Glu

(2) INFORMATION FOR SEQ ID NO:3603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3603:

Met Asn Arg Tyr Gly Leu Leu Gly Glu Gly Gln Asn Lys Leu Asp Tyr
1 5 10 15
Val Leu Ala Leu Thr Val Glu Asn Phe Leu Gln Arg Arg Leu Gln Thr
20 25 30
Ile Val Phe Lys Asn Gly Met Ala Lys Ser Ile His His Ala Arg Val
35 40 45
Leu Ile Arg Gln Arg His Ile Arg Val Gly Arg Gln Leu Val Asn Ile
50 55 60
Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe Ser
65 70 75 80
Leu Thr Ser Pro Leu Gly Gly Gly Pro Ala Gly Arg Val Lys Arg Lys
85 90 95
Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Glu Glu Asp Glu Glu
100 105 110

(2) INFORMATION FOR SEQ ID NO:3604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..851

(D) OTHER INFORMATION: / Ceres Seq. ID 1577526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3604:

```
aaagagctcccc caactcgccc ccccccattc agctccgacc ctagggtttc catccggctc      60
ttccggaagc ttccgaaaaa gggccacgac gagctcgccc acgcccgcgc ccccgccccc      120
gcggggggag accactcccc ggccttctcg ttcagcatct ggccgcccgc gcagcgcaag      180
cgngacgsg ntgggtggcg gctctgtgga gacgctcgcg ggagacacca tcctctgcaa      240
gcgctacggt gcgggtgccg ccgcccgcgc cgagccccgc gcgcccgcgc tcgaggccga      300
ggccttcgac gccgcggcct ccacgggagg cgcccgcgcc gcctccgctg aggaggggat      360
cgaggcgctg cagttcctac tccaaggagg tgagccgcgc cctcctyvgc ttctgtaagt      420
yccGctccgc ggagcccaag gccggtgaca cgccgctgga ggagggccgc gcccttggcg      480
cgcccaggcg cgaggccgcg cagcccgcgc cgtgagcgcc gdacagccat tcgttccgtt      540
ttgtatttcc tgcagcctgt gtttggcttg ggtctgagtt tgtatgactt gaacgttagc      600
tgtttgcaca tctatgcaat tcttgttctt ccatgaatag ccccgttcta gtgcgtgttc      660
ctgtttttct gggaaatccc gcccgatccc gaggttgtca aaccatcgca gcattgacct      720
ctgtctgtgt gcagcttoga gtgatggtcg aattgttccg gagaccgaat tgacaagcaa      780
ttaagattcc tcccatcttt caagccacat ttatatgtat aataataatc tgaccgttga      840
tttgaatttc t
```

(2) INFORMATION FOR SEQ ID NO:3605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1577527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3605:

```
Lys Ser Ser Pro Pro Arg Pro Pro Ser Ser Ser Asp Pro Arg Val
1      5      10      15
Ser Ile Arg Leu Phe Arg Lys Leu Pro Lys Met Ala Thr Asp Glu Leu
20      25      30
Ala His Ala Val Ala Pro Ala Pro Ala Gly Gly Asp His Ser Pro Ala
35      40      45
Phe Ser Phe Ser Ile Trp Pro Pro Thr Gln Arg Thr Arg Xaa Xaa Xaa
50      55      60
Gly Ala Ala Pro Arg Gly Asp Ala Arg Gly Arg His His Pro Leu Gln
65      70      75      80
Ala Leu Arg Cys Gly Ala Gly Arg Arg Arg Arg Ala Arg Gly Ala Arg
85      90      95
His Arg Gly Arg Gly Leu Arg Arg Arg Gly Leu His Gly Arg Arg
100      105      110
Arg Arg Leu Arg Gly Gly Asp Arg Gly Ala Ala Val Pro Thr Pro
115      120      125
Arg Arg
130
```

(2) INFORMATION FOR SEQ ID NO:3606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1577528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3606:

Arg Ala Pro His Leu Ala Pro Pro His Pro Ala Pro Thr Leu Gly Phe
1 5 10 15
Pro Ser Gly Ser Ser Gly Ser Phe Arg Lys Trp Pro Pro Thr Ser Ser
20 25 30
Pro Thr Pro Ser Pro Pro Pro Arg Pro Gly Glu Thr Thr Pro Arg Pro
35 40 45
Ser Arg Ser Ala Ser Gly Arg Arg Arg Ser Ala Arg Xaa Asp Xaa Xaa
50 55 60
Val Arg Arg Leu Val Glu Thr Leu Ala Gly Asp Thr Ile Leu Cys Lys
65 70 75 80
Arg Tyr Gly Ala Val Pro Ala Ala Asp Ala Gly Pro Ala Ala Arg Ala
85 90 95
Ile Glu Ala Glu Ala Phe Asp Ala Ala Ala Ser Thr Gly Gly Ala Ala
100 105 110
Ala Ala Ser Val Glu Glu Gly Ile Glu Ala Leu Gln Phe Leu Leu Gln
115 120 125
Gly Gly Glu Pro Pro Pro Pro Xaa Leu Arg Gln Xaa Pro Leu Arg Gly
130 135 140
Arg Gln Gly Arg
145

(2) INFORMATION FOR SEQ ID NO:3607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3607:

Met Ala Thr Asp Glu Leu Ala His Ala Val Ala Pro Ala Pro Ala Gly
1 5 10 15
Gly Asp His Ser Pro Ala Phe Ser Phe Ser Ile Trp Pro Pro Thr Gln
20 25 30
Arg Thr Arg Xaa Xaa Xaa Gly Ala Ala Pro Arg Gly Asp Ala Arg Gly
35 40 45
Arg His His Pro Leu Gln Ala Leu Arg Cys Gly Ala Gly Arg Arg Arg
50 55 60
Arg Ala Arg Gly Ala Arg His Arg Gly Arg Gly Leu Arg Arg Arg Gly
65 70 75 80
Leu His Gly Arg Arg Arg Arg Arg Leu Arg Gly Gly Gly Asp Arg Gly
85 90 95
Ala Ala Val Pro Thr Pro Arg Arg
100

(2) INFORMATION FOR SEQ ID NO:3608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..842
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3608:

agtgttgtgt cctagcgcgc cgcgcgcgc aactcgctt gcgtgactga aagctcgctg 60
gcttcgcgtc acgcgagaga cgagagcatg gacaccagc tgaagcttcg ttgttggttg 120

```

aaggtgatgg gcaggaccgg ctccaggggt caggtgaccc aggtcagagt taagtctctg 180
gatgaccaga accggctcat catgaggaat gtcaaggcac ttgctcacc ttgacagagaa 240
gaacccccc cgtatctctt aggggtgagg gctctctcgc cgcataaac gctatggggt 300
gcttgctgat gggtcagaaca agcttgatta tggctctgcc ctacccgctg agaacttctt 360
cgcaaggcgg cttcaaacac ttgtcttcaa ggctggcatg gccaaagtcca ttaccatgac 420
tcgtgtcttg atcaagcagc gtcacatcag ggttgccagg caaattgtca acgtcccatc 480
attcatggtg aggggtggag ctgagaagca cattgacttt tcaactgtcaa gccatttcgg 540
tgaggggccc gcaGgaaggg tgaagagaaa gaatcagaag aaggcgaagg gtggcgggca 600
tgctggcgat gaggatgagg agtgaggatg gacaagtagc gttaccatca ataataatat 660
tatctagatt tcttgaactt gttcgaatga tgagtgccta gctgtgtgat ctgacgcaga 720
gttcctgtgt ctgactctgt gtcattggat gtccatttta tcttgtgtga ttatcagcct 780
ttacataact gctatgtttg gatatttca attgtgttgc aatttatagt ggtgtgtttt 840
tg

```

(2) INFORMATION FOR SEQ ID NO:3609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3609:

```

Met Ser Arg His Leu Leu Thr Leu Asp Glu Lys Asn Pro Arg Arg Ile
1          5          10          15
Phe Glu Gly Glu Ala Leu Leu Arg Arg Met Asn Arg Tyr Gly Leu Leu
20          25          30
Ala Glu Gly Gln Asn Lys Leu Asp Tyr Val Leu Ala Leu Thr Ala Glu
35          40          45
Asn Phe Leu Ala Arg Arg Leu Gln Thr Leu Val Phe Lys Ala Gly Met
50          55          60
Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His Ile
65          70          75          80
Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg Val
85          90          95
Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly Gly
100          105          110
Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser Gly
115          120          125
Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu
130          135

```

(2) INFORMATION FOR SEQ ID NO:3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3610:

```

Met Asn Arg Tyr Gly Leu Leu Ala Glu Gly Gln Asn Lys Leu Asp Tyr
1          5          10          15
Val Leu Ala Leu Thr Ala Glu Asn Phe Leu Ala Arg Arg Leu Gln Thr
20          25          30
Leu Val Phe Lys Ala Gly Met Ala Lys Ser Ile His His Ala Arg Val
35          40          45

```

Leu Ile Lys Gln Arg His Ile Arg Val Gly Arg Gln Ile Val Asn Val
50 55 60
Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe Ser
65 70 75 80
Leu Ser Ser Pro Phe Gly Gly Gly Pro Ala Gly Arg Val Lys Arg Lys
85 90 95
Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu
100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:3611:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1577542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3611:

Met Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His
1 5 10 15
Ile Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg
20 25 30
Val Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly
35 40 45
Gly Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser
50 55 60
Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:3612:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1577548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3612:

aaaacagaca ggaagccgc cgaacatcac aaggtgcga acctctaga agctcgagga 60
gatgtctctc aagctgtcgg cgtggttcgt gaacccgcgg aggaatycbg tcgcgcgtct 120
ccaccggaac gccgtgcct cccgcctccg caaatacggg ctcaggtagc acgacctcta 180
cgacccgtac cagcacctag acatcaagga ggcgCtggcg cggtgcgcg gggagtggt 240
ggacgcccgt aaccagcgcc tcaagcgggc catggacctc tccatgaagc accagtacct 300
accgaagcac gtccaggcta tacagacgccc attcaggagc tacctttttg acatgcttgc 360
tcttgtgaaa aaggagagcg cagagcgtga agcattggga gcgcttcac tctaccagag 420
aaccatccaa taaagtcct ctttgcatag tccaatcaat agtgcacgcg atgatcagca 480
gaggctgata ctgtaagtgt tattgtgttt ttctcaggaa atctctacta cttattaaga 540
cgataaggggt agcctgcgct tctgacgtc

(2) INFORMATION FOR SEQ ID NO:3613:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1577549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3613:

```
Met Leu Ser Lys Leu Ser Ala Trp Phe Val Asn Pro Arg Arg Asn Xaa
1      5      10      15
Xaa Ala Arg Leu His Arg Asn Ala Val Ala Ser Arg Leu Arg Lys Tyr
20      25      30
Gly Leu Arg Tyr Asp Asp Leu Tyr Asp Pro Tyr His Asp Leu Asp Ile
35      40      45
Lys Glu Ala Leu Ala Arg Leu Pro Arg Glu Val Val Asp Ala Arg Asn
50      55      60
Gln Arg Leu Lys Arg Ala Met Asp Leu Ser Met Lys His Gln Tyr Leu
65      70      75      80
Pro Asp Asp Val Gln Ala Ile Gln Thr Pro Phe Arg Ser Tyr Leu Phe
85      90      95
Asp Met Leu Ala Leu Val Lys Lys Glu Ser Ala Glu Arg Glu Ala Leu
100      105      110
Gly Ala Leu Pro Leu Tyr Gln Arg Thr Ile Pro
115      120
```

(2) INFORMATION FOR SEQ ID NO:3614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..704

(D) OTHER INFORMATION: / Ceres Seq. ID 1577550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3614:

```
gtgctttctt agaggtgggt tggctttccc tcccctcgg gttcgggttc gggttcgtga      60
ggttctcogg ggttcgggtt cgtgggtgav cggatcgaga tggcggcgtc ggaatgttgag      120
taccgctgct tegtccggcag ctacagcvgt ggcggcggcg gctacgggtg cggcgggcgcc      180
accaattgct cgccttcgcc cttctgtct ccttcgtcc gtagcagacc aggaacgcc      240
aaggcgctaG cgtctccaag atgggtcgtc aaaacgacat tgacttactc aatccaccgg      300
cagagcttga gaagctaaag cacaagaaga agcggctagt ccagtccccc aactccttct      360
tcatggatgt caagtgccag ggctgtttca gcataaccac ttgtgttcag cactcccgaga      420
ctgtggttgt gtgccccaggc tgccaaactg ttctgtgcc aacctaccgt gggaaggcca      480
ggctcacoga ggggtgtccc ttccgtcgca agggcgatta ggtCctgctt ctcttaacgt      540
gagaagagat aaatttggtg ttttgcaact ttctcaggat atgtactgta ctcggtgagg      600
attttgttaa ttattatggc tgtagcgtg gcctgacaat gcttgtgtgt maacctgcac      660
tttgtttgag cgtagtgaac tataatatgg tgcgttttgg cttt
```

(2) INFORMATION FOR SEQ ID NO:3615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1577551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3615:

```
Cys Phe Leu Arg Gly Gly Leu Ala Ser Pro Pro Pro Val Arg Val
1      5      10      15
Arg Val Arg Glu Val Leu Arg Gly Ser Val Ser Trp Val Xaa Gly Ser
20      25      30
```

Arg Trp Arg Arg Arg Met Leu Ser Thr Ala Ala Ser Ser Ala Ala Thr
35 40 45
Xaa Val Ala Ala Ala Ala Thr Val Ala Ala Ala Pro Pro Leu Ala Arg
50 55 60
Leu Arg Pro Phe Cys Leu Pro Ser Ser Val Ala Asp Gln Glu Arg Pro
65 70 75 80
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3616:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1577552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3616:

Met Ala Ala Ser Asp Val Glu Tyr Arg Cys Phe Val Gly Ser Tyr Ser
1 5 10 15
Xaa Gly Gly Gly Tyr Gly Gly Gly Gly Ala Thr Thr Cys Ser Pro
20 25 30
Ser Pro Leu Leu Ser Pro Phe Val Arg Ser Arg Pro Gly Thr Pro Lys
35 40 45
Ala Leu Ala Ser Pro Arg Trp Cys Cys Lys Thr Thr Leu Thr Tyr Ser
50 55 60
Ile His Arg Gln Ser Leu Arg Ser
65 70

(2) INFORMATION FOR SEQ ID NO:3617:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1577553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3617:

Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu
1 5 10 15
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser
20 25 30
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Val
35 40 45
Phe Ser His Ser Gln Thr Val Val Val Cys Pro Gly Cys Gln Thr Val
50 55 60
Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys Ser
65 70 75 80
Phe Arg Arg Lys Gly Asp
85

(2) INFORMATION FOR SEQ ID NO:3618:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 941 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..941

(D) OTHER INFORMATION: / Ceres Seq. ID 1577582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3618:

```
agggcagggc  acttgcaaa  gatttatcct  cccaaagagc  aacgagagat  agggattttg  60
cttttgcatg  gtctattggt  ttgcccgcgt  aaagagctcg  ttaaatatgg  acgtntctgga  120
tcactcgagc  gatgaggagg  agcagcagga  ccggtgcggc  accagcagcg  gcagatcagg  180
ctccaggctc  ggcgcgggg  csggcggcag  aagcggaggt  caggcggcag  cggcagaacc  240
tgctgctcat  ggactgcgtc  ggccggcaacg  gcggcgacgg  ggacggcgcg  ttggaggaca  300
ccgcgcgcgt  gccagactac  gagctcttgt  ccagtcocgc  ccgcctccac  gacgacgccca  360
agaatccgcc  tcggcgctg  ctggtttcag  avgaggagga  gcagcagaag  gcgcggcgcca  420
agcaggggaa  gGcgtcccc  ccacagcctc  cgcccgtgcc  actgccacag  cggcagcaga  480
agccgcgcgt  gaggctgac  gactacgtga  ggtcaaggaa  cagktcgggc  ggcgcagggc  540
cgggggctcg  tgggtggcgc  gcctgggtct  acggcgactc  caagagctcc  gaggcaggcg  600
aggaaggggg  cggcgaggg  aagaagata  agaagaagaa  gcggtcgctc  tggctgcggc  660
accccgaccg  ccggtggcgc  gtgcagggat  tctactagcg  cgttcacgt  ctccgacgtc  720
tagtaaaacc  gtgttagtca  tgatgcgcct  ctgactcatg  cgttggtttg  gttgctccgg  780
gccctgtttg  gaagtgaagt  tttttcata  gtttttgaga  aatactatag  tatcogttaa  840
tattagagta  ttctggacta  ttaatatgatt  attagaaaat  agagtttcta  atatcatggt  900
ttttttaagt  attgatata  tagttctgga  cctaagtttt  t
```

(2) INFORMATION FOR SEQ ID NO:3619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1577583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3619:

```
Met Val His Trp Phe Ala Ala Ser Lys Ser Ser Leu Asn Met Asp Xaa
1          5          10          15
Leu Asp His Ser Asp Asp Glu Glu Glu Gln Gln Asp Arg Cys Gly Thr
20          25          30
Ser Ser Gly Arg Ser Gly Ser Arg Leu Gly Ala Arg Xaa Gly Gly Arg
35          40          45
Ser Gly Gly Gln Ala Ala Ala Pro Glu Pro Ala Ala His Gly Leu Arg
50          55          60
Arg Arg Gln Arg Arg Arg Arg Gly Arg Arg Val Gly Gly His Arg Ala
65          70          75          80
Ala Ala Arg Leu Arg Ala Leu Val Pro Val Arg Pro Pro Pro Arg Arg
85          90          95
Arg Gln Glu Ser Ala Ser Gly Ala Ala Gly Cys Arg Xaa Gly Gly Ala
100         105         110
Ala Glu Gly Ala Gly Gln Ala Gly Glu Gly Val Pro Ala Thr Ala Ser
115         120         125
Ala Arg Ala Thr Ala Thr Ala Ala Ala Glu Ala Gly Val Glu Ala Asp
130         135         140
Arg Val Arg Glu Val Lys Glu Gln Xaa Gly Arg Arg Arg Ala Gly Gly
145         150         155         160
Arg Trp Val Arg Arg Leu Val
165
```

(2) INFORMATION FOR SEQ ID NO:3620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1577584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3620:

Met Asp Xaa Leu Asp His Ser Asp Asp Glu Glu Glu Gln Gln Asp Arg
1 5 10 15
Cys Gly Thr Ser Ser Gly Arg Ser Gly Ser Arg Leu Gly Ala Arg Xaa
20 25 30
Gly Gly Arg Ser Gly Gly Gln Ala Ala Ala Pro Glu Pro Ala Ala His
35 40 45
Gly Leu Arg Arg Arg Gln Arg Arg Arg Arg Gly Arg Arg Val Gly Gly
50 55 60
His Arg Ala Ala Ala Arg Leu Arg Ala Leu Val Pro Val Arg Pro Pro
65 70 75 80
Pro Arg Arg Arg Gln Glu Ser Ala Ser Gly Ala Ala Gly Cys Arg Xaa
85 90 95
Gly Gly Ala Ala Glu Gly Ala Gly Gln Ala Gly Glu Gly Val Pro Ala
100 105 110
Thr Ala Ser Ala Arg Ala Thr Ala Thr Ala Ala Ala Glu Ala Gly Val
115 120 125
Glu Ala Asp Arg Val Arg Glu Val Lys Glu Gln Xaa Gly Arg Arg Arg
130 135 140
Ala Gly Gly Arg Trp Val Arg Arg Leu Val
145 150

(2) INFORMATION FOR SEQ ID NO:3621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1577585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3621:

Met Arg Arg Ser Ser Arg Thr Gly Ala Ala Pro Ala Ala Asp Gln
1 5 10 15
Ala Pro Gly Ser Ala Arg Gly Xaa Ala Ala Glu Ala Glu Val Arg Arg
20 25 30
Gln Arg Gln Asn Leu Leu Leu Met Asp Cys Val Gly Gly Asn Gly Gly
35 40 45
Asp Gly Asp Gly Ala Leu Glu Asp Thr Ala Pro Leu Pro Asp Tyr Glu
50 55 60
Leu Leu Ser Gln Ser Ala Arg Leu His Asp Asp Ala Lys Asn Pro Pro
65 70 75 80
Pro Ala Leu Leu Val Ala Xaa Glu Glu Glu Gln Gln Lys Ala Pro Ala
85 90 95
Lys Gln Gly Lys Ala Ser Pro Pro Gln Pro Pro Pro Val Pro Leu Pro
100 105 110
Gln Arg Gln Gln Lys Pro Ala Trp Arg Leu Ile Glu Tyr Val Arg Ser
115 120 125
Arg Asn Xaa Ser Gly Gly Ala Gly Pro Gly Val Gly Gly Cys Gly Ala
130 135 140
Trp Ser Asp Gly Asp Ser Lys Ser Ser Glu Asp Gly Glu Asp Gly Gly
145 150 155 160
Gly Glu Gly Lys Lys Asp Lys Lys Lys Lys Arg Ser Ser Trp Leu Pro
165 170 175
Asp Pro Asp Arg Arg Trp Pro Val Gln Gly Phe Tyr

180 185
(2) INFORMATION FOR SEQ ID NO:3622:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..854
(D) OTHER INFORMATION: / Ceres Seq. ID 1577601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3622:
acttgctcca tatcccatcc atcacagcta gctagcgtac agacgaataa tctcttcttc 60
acctcaactag ctaaacaccag ctacgagctc gatcgctctg tcttgcaata atggccgctc 120
gctctctctc ccacgacgctg gtccggcgcg cggctcctggc agcggcgctc ctgctgctgg 180
cggcgggggc cggacgcgcg tcggcgcgcg tgagctgcgg cgaggtgacg tcgtcggtgg 240
cgccgtgcct cgggtacgcg atgggcagcg cggcgctgcgc ctccgcgggc tgctgcagcg 300
gggtgcgctc gctcaacagc cgcgcgtcgt cggcgcgagg ccgncaggcc acctgcaact 360
gcctcaagag catgacggcg cggctcggcg gcggcgctcag Catggccaac gccgccacca 420
tccccggcaa gtccggcgctc tccgtcggcg tgcccatcag cccaccgctc gactgcacca 480
agatcaactg atcgatggaa ccatagtggg ggtagctcgc tctgttgatg gcagcgtacg 540
tgcccatcag cagcatgcag tcgtcgtcgt agcagagatg tcttagctac gtgtgtgtca 600
tgcatcagac tggcacataa taaagaagta gatcatgca ccaactagtga tcaactcgtc 660
tagtgcctc cgttcgctg ttgtcgtcgt cgtcgtcgtg gtgtacctcg tacgtgacat 720
gccgtagcac ttagctagc agacgagcac ctcaatgtcc ttgggtttgc tttgctggct 780
ctctgttttc gtctcgtgtt gcttttaatc tggcacaggt ttctaaatta taataatgaa 840
tacttttttg tctt
(2) INFORMATION FOR SEQ ID NO:3623:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1577602
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3623:
Met Ala Ala Arg Ser Ser Ser Gln Gln Leu Val Ala Ala Ala Val Leu
1 5 10 15
Ala Ala Ala Xaa Leu Leu Leu Ala Ala Gly Ala Gly Thr Ala Ser Ala
20 25 30
Ala Val Ser Cys Gly Glu Val Thr Ser Ser Val Ala Pro Cys Leu Gly
35 40 45
Tyr Ala Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly
50 55 60
Val Arg Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala
65 70 75 80
Thr Cys Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val
85 90 95
Ser Met Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val
100 105 110
Gly Val Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn
115 120 125
(2) INFORMATION FOR SEQ ID NO:3624:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577603
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3624:
Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly Val Arg
1 5 10 15
Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala Thr Cys
 20 25 30
Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val Ser Met
 35 40 45
Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val Gly Val
50 55 60
Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn
65 70 75

(2) INFORMATION FOR SEQ ID NO:3625:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..572
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577610
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3625:
aagaaaaagcc tccattcccg agtctccagc caaccgcac cagtcacacc catccccctc 60
gaccocgaca accccagatc cgcaccgat ggcgcccaag gccgagaaga agccagcgca 120
gaagaagccg cgcccgagg agaaggcgga gaagacgacc gcagGtaaga ggccttggt 180
ttgtgaacta ctccgacagt gatgctgcca aggaagctat ttctgcaatg gatggcaagg 240
aaattgatgg cgcccgagta cgtgtcaaca tggctaata gagaacctgt gggaaccgtg 300
gtggtggcgg ctatggtggc ggcggctatg gaggtggtgg ctacggagggt ggtggcggct 360
acggagggtg tggctatggt ggtggcagcc aaagctatga tgcttgaagg gggcaggatc 420
ctattaagtc attatcaacc aagatatttg aaataatgaa ctttaggact tggtagcag 480
ttttatgtta agcatgttca gggtttgcta ttctgtttat gctgaattgt tggaactcct 540
agatgcagaa tattacgtat tggttttggt cc

(2) INFORMATION FOR SEQ ID NO:3626:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..134
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577611
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3626:
Glu Lys Pro Pro Phe Pro Ser Leu Gln Pro Thr Ala Ser Ser Pro Pro
1 5 10 15
His Pro Pro Arg Pro Arg Gln Pro Arg Val Pro Thr Arg Trp Arg Pro
 20 25 30
Arg Pro Arg Arg Ser Gln Arg Arg Arg Ser Arg Arg Pro Arg Arg Arg
35 40 45
Arg Arg Arg Arg Pro Gln Val Arg Gly Phe Gly Phe Val Asn Tyr Ser
50 55 60
Asp Ser Asp Ala Ala Lys Glu Ala Ile Ser Ala Met Asp Gly Lys Glu
65 70 75 80

Ile Asp Gly Arg Gln Val Arg Val Asn Met Ala Asn Glu Arg Pro Ala
85 90 95
Gly Asn Arg Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly
100 105 110
Gly Tyr Gly Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly
115 120 125

Ser Gln Ser Tyr Asp Ala
130

(2) INFORMATION FOR SEQ ID NO:3627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1577612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3627:

Met Leu Pro Arg Lys Leu Phe Leu Gln Trp Met Ala Arg Lys Leu Met
1 5 10 15
Gly Gly Arg Tyr Val Ser Thr Trp Leu Met Arg Asp Leu Leu Gly Thr
20 25 30
Val Val Val Ala Ala Met Val Ala Ala Met Glu Val Val Ala Thr
35 40 45
Glu Val Val Ala Ala Thr Glu Val Val Ala Met Val Val Ala Ala Lys
50 55 60
Ala Met Met Leu Glu Gly Gly Arg Ile Leu Leu Ser His Tyr Gln Pro
65 70 75 80
Arg Tyr Leu Lys

(2) INFORMATION FOR SEQ ID NO:3628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1577613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3628:

Met Ala Arg Lys Leu Met Gly Gly Arg Tyr Val Ser Thr Trp Leu Met
1 5 10 15
Arg Asp Leu Leu Gly Thr Val Val Val Ala Ala Met Val Ala Ala Ala
20 25 30
Met Glu Val Val Ala Thr Glu Val Val Ala Ala Thr Glu Val Val Ala
35 40 45
Met Val Val Ala Ala Lys Ala Met Met Leu Glu Gly Gly Arg Ile Leu
50 55 60
Leu Ser His Tyr Gln Pro Arg Tyr Leu Lys
65 70

(2) INFORMATION FOR SEQ ID NO:3629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..731

(D) OTHER INFORMATION: / Ceres Seq. ID 1577614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3629:

aaaaaacctta	gcagccacc	ggtttccct	cgctccaggt	ggcggcgcg	tcacctggt	60
ttgttcttac	tcctcccggt	tcctcacta	gtcgttactg	acttctcgct	tgctgtctcc	120
agatctccct	tcgcagccgg	ccagggaccc	cttcacagcg	cgggagatgg	ctgatcagga	180
ggccccagtt	gcagttgagg	caccaacccc	agttcttgga	gagccaatgg	acttgatgac	240
tgcgctcgag	ctggtgatga	agaagtcaag	tgctcatgat	ggacttggtg	agggtctctcg	300
cgagggtgcc	aaggccattg	agaagcatgc	tgctcagctt	tcgcttcttg	ctgaggactg	360
tgaccagcca	gattatgtca	agctggtgaa	ggcgctctgt	gctgaacaca	atgttcacct	420
tgctcactgtt	cctgctgcta	agactcttgg	cgagtgggct	gggctttgca	agattgactc	480
cgaggggcaag	caaaggaagg	ttgtaggctg	ctcctgtgtc	gttgccaagg	actacgggtga	540
agaatctgag	ggccttaaga	tagtgcagga	gtatgtcaag	tcgcactaga	tgtAacacgt	600
ttcagtaata	ctctacattt	ggatctgggc	ttaatattat	gcttgcgtct	tgggcttgcg	660
atggagattag	gacaattttac	tacaagagcc	catgaggata	tgagcaattt	ggaattctaa	720
atgtttgtgt	t					

(2) INFORMATION FOR SEQ ID NO:3630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3630:

Met	Ala	Asp	Gln	Glu	Ala	Pro	Val	Ala	Val	Glu	Ala	Pro	Thr	Pro	Val
1		5					10				15				
Leu	Gly	Glu	Pro	Met	Asp	Leu	Met	Thr	Ala	Leu	Gln	Leu	Val	Met	Lys
		20					25				30				
Lys	Ser	Ser	Ala	His	Asp	Gly	Leu	Val	Lys	Gly	Leu	Arg	Glu	Ala	Ala
		35					40				45				
Lys	Ala	Ile	Glu	Lys	His	Ala	Ala	Gln	Leu	Cys	Val	Leu	Ala	Glu	Asp
		50					55				60				
Cys	Asp	Gln	Pro	Asp	Tyr	Val	Lys	Leu	Val	Lys	Ala	Leu	Cys	Ala	Glu
		65					70				75				
His	Asn	Val	His	Leu	Val	Thr	Val	Pro	Ala	Ala	Lys	Thr	Leu	Gly	Glu
		85					90				95				
Trp	Ala	Gly	Leu	Cys	Lys	Ile	Asp	Ser	Glu	Gly	Lys	Ala	Arg	Lys	Val
		100					105				110				
Val	Gly	Cys	Ser	Cys	Val	Val	Val	Lys	Asp	Tyr	Gly	Glu	Glu	Ser	Glu
		115					120				125				
Gly	Leu	Asn	Ile	Val	Gln	Glu	Tyr	Val	Lys	Ser	His				
		130					135				140				

(2) INFORMATION FOR SEQ ID NO:3631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3631:

Met Asp Leu Met Thr Ala Leu Gln Leu Val Met Lys Ser Ser Ala

1 5 10 15
His Asp Gly Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu
20 25 30
Lys His Ala Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro
35 40
Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His
50 55 60
Leu Val Thr Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu
65 70 75 80
Cys Lys Ile Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser
85 90 95
Cys Val Val Val Lys Asp Tyr Gly Glu Ser Glu Gly Leu Asn Ile
100 105 110
Val Gln Glu Tyr Val Lys Ser His
115 120

(2) INFORMATION FOR SEQ ID NO:3632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3632:

Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Ser Ala His Asp Gly
1 5 10 15
Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu Lys His Ala
20 25 30
Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro Asp Tyr Val
35 40 45
Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His Leu Val Thr
50 55 60
Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile
65 70 75 80
Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser Cys Val Val
85 90 95
Val Lys Asp Tyr Gly Glu Glu Ser Glu Gly Leu Asn Ile Val Gln Glu
100 105 110
Tyr Val Lys Ser His
115

(2) INFORMATION FOR SEQ ID NO:3633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3633:

aaagtgccaaa	atcatcgctgt	crccgcccagt	rgacgcggttc	gactccggccc	gcgcgccctgt	60
ctctctctgc	ccaccgcgcac	cggccatttgc	cctcgctctgc	tctggccacc	gcaccttcca	120
ccgccccccgc	gtgctctctcc	gcagttctggc	cggttgacc	acctgcwccc	caccaccgcgc	180
gccccaccaca	cttatccacc	gttgcmggctc	gtcgcmccam	ctgctccccc	actgacaccg	240
gtcgaggtat	aatctcacc	tgggtgaagc	ttcaccgcac	tgctccgata	acaccgaacc	300
aaacccatcc	gagcgcatat	accagcaaaa	aaagtggaca	catttttttc	agcctaggtt	360

tNtccgCtgc gcccccctgtt ttccgaatcc ttccctatgc gatcataact gacgcccoga 420
atcgCcgccgc gggccggggag gagatccatc acgttttctg ctagggtttt gtatttggac 480
tagacagagc ggaaatctgg tgggtgtgat tctgtaacca gaagatcaga aactacggag 540
gagtgggggtt ttgtgattgg ttaccgatag gggttttgat tcatcgccac ccaaatgttg 600
gttgattttt tctgcagtt tctctcaatg tatttatggt catggtagta ctggattatg 660
gatacatttt ttccaagtga ttcataatct gcatcactcc tttttaaaaa agatcatcaa 720
tgaggagtga tgatatgatg atttttttat ttatctgtta acatocagtaa catcataata 780
gttttttttc

(2) INFORMATION FOR SEQ ID NO:3634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1577623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3634:

Lys Gly Asn His Arg Cys Xaa Ala Ser Xaa Arg Val Arg Leu Arg
1 5 10 15
Pro Pro Pro Leu Leu Leu Pro Thr Arg Thr Gly His Cys Pro Arg
20 25 30
Leu Leu Cys His Pro His Leu Pro Pro Pro Arg Ala Pro Pro Gln
35 40 45
Ser Gly Arg Cys Thr His Leu Xaa Pro Thr Thr Ala Ala Pro Pro Thr
50 55 60
Tyr Pro Pro Leu Xaa Val Val Xaa Pro Xaa Ala Pro Pro Leu Thr Pro
65 70 75 80
Val Glu Val

(2) INFORMATION FOR SEQ ID NO:3635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3635:

Lys Ala Lys Ile Ile Ala Xaa Pro Pro Xaa Asp Ala Phe Asp Ser Gly
1 5 10 15
Arg Arg Pro Cys Ser Ser Cys Pro Pro Ala Pro Ala Ile Ala Leu Ala
20 25 30
Cys Ser Ala Thr Arg Thr Phe His Arg Pro Arg Val Leu Leu Arg Ser
35 40 45
Leu Ala Val Ala Pro Thr Cys Xaa Pro Pro Pro Pro Pro His Pro Leu
50 55 60
Ile His Arg Cys Xaa Ser Ser Xaa Xaa Leu Leu Pro His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1577625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3636:

Arg	Pro	Lys	Ser	Ser	Leu	Xaa	Arg	Gln	Xaa	Thr	Arg	Ser	Thr	Pro	Ala
1			5						10					15	
Ala	Ala	Pro	Ala	Pro	Pro	Ala	His	Pro	His	Arg	Pro	Leu	Pro	Ser	Pro
			20					25					30		
Ala	Leu	Pro	Pro	Ala	Pro	Ser	Thr	Ala	Pro	Ala	Cys	Ser	Ser	Ala	Val
			35				40					45			
Trp	Pro	Leu	His	Pro	Pro	Xaa	Pro	His	His	Arg	Arg	Pro	Thr	His	Leu
			50			55					60				
Ser	Thr	Val	Xaa	Gly	Arg	Arg	Xaa	Xaa	Cys	Ser	Pro	Thr	Asp	Thr	Gly
			65		70				75					80	
Arg	Gly	Ile	Ile	Ser	Pro	Trp	Val	Lys	Leu	His	Pro	Thr	Ala	Pro	Ile
			85					90						95	
Thr	Pro	Asn	Gln	Thr	His	Pro	Ser	Ala	Tyr	Thr	Gln	Gln	Lys	Ser	Gly
			100					105					110		
His	Ile	Phe	Tyr	Ser	Leu	Gly	Xaa	Ser	Ala	Ala	Pro	Pro	Val	Phe	Glu
			115				120						125		
Ile	Leu	Ser	Leu	Ala	Ile	Ile	Thr	Asp	Ala	Pro	Asn	Arg	Arg	Ala	Ala
			130			135					140				
Gly	Glu	Glu	Ile	His	His	Val	Phe	Cys							
			145			150									

(2) INFORMATION FOR SEQ ID NO:3637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..798
(D) OTHER INFORMATION: / Ceres Seq. ID 1577634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3637:

aacctcgtcg	tgtctcgggt	tggccttggt	tcctctctccc	cgacgaccac	cccgcgcttc	60
tcctctctccc	ccgtcccaacc	ttccgagagg	ctcgagccct	gatcccaacg	tgaggcgccg	120
gggtgttagga	gtttagcgat	ggcgaggtgg	cggccggcgg	cgctgctggt	agtggcgctg	180
acagcggttc	tgtcggcrgc	gcrgcggcgg	gatgcgctct	cagtgacggt	gaccgacacc	240
gagtcgcatcc	acccgcctcg	cgcacccggg	tccgcgtgcc	tttcccaacc	tactctcgcg	300
Gctctcgcca	gccagctctag	ggtttcggtc	cggcgctgct	tatccgcgcc	cgccggccat	360
gtcgaagcaa	ggagggaagg	ccaagccgct	gaaggcgccc	aaggccgaca	agaaggagta	420
cgacgagact	gatcttgcat	atctgcagaa	gaagaaaagt	gaggaaaaag	cactgaagga	480
gcttaaggcc	aaggcacaga	agggcgcgat	tgggggctcg	ggtctgaaga	aaagtggaaa	540
gaaatgagac	tggtcacccg	tctccaatac	ctagaggatg	ataaggcagc	tgtctatctg	600
tgttgcgctt	cactaagtgt	gattgtaaca	gtggtacctc	ttgtgttctg	tgttccgcga	660
tgttgcagtt	ggttgcttga	tcgaaaagat	tttcaacctc	ccatctgcta	gctatgatac	720
agatggtccc	ctgataataa	tgatgacata	ttctgtgatg	gatgccacag	cattttttgt	780
ttttgttttt	gcattcag					

(2) INFORMATION FOR SEQ ID NO:3638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1577635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3638:

Met	Ala	Arg	Trp	Arg	Pro	Ala	Ala	Leu	Leu	Val	Val	Ala	Leu	Thr	Ala	
1																
Val	Leu	Ser	Xaa	Ala	Xaa	Arg	Ala	Asp	Ala	Leu	Ser	Val	Thr	Val	Thr	
Asp	Thr	Glu	Cys	Ile	His	Pro	Pro	Arg	Ala	Pro	Gly	Ser	Ala	Cys	Leu	
Ser	Pro	Pro	Thr	Leu	Ala	Ala	Leu	Ala	Ser	Gln	Ser	Arg	Val	Ser	Val	
Pro	Ala	Cys	Leu	Ser	Ala	Pro	Ala	Gly	His	Val	Glu	Ala	Arg	Arg	Gly	
65																
Gly	Gln	Ala	Ala	Glu	Gly	Ala	Gln	Gly	Arg	Gln	Glu	Gly	Val	Arg	Arg	
Asp																

(2) INFORMATION FOR SEQ ID NO:3639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1577636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3639:

Met	Ser	Lys	Gln	Gly	Gly	Lys	Ala	Lys	Pro	Leu	Lys	Ala	Pro	Lys	Ala	
1																
Asp	Lys	Lys	Glu	Tyr	Asp	Glu	Thr	Asp	Leu	Ala	Tyr	Leu	Gln	Lys	Lys	
Lys	Asp	Glu	Glu	Lys	Ala	Leu	Lys	Glu	Leu	Lys	Ala	Lys	Ala	Gln	Lys	
Gly	Ala	Ile	Gly	Gly	Ser	Gly	Leu	Lys	Lys	Ser	Gly	Lys	Lys			
50																

(2) INFORMATION FOR SEQ ID NO:3640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1577637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3640:

Met	Arg	Leu	Val	Thr	Arg	Leu	Gln	Tyr	Leu	Glu	Asp	Asp	Lys	Ala	Ala	
1																
Val	Tyr	Leu	Cys	Cys	Ala	Ser	Leu	Ser	Val	Ile	Val	Thr	Val	Val	Pro	
Leu	Val	Phe	Cys	Val	Pro	Arg	Cys	Cys	Ser	Trp	Leu	Leu	Asp	Arg	Lys	
Met	Phe	Gln	Pro	Pro	Ile	Cys										
50																

(2) INFORMATION FOR SEQ ID NO:3641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..810
(D) OTHER INFORMATION: / Ceres Seq. ID 1577653

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3641:

gtcgagttcg	acctcgatt	tggcgaatg	ccccggcgcc	ctctcccccc	gcagcgcgtc	60
ccgtacgcct	ccttcgctcc	aggaagggga	aggagcgcg	sgggaaacg	gagcaggaat	120
ctggcgctct	ccgcttccct	ctccaaacgt	gcagcagtcg	catccctgac	aacagattcG	180
ggagaaagaa	ggcccaatga	taatggaaat	tccactggac	caaatccgga	ggccactgat	240
gcgaacgcgg	gccaaatgat	cagtcgaagt	gcaagaactc	atgggcagta	tcogtctcat	300
cggcctccaa	gtacctattg	atgtgttggg	ggtcgatggg	gtctattatg	gcttctcttg	360
atgcaccgcg	tacgaggtct	accacgcgct	tggtctccca	accatccgct	gcaagttctg	420
ccgtggggaca	aaggaaacac	tgaggcacca	tatgcgatga	gttatatttt	attcagttac	480
aaagtgatct	gtgtatctag	agctaaaaca	gaagcttcca	tggtcttttc	gtcgtctcgt	540
ctgcaattct	ccatacctgt	aaatgtttgc	caaacagagt	ggtgaatagt	acttctgtac	600
ccagcagcat	cagaaaaatg	taattttgcc	tacaacactc	ttttcgatca	gtggatggat	660
gagtaaccac	cgctcagtag	atcattccat	ttctacgaga	tttttgtaaa	aaaagaaaaa	720
tgcagcagca	gtcggcacgc	tgtgtcattt	agatcatcta	gaaaaccaga	aaaaacgagt	780
catgtaacct	gtttggctcg	tgcaaaaaat				

- (2) INFORMATION FOR SEQ ID NO:3642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..85
(D) OTHER INFORMATION: / Ceres Seq. ID 1577654

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3642:

Val	Glu	Phe	Asp	Pro	Gly	Phe	Gly	Asp	Xaa	Pro	Arg	Arg	Pro	Pro
1			5					10					15	
Pro	Gln	Arg	Val	Pro	Tyr	Ala	Ser	Phe	Ala	Pro	Gly	Arg	Gly	Ser
			20				25					30		
Ala	Xaa	Gly	Thr	Arg	Ser	Arg	Asn	Leu	Ala	Leu	Ser	Ala	Ser	Ser
			35				40				45			
Asn	Gly	Ala	Ala	Val	Pro	Ser	Leu	Thr	Thr	Asp	Ser	Gly	Glu	Gly
			50				55				60			
Pro	Ser	Asp	Asn	Gly	Asn	Ser	Thr	Gly	Pro	Asn	Pro	Glu	Ala	Thr
			65				70				75			80
Ala	Asn	Ala	Gly	Gln										
				85										

- (2) INFORMATION FOR SEQ ID NO:3643:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..85
(D) OTHER INFORMATION: / Ceres Seq. ID 1577655

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3643:

Met	Glu	Ile	Pro	Leu	Asp	Gln	Ile	Arg	Arg	Pro	Leu	Met	Arg	Thr	Arg
1			5					10					15		
Ala	Asn	Asp	Pro	Val	Lys	Val	Gln	Glu	Leu	Met	Gly	Ser	Ile	Arg	Val
			20					25					30		

Ile Gly Leu Gln Val Pro Ile Asp Val Leu Glu Val Asp Gly Val Tyr
35 40 45
Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His Gln Arg Leu Gly
50 55 60
Leu Pro Thr Ile Arg Cys Lys Val Arg Arg Gly Thr Lys Glu Thr Leu
65 70 75 80
Arg His His Met Arg
85

(2) INFORMATION FOR SEQ ID NO:3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3644:

Met Pro Pro Leu Arg Gly Ser Pro Ala Pro Trp Ser Pro Asn His Pro
1 5 10 15
Leu Gln Ser Ser Pro Trp Asp Lys Gly Asn Thr Glu Ala Pro Tyr Ala
20 25 30
Met Ser Tyr Ile Leu Phe Ser Tyr Lys Val Ile Cys Val Ser Arg Ala
35 40 45
Lys Thr Glu Ala Ser Met Val Phe Ser Ser Ser Arg Leu Gln Phe Ser
50 55 60
Ile Pro Val Asn Val Val Gln Thr Glu Trp
65 70

(2) INFORMATION FOR SEQ ID NO:3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3645:

atgttatgta atatagtagt aagttatgaa gtccgaccga taccaccgcg ctagactgtg 60
gcctgcaccc ctcacgcgtc ggctcgatcg ctgatcagtt ctgcrgccgg cgacgtgtgc 120
tagctcaaga cgacgacatg ggctcggcgg tgaagatcgg gacgtggggg gccgacggcgG 180
ggagcccccgt cgacatcaag gtggcgcccg ggccggctgga gagcatcacc atcccgctgga 240
accagagggt ggctgacaaa gcatacaaga agagccactt gggcaatgag tggaaaaaac 300
cttttgctgg atcatctcac gccaaaggga tcgtttctgga gaagattggt attgaggcca 360
agcagcgaat tcgggccatc cgtaagtgtg cccgtgttca gctggtgaag aatggaaaga 420
agattgtcgc ctttgtgccg aatgatgggt gccataacta catcgaggag aatgatgagg 480
tgattgattgc tggatttggg cgtaagggtc atgctgtggg agacattcct ggtgtcaggt 540
tcaaggttgt taagggtgtc ggtgtgtcgc tgcttgcact ctccaaggag aagaaggaga 600
agCcaagggtc ttatgatcac ttccgtagtc aagaatgggt taaactgccc aaggctctat 660
gtttaaagtt ctgctagcaa cagagctgtt aattctgagc tgtacctttt tgttaacatt 720
gttacagtct tacagagttc tgtttccatt ttgaagatat taatatggcg

(2) INFORMATION FOR SEQ ID NO:3646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1.158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577662
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3646:

Met	Gly	Ser	Ala	Val	Lys	Ile	Gly	Thr	Trp	Gly	Gly	Asp	Gly	Gly	Ser	
1				5				10					15			
Pro	Cys	Asp	Ile	Thr	Val	Ala	Pro	Arg	Arg	Leu	Glu	Ser	Ile	Thr	Ile	
				20				25					30			
Arg	Trp	Asn	Gln	Arg	Trp	Ala	Asp	Lys	Ala	Tyr	Lys	Lys	Ser	His	Leu	
				35				40					45			
Gly	Asn	Glu	Trp	Lys	Lys	Pro	Phe	Ala	Gly	Ser	Ser	His	Ala	Lys	Gly	
				50				55				60				
Ile	Val	Leu	Glu	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Gln	Pro	Asn	Ser	Ala	
				65				70				75			80	
Ile	Arg	Lys	Cys	Ala	Arg	Val	Gln	Leu	Val	Lys	Asn	Gly	Lys	Lys	Ile	
				85				90					95			
Ala	Ala	Phe	Val	Pro	Asn	Asp	Gly	Cys	Leu	Asn	Tyr	Ile	Glu	Glu	Asn	
				100				105					110			
Asp	Glu	Val	Leu	Ile	Ala	Gly	Phe	Gly	Arg	Lys	Gly	His	Ala	Val	Gly	
				115				120					125			
Asp	Ile	Pro	Gly	Val	Arg	Phe	Lys	Val	Val	Lys	Val	Ser	Gly	Val	Ser	
				130				135					140			
Leu	Leu	Ala	Leu	Phe	Lys	Glu	Lys	Lys	Glu	Lys	Pro	Arg	Ser			
				145				150					155			

(2) INFORMATION FOR SEQ ID NO:3647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 969 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1.969

 (D) OTHER INFORMATION: / Ceres Seq. ID 1577663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3647:

acataaaccg	ccatamccac	nccctcgcc	gcctgertcc	acctccgcc	ccgcgcctcc	60
ccgcgtcccc	ccctctctac	gcagatcgtc	caggtaagat	gtcgtccgag	gcgggtgaag	120
tggcggtgcc	ggagtcggta	ctccgcaagc	ggaagcgcn	aggagcagtg	ggccgccgag	180
aaagaaggaa	agtcctctgc	cgagaggaag	aagtccatcg	agaaccggaa	gctcatcttc	240
acccgcgcga	agcagtagcc	cgaggagtag	gatgccacag	agaaggaaat	ggtacagctt	300
aagcgtgagg	cccgtttgaa	gggtgttttc	tatgtcagtc	ctgagGcaaa	gctgctattt	360
gtgatccgca	tccgtggtat	caatgccatg	catcttaaga	ccaggaaagt	attgcagctt	420
ctgcgtttga	ggcagatatt	caatggcgtg	ttctctgaaa	tcaacaaggc	taccattaac	480
gtctCttcgca	gggttagacc	ttatgttgca	tatgggtacc	Cgaacttgaa	gagtgctcagg	540
gagttgatct	acaagagggg	ctacggaaaa	ctgaacaagc	agaggatccc	tctgtctaac	600
aaccgaagtca	tcgaggaggg	cttggggcaag	cacaacatca	tttgattga	ggatcttggt	660
catgagatca	tgactgtcgg	cccacacttc	aaggagggca	acaacttctt	ttggccattt	720
aagctgaagg	caccgtcggy	aggtctgaag	aagaagagga	accactatgt	ggagggtggt	780
gatgccggtga	accgtgagaa	ttacatcaac	gagctcatca	aaaggatgaa	ttaggttcac	840
gatcaagctc	tattgtgttc	taagaaactt	tctgtgctct	cccaatttta	cattattagg	900
aagcggatga	atatgcatgc	agttttgttg	tttgaaacta	gatgtgtatg	gaagaacaat	960
gatcttttc						

(2) INFORMATION FOR SEQ ID NO:3648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..99
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577664
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3648:

Ile	Thr	Arg	His	Xaa	His	Xaa	Pro	Arg	Arg	Leu	Xaa	Pro	Pro	Pro	Pro
1			5							10				15	
Pro	Ala	Leu	Pro	Ala	Ser	Pro	Leu	Ser	Tyr	Ala	Asp	Arg	Pro	Gly	Lys
			20					25					30		
Met	Ser	Ser	Glu	Ala	Val	Lys	Val	Ala	Val	Pro	Glu	Ser	Val	Leu	Arg
			35				40					45			
Lys	Arg	Lys	Arg	Xaa	Gly	Ala	Val	Gly	Arg	Arg	Glu	Glu	Gly	Glu	Val
			50			55					60				
Pro	Gly	Arg	Glu	Glu	Glu	Val	His	Arg	Glu	Pro	Glu	Ala	His	Leu	His
			65			70				75				80	
Pro	Arg	Gln	Ala	Val	Arg	Arg	Gly	Val	Arg	Cys	Pro	Gly	Glu	Gly	Thr
			85					90						95	

Gly Thr Ala

(2) INFORMATION FOR SEQ ID NO:3649:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1577665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3649:

Met	His	Pro	Lys	Thr	Arg	Lys	Ile	Leu	Gln	Leu	Leu	Arg	Leu	Arg	Gln
1			5					10					15		
Ile	Phe	Asn	Gly	Val	Phe	Leu	Lys	Val	Asn	Lys	Ala	Thr	Ile	Asn	Met
			20					25					30		
Leu	Arg	Arg	Val	Glu	Pro	Tyr	Val	Ala	Tyr	Gly	Tyr	Pro	Asn	Leu	Lys
			35				40					45			
Ser	Val	Arg	Glu	Leu	Ile	Tyr	Lys	Arg	Gly	Tyr	Gly	Lys	Leu	Asn	Lys
			50			55				60					
Gln	Arg	Ile	Pro	Leu	Ser	Asn	Asn	Gln	Val	Ile	Glu	Glu	Gly	Leu	Gly
			65			70			75					80	
Lys	His	Asn	Ile	Ile	Cys	Ile	Glu	Asp	Leu	Val	His	Glu	Ile	Met	Thr
			85			90							95		
Val	Gly	Pro	His	Phe	Lys	Glu	Ala	Asn	Asn	Phe	Leu	Trp	Pro	Phe	Lys
			100				105						110		
Leu	Lys	Ala	Pro	Leu	Gly	Gly	Leu	Lys	Lys	Lys	Arg	Asn	His	Tyr	Val
			115			120						125			
Glu	Gly	Gly	Asp	Ala	Gly	Asn	Arg	Glu	Asn	Tyr	Ile	Asn	Glu	Leu	Ile
			130			135					140				

Lys Arg Met Asn
145

(2) INFORMATION FOR SEQ ID NO:3650:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3650:

Met Leu Arg Arg Val Glu Pro Tyr Val Ala Tyr Gly Tyr Pro Asn Leu
1 5 10 15
Lys Ser Val Arg Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn
20 25 30
Lys Gln Arg Ile Pro Leu Ser Asn Asn Gln Val Ile Glu Glu Gly Leu
35 40 45
Gly Lys His Asn Ile Ile Cys Ile Glu Asp Leu Val His Glu Ile Met
50 55 60
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe
65 70 75 80
Lys Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Arg Asn His Tyr
85 90 95
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Tyr Ile Asn Glu Leu
100 105 110
Ile Lys Arg Met Asn
115

(2) INFORMATION FOR SEQ ID NO:3651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1577678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3651:

atcattggtc tgctagcaga aacctcagag atatgttaca gagaaataaa ggacatcaag 60
tgcatcaact gccttcacaa gccagaaggt tccatgtttg tcaatgttgaa attaaatttg 120
tatcttttgg aggggattca tgacgatatt gatttttgct gcaagCtggc aaaagaagag 180
tctgtgattt tgtgtccagg gactgttttg ggaatggaaa actggatccg catcactttc 240
gchattgatt catctttctc tcttgatggt cttgagagga tcaaatottt ctgccaaagg 300
cataagaaga agaatttgct taatggccat taactgtatc tacgttcaaa gttaccacag 360
tccattgttt ttcatgtgat catcaacaaa tgtggaactt tgaatccct ctgaattaat 420
aaagttttcc ttg

(2) INFORMATION FOR SEQ ID NO:3652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1577679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3652:

Ile Ile Gly Leu Leu Ala Glu Thr Ser Glu Ile Cys Tyr Arg Glu Ile
1 5 10 15
Lys Asp Ile Lys Cys Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met
20 25 30
Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp
35 40 45
Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu
50 55 60
Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe
65 70 75 80

Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser
85 90 95
Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
100 105 110

(2) INFORMATION FOR SEQ ID NO:3653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3653:

Met Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His
1 5 10 15
Asp Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile
20 25 30
Leu Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr
35 40 45
Phe Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys
50 55 60
Ser Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3654:

Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp Asp Ile
1 5 10 15
Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro
20 25 30
Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe Xaa Ile
35 40 45
Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser Phe Cys
50 55 60
Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His
65 70 75

(2) INFORMATION FOR SEQ ID NO:3655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1045
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3655:

atcaagtcgg ctatcttctc cggccatcgg tcgcaccccc acgtgggggc ggcgccggtc

ccgcagcagc	agcagctggg	gagcaccgct	togttccact	cgacacccat	tctgcagcgg	120
aagcacaca	cccagtgcca	caacagattc	aactattata	cgagacgtag	gaggaaaccga	180
gaaactaaaa	gggtcaatgct	acggaacatg	tcagaatatg	cagagctctct	ctttcagagtg	240
tgggcgtgatg	aagatgagaa	aaatgctgca	tctgctgggc	cttcacgtgtt	tagaggacat	300
cgttgggtca	gaaattcaag	caacaatggt	ttccgtacac	acgattttta	tacggggaat	360
ttcaaaaagca	aaggaggattt	tgagtttttg	acaagtgatg	aggatgaacc	agagaactctg	420
tttctgtaag	tttttcgaga	ccagcacaca	tattattggt	ctttttcatc	tgataattttt	480
cagagGaaat	ccaaacgtgc	tcgctcacaa	aaatccagaa	actggagttt	tgaacacagc	540
gaggaggatg	aagtatcagc	tcacatcagag	gtatcttttg	cacgcacaagc	atgtgacatt	600
agcacttctg	gtccgcttaa	acttgaagat	gttaaaaagc	cataccgagc	ctttggggttg	660
agatggcatc	cagatcgcca	caatggatca	tctaagtcta	cagcgggagga	gaaattccaag	720
cattgcagtg	cagacatacaa	gaccttatgt	gatagtttgg	ccgctgcata	gataattttg	780
aaagaagatg	gactctggat	gagccctctc	caaatcttct	agctgcaaat	tctgaagagc	840
tgccacatgc	ttgtggtagc	tcggaccatc	ccaatcccaa	gagcggggag	tcgactttct	900
tggttattga	ggcgattgag	tcaattcaaa	attgaccgga	taatatatgt	actgtaccgt	960
gtaaaaattt	ttgtcacagc	tcattgtgtg	attattttta	tagatatgaa	gatattgttc	1020
acaccaactca	ataaattttc	ttggc				

(2) INFORMATION FOR SEQ ID NO:3656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3656:

Ile	Lys	Ser	Ala	Ile	Phe	Ser	Gly	His	Arg	Ser	His	Pro	His	Val	Gly
1				5					10					15	
Ala	Ala	Ala	Val	Pro	Gln	Gln	Gln	Gln	Leu	Gly	Ser	Thr	Ala	Ser	Phe
			20				25						30		
His	Ser	Thr	Pro	Ile	Leu	Gln	Arg	Lys	His	Lys	Thr	Gln	Trp	His	Asn
			35				40					45			
Arg	Phe	Asn	Tyr	Tyr	Thr	Arg	Arg	Arg	Asn	Arg	Glu	Thr	Lys	Arg	
			50				55				60				
Ser	Met	Leu	Arg	Asn	Met	Ser	Glu	Tyr	Ala	Glu	Ser	Leu	Phe	Gln	Ser
65				70					75					80	
Trp	Arg	Asp	Glu	Asp	Glu	Lys	Asn	Ala	Ala	Ser	Ala	Gly	Pro	Ser	Trp
			85						90					95	
Phe	Arg	Gly	His	Arg	Trp	Val	Arg	Asn	Ser	Ser	Asn	Asn	Gly	Phe	Arg
			100					105					110		
Thr	His	Asp	Phe	Tyr	Tyr	Gly	Asn	Phe	Lys	Ser	Lys	Gly	Gly	Phe	Glu
			115				120					125			
Phe	Cys	Thr	Ser	Asp	Glu	Asp	Glu	Pro	Glu	Asn	Leu	Phe	Arg	Asn	Val
			130				135				140				
Phe	Arg	Asp	Gln	His	Thr	Tyr	Trp	Ser	Phe	Ser	Ser	Asp	Asn	Phe	
145				150					155					160	
Gln	Arg	Asn	Ser	Lys	Arg	Ala	Arg	Ser	Gln	Lys	Ser	Arg	Asn	Trp	Ser
			165						170					175	
Phe	Glu	Thr	Asp	Glu	Glu	Asp	Glu	Val	Ser	Ala	Pro	Ser	Glu	Val	Ser
			180					185					190		
Leu	Ala	Arg	Gln	Ala	Leu	Gly	Leu	Ser	Thr	Ser	Gly	Pro	Leu	Lys	Leu
			195				200					205			
Glu	Asp	Val	Lys	Ser	Ala	Tyr	Arg	Ala	Cys	Ala	Leu	Arg	Trp	His	Pro
			210				215					220			
Asp	Arg	His	Asn	Gly	Ser	Ser	Lys	Ser	Thr	Ala	Glu	Glu	Lys	Phe	Lys
225				230						235				240	
His	Cys	Ser	Ala	Ala	Tyr	Lys	Thr	Leu	Cys	Asp	Ser	Leu	Ala	Ala	Ala
			245					250					255		

(2) INFORMATION FOR SEQ ID NO:3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1577690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3657:

Ser Ser Arg Leu Ser Ser Pro Ala Ile Gly Arg Thr Pro Thr Trp Gly
1 5 10 15
Arg Arg Arg Ser Arg Ser Ser Ser Ser Trp Gly Ala Pro Leu Arg Ser
20 25 30
Thr Arg His Pro Phe Cys Ser Gly Ser Thr Arg Pro Ser Gly Thr Thr
35 40 45
Asp Ser Thr Ile Ile Arg Asp Val Gly Gly Thr Glu Lys Leu Lys Gly
50 55 60
Gln Cys Tyr Gly Thr Cys Gln Asn Met Gln Ser Leu Ser Phe Arg Val
65 70 75 80
Gly Val Met Lys Met Arg Lys Met Leu His Leu Leu Gly Leu His Gly
85 90 95
Leu Glu Asp Ile Val Gly Ser Glu Ile Gln Ala Thr Met Val Ser Val
100 105 110
His Thr Ile Phe Ile Thr Gly Ile Ser Lys Ala Lys Glu Asp Leu Ser
115 120 125
Phe Ala Gln Val Met Arg Met Asn Gln Arg Ile Cys Phe Val Met Phe
130 135 140
Phe Glu Thr Ser Thr His Ile Ile Gly Leu Phe His Leu Ile Ile Phe
145 150 155 160
Arg Gly Thr Pro Asn Val Leu Ala His Lys Asn Pro Glu Thr Gly Val
165 170 175
Leu Lys Gln Thr Arg Arg Met Lys Tyr Gln Leu His Gln Arg Tyr Leu
180 185 190
Trp His Asp Lys Leu Leu Gly
195

(2) INFORMATION FOR SEQ ID NO:3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1577691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3658:

Met Leu Arg Asn Met Ser Glu Tyr Ala Glu Ser Leu Phe Gln Ser Trp
1 5 10 15
Arg Asp Glu Asp Glu Lys Asn Ala Ala Ser Ala Gly Pro Ser Trp Phe
20 25 30
Arg Gly His Arg Trp Val Arg Asn Ser Ser Asn Asn Gly Phe Arg Thr
35 40 45
His Asp Phe Tyr Tyr Gly Asn Phe Lys Ser Lys Gly Gly Phe Glu Phe
50 55 60
Cys Thr Ser Asp Glu Asp Glu Pro Glu Asn Leu Phe Arg Asn Val Phe

65	70	75	80
Arg Asp Gln His Thr Tyr Tyr Trp Ser Phe Ser Ser Asp Asn Phe Gln			
	85	90	95
Arg Asn Ser Lys Arg Ala Arg Ser Gln Lys Ser Arg Asn Trp Ser Phe			
	100	105	110
Glu Thr Asp Glu Glu Asp Glu Val Ser Ala Pro Ser Glu Val Ser Leu			
	115	120	125
Ala Arg Gln Ala Leu Gly Leu Ser Thr Ser Gly Pro Leu Lys Leu Glu			
	130	135	140
Asp Val Lys Ser Ala Tyr Arg Ala Cys Ala Leu Arg Trp His Pro Asp			
	145	150	155
Arg His Asn Gly Ser Ser Lys Ser Thr Ala Glu Lys Phe Lys His			
	165	170	175
Cys Ser Ala Ala Tyr Lys Thr Leu Cys Asp Ser Leu Ala Ala Ala			
	180	185	190

(2) INFORMATION FOR SEQ ID NO:3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..875

- (D) OTHER INFORMATION: / Ceres Seq. ID 1577698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3659:

atcggtgccc	cattggccac	tggccccctag	ccctcgccct	ccctttttcta	ttgctccgaa	60
gcgccagttg	cgagctgtct	cctccactct	tctccttcac	tgtcgagccc	gccccctgtg	120
gaagcttcga	ggctgctgct	gctgcgccca	tgccgcgga	aggcaagacg	ccgtccctcg	180
ccgaggagta	ttcaactcca	ccacaggaag	ttccagtgga	aaaggcagct	gaggagaagc	240
cctctagtgg	tactgagtct	gaagctgctc	cctcaaccCa	atgatgaaac	tcctccatct	300
gtagaagaca	agaatggaac	ttctgaagta	caagatgctg	ctgaaaaatcc	agaggcgagaa	360
gaaactaaca	ctgctgcaga	ggaaacacct	gctgtagagg	aagcaagtga	gactaccgag	420
gaggaagagg	ctgagaaacc	tgagatcaag	atcgaaacag	ctccagcaga	ttttcgtttc	480
ccaacaacaa	accaaaacag	gcattgtttc	acacgctatg	ttgaatatca	caggtgtgtg	540
gctgcataag	gtgaggtatg	acctgagtgt	gataagttcg	ccaagtacta	tcgatccctg	600
tgcccagggt	aatgggttga	tcgctggaac	gagcaacgcg	aaaacggcac	cttcctctgga	660
cctctgtaac	cctacaatgc	aaaagaagta	tgaactcaag	atgttgctgc	ggcttctctt	720
ccttggtaac	tggcgccaag	ttaccttttt	tggagctctc	tacagataaa	gaaatccctt	780
ttggcttgaa	gaatgcctgt	tgtctcttcc	taacggctcat	gtgtgctgct	gctgagaagc	840
tagcgtoaca	gttaacaatt	ttctttatca	agttc			

(2) INFORMATION FOR SEQ ID NO:3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

- (D) OTHER INFORMATION: / Ceres Seq. ID 1577699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3660:

Arg Val Pro Ile Gly His Trp Pro Leu Ala Leu Pro Phe Leu							
1	5	10	15	20	25	30	
Leu Leu Arg Ser Pro Ser Cys Glu Leu Ser Pro Pro Leu Phe Ser Phe							
	35	40	45				
Thr Val Ala Ala Ala Pro Cys Arg Ser Phe Glu Ala Ala Ala Ala							
	50	55	60	65	70	75	
Pro Met Ala Ala Glu Gly Lys Thr Pro Ser Leu Ala Glu Glu Tyr Ser							

50	55	60
Leu Pro Pro Gln Glu Val	Pro Val Glu Lys	Ala Ala Glu Glu Lys Pro
65	70	75
Ser Ser Gly Thr Glu Ser	Glu Ala Ala Pro	Ser Thr Gln
85	90	

(2) INFORMATION FOR SEQ ID NO:3661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1577700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3661:

Met Leu Asn Ile Thr Gly Val Trp Leu Gln Lys Val Arg Met His Leu	
1	5 10 15
Ser Val Ile Ser Ser Pro Ser Thr Ile Asp Pro Cys Ala Gln Val Asn	
	20 25 30
Gly Leu Ile Ala Gly Thr Ser Asn Ala Lys Thr Ala Pro Ser Leu Asp	
	35 40 45
Leu Cys Asn Pro Thr Met Gln Lys Lys Tyr Glu Leu Thr Met Leu Cys	
	50 55 60
Arg Leu Leu Phe Leu Gly Asn Trp Arg Gln Val Thr Phe Phe Gly Ala	
65	70 75 80
Leu Tyr Arg Ile Arg Asn Pro Phe Trp Leu Glu Glu Cys Pro Val Ala	
	85 90 95
Leu Pro Asn Gly His Val Val Arg Cys	
	100 105

(2) INFORMATION FOR SEQ ID NO:3662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3662:

Met His Leu Ser Val Ile Ser Ser Pro Ser Thr Ile Asp Pro Cys Ala	
1	5 10 15
Gln Val Asn Gly Leu Ile Ala Gly Thr Ser Asn Ala Lys Thr Ala Pro	
	20 25 30
Ser Leu Asp Leu Cys Asn Pro Thr Met Gln Lys Lys Tyr Glu Leu Thr	
	35 40 45
Met Leu Cys Arg Leu Leu Phe Leu Gly Asn Trp Arg Gln Val Thr Phe	
	50 55 60
Phe Gly Ala Leu Tyr Arg Ile Arg Asn Pro Phe Trp Leu Glu Glu Cys	
65	70 75 80
Pro Val Ala Leu Pro Asn Gly His Val Val Arg Cys	
	85 90

(2) INFORMATION FOR SEQ ID NO:3663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1577714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3663:

```
gtcgtctctcc gaactctgat tgaggaggag tgaagcttct ttctctcttc ctccagtcac 60
ccattgcaaa aagtagaagc agggaaggaa ttggaagcat gaacaagcag cagcaggcgt 120
acgggtacgg aaatgggcag caggccgacg tcccaggcta ctgctgtttc catccccggg 180
aggtcgggct cgcgctctgc gctcactgcc tcaaggatcg cctcctcctc ctctcggccg 240
ctgccacaaa caataagatc gacgacgacg cccgccgcaa aagcaggagc agggagcagg 300
gcattctcct ccccaaggtc ttccgcgtcg gctcctcctt cctccagcgc ctcgactccc 360
gccaccaccg gggacgaggg cgggacaaca actgctactc cgaacgacgc gacgccaccg 420
cctccgtctc aagcctcgat gattccttca tctccatcaa attcaggagg aacggcaagg 480
cgacgtggga cagccagcag cagcacaagg cggcagCtcc cgcgaggtct cgtcgacgac 540
gaccattgta cggttgagc acgtcaagcg tktcggcgtc acccgggtgc gcaaacagg 600
gggtggccgc atgctgcagc tggcgcgctg gaggaggtcg tccgctgctg cgggtgggct 660
ggacggcaag aaggcgcgcg cgcgcgcgcg tgagcggtcc aaggccagag ggagaggctg 720
gattccggag ctcaactcga ggccggcgca cgggagccgc gcgtggtagg tcgcgctcgt 780
cggtaaggag gcccggtcgg tcggggcgcg gccagcccat gcattgatgc atggtgtccg 840
atggtatgat ggaatcgca gcttcccccc ttgctttgga tggagacgta gtaattgctt 900
gcttgtgctt tgtaccagt gagatgagtg agtgctcctc tttaactact ataggctact 960
atcgtacagc ttaatacgac ctagtgtgt gtgtggattg ctatgcgtg
```

(2) INFORMATION FOR SEQ ID NO:3664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3664:

```
Met Asn Lys Gln Gln Gln Ala Tyr Gly Tyr Gly Asn Gly Gln Ala
1 5 10 15
Asp Val Pro Gly Tyr Cys Cys Phe His Pro Arg Glu Val Gly Val Gly
20 25 30
Val Cys Ala His Cys Leu Lys Asp Arg Leu Leu Leu Leu Ala Ala
35 40 45
Ala Asn Asn Asn Lys Ile Asp Asp Ala Arg Arg Lys Ser Arg Ser
50 55 60
Arg Ser Arg Ser Ile Ser Leu Pro Lys Val Phe Ala Leu Gly Ser Ser
65 70 75 80
Phe Leu Gln Arg Leu Asp Ser Arg His His Arg Gly Arg Gly Arg Asp
85 90 95
Asn Asn Cys Tyr Ser Asp Asp Asp Ala Thr Ala Ser Val Ala Ser
100 105 110
Leu Asp Asp Ser Phe Ile Ser Ile Lys Phe Glu Asp Asn Gly Lys Ala
115 120 125
Thr Trp Asp Ser Gln Ser Gln His Lys Ala Ala Ala Pro Ala Arg Ser
130 135 140
Arg Arg Arg Arg Pro Trp
145 150
```

(2) INFORMATION FOR SEQ ID NO:3665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1577716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3665:

Met	Gly	Ser	Arg	Pro	Thr	Ser	Gln	Ala	Thr	Ala	Val	Ser	Ile	Pro	Gly	
1				5					10					15		
Arg	Ser	Ala	Ser	Ala	Ser	Ala	Leu	Thr	Ala	Ser	Arg	Ile	Ala	Ser	Ser	
				20				25					30			
Ser	Ser	Ser	Pro	Leu	Pro	Thr	Thr	Ile	Arg	Ser	Thr	Thr	Thr	Pro	Ala	
				35				40					45			
Ala	Lys	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Ser	Pro	Ser	Pro	Arg	Ser	Ser	
	50						55					60				
Arg	Ser	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Ser	Thr	Pro	Ala	Thr	Thr	Gly	
	65						70				75				80	
Asp	Glu	Gly	Gly	Thr	Thr	Thr	Ala	Thr	Pro	Thr	Thr	Thr	Thr	Pro	Pro	
				85					90					95		
Pro	Pro	Ser	Gln	Ala	Ser	Met	Ile	Pro	Ser	Ser	Pro	Ser	Asn	Ser	Arg	
				100				105					110			
Thr	Thr	Ala	Arg	Arg	Gly	Thr	Ala	Arg	Ala	Ser	Thr	Arg	Arg	Gln		
				115				120					125			
Leu	Pro	Arg	Gly	Leu	Val	Asp	Asp	His	Gly	Ser	Gly	Gly	Ala	Arg		
	130					135					140					
Gln	Ala	Xaa	Arg	Arg	His	Pro	Val	Ala	Gln	Thr	Gly	Gly	Gly	Pro	His	
	145					150				155					160	
Ala	Ala	Ala	Gly	Ala	Leu	Glu	Glu	Val	Val	Arg	Cys	Cys	Gly	Trp	Ala	
				165					170					175		
Gly	Arg	Gln	Glu	Gly	Gly	Gly	Gly	Gly	Gly							
				180					185							

(2) INFORMATION FOR SEQ ID NO:3666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1577717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3666:

aactaggcaa	ctaactccgtc	tcacgcctct	cctgtccctt	ctcgcgcCtc	tgcgcccgcc	60
tctgtccctcg	cctctctccat	cgcacccagc	tttctctccc	acccaccacac	cactctctacc	120
cgccacagtc	gtgtagtcgc	ggcggcgagat	atgcaggccg	ccgccgcctt	caaccaggca	180
gccttcacgc	ccgcctcgct	gcacgcgcctc	ccgagggccc	tccactagc	tgttcggag	240
gatgtctttg	cggggataag	agggcgccct	tttacacggc	cccggtgtgtg	cgggagcctc	300
tctgtccggcg	tcggcagcta	caacagcgag	cacactccag	tatttccaa	acaacaatca	360
tgggatccct	acaagctctt	tggtgttgat	caagatgcac	ctgaagaaga	ggtccggagt	420
gcacggaatt	ttcttctaaa	acaatacgcc	ggatatgaag	aaagtgaaga	ggccattgaa	480
ggtgcttatg	acaagataat	aatgaatagc	tacacagacc	gtaagaatac	caaatctaat	540
ctgaaaagca	agctaaaaga	gcaagttgaa	ggatccccat	catggcctt		

(2) INFORMATION FOR SEQ ID NO:3667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1577718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3667:

Leu	Gly	Asn	Tyr	Ser	Val	Ser	Arg	Leu	Ser	Cys	Pro	Leu	Ser	Pro	Leu
1				5				10						15	
Ser	Pro	Arg	Leu	Cys	Leu	Arg	Leu	Leu	His	Arg	Thr	Gln	Leu	Ser	Ser
			20					25					30		
Pro	Pro	His	His	His	Ser	Tyr	Pro	Ala	Thr	Ser	Cys	Ser	Arg	Gly	Gly
			35					40				45			
Gly	Tyr	Ala	Gly	Arg	Arg	Arg	Leu	Gln	Pro	Gly	Ser	Leu	His	Arg	Pro
			50			55				60					
Leu	Ala	Ala	Ser	Pro	Pro	Glu	Ala	Pro	Pro	Pro	Ser	Cys	Cys	Gly	Gly
65						70				75				80	
Cys	Phe	Cys	Gly	Asp	Lys	Arg	Arg	Ala	Phe	Tyr	Thr	Ala	Pro	Val	Leu
				85					90					95	
Arg	Glu	Pro	Leu	Cys	Arg	Arg	Arg	Gln	Leu	Gln	Gln	Ala	Ala	His	Ser
			100					105					110		
Ser	Ile	Ser	Lys	Thr	Thr	Ile	Met	Gly	Ser	Leu	Gln	Ala	Ser	Trp	Cys
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1577719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3668:

Met	Gln	Ala	Ala	Ala	Ala	Phe	Asn	Gln	Ala	Ala	Phe	Thr	Ala	Arg	Ser
1														15	
Leu	His	Arg	Pro	Pro	Arg	Pro	Leu	His	Leu	Ala	Val	Ala	Glu	Asp	Ala
			20					25					30		
Phe	Ala	Gly	Ile	Arg	Gly	Ala	Pro	Phe	Thr	Arg	Pro	Arg	Cys	Cys	Gly
			35				40					45			
Ser	Leu	Ser	Val	Gly	Val	Gly	Ser	Tyr	Asn	Ser	Glu	His	Thr	Pro	Val
			50			55				60					
Phe	Pro	Arg	Gln	Gln	Ser	Trp	Asp	Pro	Tyr	Lys	Leu	Leu	Gly	Val	Asp
65						70				75				80	
Gln	Asp	Ala	Ser	Glu	Glu	Glu	Val	Arg	Ser	Ala	Arg	Asn	Phe	Leu	Leu
				85					90				95		
Lys	Gln	Tyr	Ala	Gly	Tyr	Glu	Glu	Ser	Glu	Glu	Ala	Ile	Glu	Gly	Ala
			100					105					110		
Tyr	Asp	Lys	Ile	Ile	Met	Asn	Ser	Tyr	Thr	Asp	Arg	Lys	Lys	Ser	Lys
			115				120					125			
Phe	Asn	Leu	Lys	Ser	Lys	Leu	Lys	Glu	Gln	Val	Glu	Gly	Ser	Pro	Ser
			130			135					140				
Trp	Leu														
145															

(2) INFORMATION FOR SEQ ID NO:3669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3669:

tatttttcta	agcatgtgaag	ggttggttgg	tgccatgttg	ttcttgaacc	ccatacacgt	60
gtttcccggt	gatttgccct	tgctcagcatg	gacactgttg	aagaagcggg	sswtgcataa	120
agtatcttaa	tggttctgtg	atggaaggtc	gaacacatcac	agttgaaaag	tcacgccgtg	180
gtcgcccaag	gacaccaact	ccctggaagct	atcttggcca	tcggtacgag	cgtaggggagc	240
gtggggaggtt	ccatagaggc	tatggtgtgtg	ggcgtgatga	gtattacggc	aatggcggcg	300
gcgggtatgg	ctaccgcaag	tctccgcctc	ccatgtactc	ttctacagg	gagagtcggg	360
attattatcc	ctctacaag	gacagccggg	actaccctcc	ctacagggac	ggcaggggact	420
actctctccc	ccacaggga	cctcgggact	actacgaaag	caggggtggc	cggggctact	480
cgccgcctcc	ttatggtgtg	ggtaggtcaa	ggagggaccg	antcggtttc	accgtagctgg	540
atgccagaaa	ggggctacog	tggaggccgc	cgggtgggtg	gcggcgagata	tgacaggtaa	600
tgtagaggtt	ttctctccgc	cggtagctgc	tgctgcgatg	gctgcgatg	gctctcgcag	660
ctctggtgat	atgggttagac	tgctgcgtgt	agctgtgtac	ttggtgtact	gtcttccgcg	720
gtatgtggat	tttgtgaaaa	ctctgtatg	agcacctttt	atttgtagcc	tgcaatgatt	780
ctctcttaag						

(2) INFORMATION FOR SEQ ID NO:3670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3670:

Met	Glu	Gly	Arg	Asn	Ile	Thr	Val	Glu	Lys	Ser	Arg	Arg	Gly	Arg	Pro
1				5				10					15		
Arg	Thr	Pro	Thr	Pro	Gly	Ser	Tyr	Leu	Gly	His	Arg	Tyr	Glu	Arg	Arg
				20				25					30		
Glu	Arg	Gly	Arg	Phe	His	Arg	Gly	Tyr	Gly	Gly	Gly	Arg	Asp	Glu	Tyr
				35				40					45		
Tyr	Gly	Asn	Gly	Gly	Gly	Gly	Tyr	Gly	Tyr	Arg	Arg	Ser	Pro	Pro	Pro
				50				55					60		
Met	Tyr	Ser	Ser	Tyr	Arg	Glu	Ser	Arg	Asp	Tyr	Tyr	Pro	Ser	Tyr	Lys
				70											80
Asp	Ser	Arg	Asp	Tyr	Pro	Pro	Tyr	Arg	Asp	Gly	Arg	Asp	Tyr	Ser	Pro
				85											95
Pro	His	Arg	Asp	Pro	Arg	Asp	Tyr	Tyr	Glu	Ser	Arg	Gly	Gly	Arg	Gly
				100											110
Tyr	Ser	Pro	Pro	Tyr	Gly	Gly	Gly	Arg	Ser	Arg	Arg	Asp	Arg	Arg	Xaa
				115											125
Gly	Phe	Thr	Val	Ser	Asp	Ala	Arg	Lys	Gly	Leu	Arg	Trp	Arg	Pro	Pro
				130											140
Gly	Gly	Trp	Arg	Arg	Ile										
				145											150

(2) INFORMATION FOR SEQ ID NO:3671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3671:

Met	Val	Val	Gly	Val	Met	Ser	Ile	Thr	Ala	Met	Ala	Ala	Ala	Gly	Met
1			5					10						15	
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Pro	Cys	Thr	Leu	Pro	Thr	Gly	Arg	Val
			20					25					30		
Gly	Ile	Ile	Ile	Pro	Pro	Thr	Arg	Thr	Ala	Gly	Thr	Thr	Leu	Pro	Thr
			35					40				45			
Gly	Thr	Ala	Gly	Thr	Thr	Leu	Leu	Pro	Thr	Gly	Thr	Leu	Gly	Thr	Thr
			50				55				60				
Thr	Lys	Ala	Gly	Val	Ala	Gly	Ala	Thr	Arg	Arg	Leu	Leu	Met	Val	Val
			65				70			75				80	
Val	Gly	Gln	Gly	Gly	Thr	Xaa	Ser	Val	Ser	Pro	Tyr	Arg	Met	Pro	Glu
			85					90					95		
Arg	Gly	Tyr	Gly	Gly	Gly	Arg	Arg	Val	Gly	Gly	Gly	Gly	Tyr	Asp	Arg
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3672:

Met	Ser	Ile	Thr	Ala	Met	Ala	Ala	Ala	Gly	Met	Ala	Thr	Ala	Gly	Leu
1					5				10					15	
Arg	Leu	Pro	Cys	Thr	Leu	Pro	Thr	Gly	Arg	Val	Gly	Ile	Ile	Ile	Pro
			20					25				30			
Pro	Thr	Arg	Thr	Ala	Gly	Thr	Thr	Leu	Pro	Thr	Gly	Thr	Ala	Gly	Thr
			35				40					45			
Thr	Leu	Leu	Pro	Thr	Gly	Thr	Leu	Gly	Thr	Thr	Thr	Lys	Ala	Gly	Val
			50				55				60				
Ala	Gly	Ala	Thr	Arg	Arg	Leu	Leu	Met	Val	Val	Val	Gly	Gln	Gly	Gly
			65				70			75				80	
Thr	Xaa	Ser	Val	Ser	Pro	Tyr	Arg	Met	Pro	Glu	Arg	Gly	Tyr	Gly	Gly
			85					90					95		
Gly	Arg	Arg	Val	Gly	Gly	Gly	Gly	Tyr	Asp	Arg					
			100				105								

(2) INFORMATION FOR SEQ ID NO:3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..926
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3673:

aaaagatctc	agccgcgcgc	gtctccgtcg	ctccgcgcga	cctcccccca	tcaccgcctc	60
actaaaaacc	taatccctag	cgcacatggc	ggctgtgtcg	gcggccacat	cgcacctcct	120
acgcacacac	cgcacacccc	acctctcctc	cctccgcgca	gantnctcat	cctcccgctg	180
tttaccctag	cagccggagc	tgctcccccga	cccgaccgcc	ggcaccctcg	acctcgccgg	240
cgcggcccca	ctccctccaa	accccgacac	ggggagcccc	ttctacaccc	agaactggcg	300
caaccagacc	gcmgccaacc	cgsmtcctc	gcttctgcgc	amcgtcgtcg	cmgmgagcmc	360

cttcggggcg	cagCacttca	tggccgcctt	ctacgatgca	cccgcagtca	cggggtcaaa	420
ggagacgttc	gccaaagtata	tggcggagCa	gcggtgggaa	gacatgaagc	acctgttcga	480
ccactgggtg	cgctccctcg	acgccgccac	ggggaagccc	aaccaccgcg	acgtcgacct	540
cttcaatcac	tacctccgcg	ccaacctcat	gaccagggcc	ctgccgcacg	agatgctcga	600
tctcgctgac	cacatgctcg	agttcgagct	ccaacccaac	actgcctcgt	acaacctcgt	660
gctcaagagc	atggtcgcca	gccaggagac	cgagggcgcc	gagaagctca	ttgaacgggt	720
agtgcgctat	tcttgtacgg	gcggcattgt	cgttgccaat	gaggcattct	gatttctgtt	780
ccggcaccta	gttttgttta	ccgtacttat	aggtgacgac	ctataatggt	ataacctgta	840
aaaccgggtg	gccactgacg	tttggcattg	acgtgaggat	atgcagcaag	ctcaaatgcg	900
gtaatgagaa	gaggacacgt	tcttct				

(2) INFORMATION FOR SEQ ID NO:3674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3674:

Lys	Arg	Ser	Gln	Pro	Pro	Ser	Ser	Pro	Ser	Leu	Arg	Arg	Thr	Ser	Pro
1				5						10				15	
His	His	Arg	Leu	Thr	Lys	Thr	Leu	Ile	Pro	Ser	Arg	His	Gly	Gly	Cys
			20				25						30		
Cys	Gly	Gly	His	Leu	Ala	Pro	Pro	Thr	Pro	Pro	Pro	Gln	Pro	Pro	Pro
		35				40						45			
Ser	Pro	Pro	Pro	Arg	Arg	Xaa	Leu	Ile	Leu	Pro	Cys	Phe	Thr	Pro	Ala
		50				55					60				
Ala	Gly	Ala	Val	Pro	Arg	Pro	Asp	Arg	Arg	His	Pro	Arg	Pro	Arg	Arg
65				70					75					80	
Arg	Gly	Pro	Thr	Pro	Ser	Lys	Pro	Gln	His	Gly	Glu	Pro	Leu	Leu	His
				85					90					95	
Pro	Glu	Leu	Ala	Gln	Pro	Ser	Arg	Xaa	Gln	Pro	Xaa	Leu	Leu	Ala	Ser
			100				105								
Xaa	Xaa	Arg	Arg	Arg	Xaa	Xaa	Xaa	Leu	Arg	Gly	Ala	Ala	Leu	His	Gly
			115				120					125			
Arg	Leu	Leu	Arg	Cys	Thr	Arg	Arg	His	Gly	Ala	Gln	Gly	Asp	Val	Arg
		130				135					140				
Gln	Val	Tyr	Gly	Gly	Ala	Ala	Val	Gly	Arg	His	Glu	Ala	Pro	Val	Arg
145					150				155					160	
Pro	Leu	Gly	Ala	Leu	Pro	Arg	Arg	Arg	His	Gly	Glu	Ala	Gln	Pro	Pro
			165						170					175	
Arg	Arg	Arg	Pro	Leu	Gln	Ser	Leu	Pro	Pro	Arg	Gln	Pro	His	Asp	Gln
			180					185					190		
Gly	Pro	Ala	Ala	Arg	Asp	Ala	Arg	Ser	Arg						
			195				200								

(2) INFORMATION FOR SEQ ID NO:3675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3675:

Met Ala Ala Val Ala Ala Ala Thr Ser His Leu Leu Arg His His Arg

```

1           5           10           15
Asn Pro His Leu Leu Leu Arg Ala Xaa Xaa Ser Ser Ser Arg Ala
20           25           30
Leu Pro Gln Gln Pro Glu Leu Ser Pro Asp Pro Thr Ala Gly Thr Pro
35           40           45
Asp Leu Ala Gly Ala Ala Pro Leu Pro Pro Asn Pro Ser Thr Gly Ser
50           55           60
Pro Phe Tyr Thr Gln Asn Trp Arg Asn Pro Ala Xaa Ala Asn Pro Xaa
65           70           75           80
Ser Ser Leu Leu Xaa Xaa Val Val Xaa Xaa Ser Xaa Phe Gly Ala Gln
85           90           95
His Phe Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys
100          105          110
Glu Thr Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys
115          120          125
His Leu Phe Asp His Trp Val Arg Ser Leu Asp Ala Thr Gly Lys
130          135          140
Pro Asn His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn
145          150          155          160
Leu Met Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His
165          170          175
Met Leu Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val
180          185          190
Leu Lys Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu
195          200          205
Ile Glu Arg
210

```

(2) INFORMATION FOR SEQ ID NO:3676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3676:

```

Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys Glu Thr
1           5           10           15
Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys His Leu
20           25           30
Phe Asp His Trp Val Arg Ser Leu Asp Ala Ala Thr Gly Lys Pro Asn
35           40           45
His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn Leu Met
50           55           60
Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His Met Leu
65           70           75           80
Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val Leu Lys
85           90           95
Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu Ile Glu
100          105          110
Arg

```

(2) INFORMATION FOR SEQ ID NO:3677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1017

(D) OTHER INFORMATION: / Ceres Seq. ID 1577771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3677:

ccgcgtaccc	aaatctctcc	gtccacggcg	acgccagacg	gcattccgtca	gccagcaaca	60
ttccaccac	acccctcccg	tcgccgacga	agaagcacag	cggagaggcg	gccgaagccg	120
acgcctcacc	aagtccaccag	tagcttctcc	gcgcctcgtc	gsccttcccg	cacttggatg	180
ctccctcgcg	cggcgccctag	agcggcgggc	gtctagcggg	cgcggcgagg	tgaacccacc	240
gatggcgac	gctctctctc	cacgcccgtt	cctcgcgcgc	ttgtcagtcg	tatccggagc	300
ctcttcatca	gcctcttctg	ccccgcgtg	tctttgggtg	ctctcgtcgc	ccggctcccc	360
gcgcggggcg	cgctggcgcg	ccggnctacc	cgcaaccocg	gcmtcgccgn	ttcaactcgc	420
acaagctctg	ccggacagct	ttggagaacc	ctgatataat	gtttctaaaa	gtgaattttg	480
atgaaaacaa	acctatgtgc	aaacgactga	atgtcaaaagt	ccttcccttc	ttccattttt	540
atcgtggagc	tgaacgggcta	cttgaggcct	tctcctgttc	cttagcttaag	tttcagaagc	600
tgaaggatgc	cattgcaatg	cacaacactg	ctcgtttgcg	cattgtgtcca	cctgtgtggag	660
ttggcgatgt	tgacttgcgt	gataacgcga	gcctccaaga	gaacacctga	gaagctagcc	720
cacggtagat	tcatagaga	gagctccacc	tcattccact	ctacgtcctg	ctcattgttt	780
tcttctacta	agattctcaat	gtaatcagtt	gtggagaaca	taagtacgct	cggttcatga	840
atcagaatga	tggattattg	taacgcattc	ttgaaaggga	aaaacatgta	ttatagcgtg	900
ataactgtac	cttttgtgtt	tgttgtacag	aacctataga	ttgtacttca	ttttaggtga	960
agacgccttt	gaacattttaa	gtccctctgt	gggcccgttt	atagagtcag	tcagttcc	

(2) INFORMATION FOR SEQ ID NO:3678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3678:

Pro	Leu	Pro	Lys	Ser	Leu	Arg	Pro	Arg	Arg	Arg	Gln	Thr	Ala	Ser	Val	1	5	10	15
Ser	Gln	Gln	His	Leu	His	His	Thr	Leu	Pro	Val	Pro	Asp	Glu	Glu	Ala	20	25	30	
Gln	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Arg	Leu	Thr	Lys	Ser	Pro	Val	Ala	35	40	45	
Ser	Pro	Arg	Ser	Cys	Xaa	Leu	Pro	Ala	Leu	Gly	Cys	Ser	Leu	Arg	Arg	50	55	60	
Arg	Leu	Glu	Arg	Arg	Pro	Ser	Ser	Gly	Arg	Pro	Glu	Val	Asn	Pro	Pro	65	70	75	80
Met	Ala	Asp	Ala	Leu	Leu	Pro	Arg	Arg	Phe	Leu	Ala	Pro	Leu	Ser	Val	85	90	95	
Val	Ser	Gly	Ala	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Pro	Pro	Cys	Leu	Trp	100	105	110	
Val	Leu	Ser	Ser	Pro	Gly	Ser	Pro	Arg	Xaa	Pro	Arg	Leu	Ala	Ala	Xaa	115	120	125	
Ser	Pro	Ala	Thr	Pro	Xaa	Ser	Pro	Xaa	His	Ser	Ala	Gln	Ala	Leu	Pro	130	135	140	
Asp	Ser	Phe	Gly	Glu	Pro											145	150		

(2) INFORMATION FOR SEQ ID NO:3679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3679:

Met	Cys	Lys	Arg	Leu	Asn	Val	Lys	Val	Leu	Pro	Phe	Phe	His	Phe	Tyr
1				5					10					15	
Arg	Gly	Ala	Asp	Gly	Leu	Leu	Glu	Ala	Phe	Ser	Cys	Ser	Leu	Ala	Lys
				20				25					30		
Phe	Gln	Lys	Leu	Lys	Asp	Ala	Ile	Ala	Met	His	Asn	Thr	Ala	Arg	Cys
				35			40					45			
Ser	Ile	Gly	Pro	Pro	Val	Gly	Val	Gly	Asp	Val	Asp	Leu	Leu	Asp	Asn
				50			55				60				
Ala	Ser	Pro	Gln	Glu	Lys	Pro	Ala	Glu	Ala	Ser	Pro	Arg			
				70						75					

(2) INFORMATION FOR SEQ ID NO:3680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..792

(D) OTHER INFORMATION: / Ceres Seq. ID 1577774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3680:

aagatttgcc	ttgcttgcc	gtgccctg	ggagccaagc	caaggacg	tagcgctcgc	60
cacgcgcgat	gtccgggctt	ctcccgccg	cgcgaccgct	gctaccgtct	cctcgcgctc	120
cttcctccgt	tggtcgggcg	aaggcagcgt	cggcatgctg	ctccagccta	aagcagtcgc	180
gccacggcgc	aagtgctgc	gccctttcca	cgtcgccgc	cggtcaggcc	gcgcgcgtct	240
tggtcgccgc	gctcgtctt	gtagcggcac	ccctggcct	gcgtgctgct	atctcaccag	300
catttgcaca	gccagtttca	gaaggcgccag	Cgctgttccg	gaaggctgtg	attggttgcc	360
atgacatggg	agggaaacatt	ctacagccag	gagccaactct	tttctgaag	gacctcgaga	420
gaaacggagt	tgccacggag	gaggaaactg	ataacatcac	atactatggg	aaaggaagaa	480
tgcccggttt	tggagagaaa	tgcaacccaa	gaggacagtg	cacCttcgcc	ccccggctat	540
cggaagacga	catcaagatc	ctagctttgt	ttgtcaagtc	gcaagcccg	aacgggtggc	600
cgaagattga	gggggatgga	gattgatcaa	actgaaaaaa	cgatgagaag	acgggtgctt	660
ttagtcatag	gaaaatggtg	acgggaagat	agtggtttga	tagtttagga	atctgtgctt	720
ctgaactgtg	taacctttta	gtctctgttt	ctgaactgaa	ctgtgaacct	tctgttcgct	780
gtttcagttt	tc					

(2) INFORMATION FOR SEQ ID NO:3681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3681:

Arg	Phe	Ala	Leu	Ala	Cys	Arg	Ala	Leu	Arg	Glu	Pro	Ser	Gln	Gly	Arg
1				5				10					15		
Leu	Ala	Leu	Ala	Thr	Arg	Asp	Val	Arg	Ala	Ser	Ser	Gly	Arg	Ala	Thr
				20				25					30		
Ala	Ala	Thr	Val	Ser	Leu	Arg	Leu	Phe	Leu	Arg	Cys	Ser	Gly	Glu	Gly
				35			40				45				
Ser	Val	Gly	Met	Leu	Leu	Gln	Pro	Lys	Ala	Val	Ala	Pro	Arg	Pro	Lys

50	55	60
Cys Cys Arg Pro Phe His Arg Arg Arg Ala Ser Gly Arg Ala Ala Leu		
65	70	75
Gly Cys Gly Ala Arg Pro Cys Ser Gly Thr Pro Trp Pro Ala Cys Cys		80
	85	90
Tyr Leu Thr Ser Ile Cys Thr Ala Ser Phe Arg Arg Arg Ser Ala Val	105	110
	100	
Pro Glu Gly Leu Tyr Trp Leu Pro		
	115	120

(2) INFORMATION FOR SEQ ID NO:3682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1577776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3682:

Met Ser Gly Leu Pro Pro Ala Ala Arg Pro Leu Leu Pro Ser Pro Cys	
1	5
Ala Ser Ser Ser Val Val Arg Ala Lys Ala Ala Ser Ala Cys Cys Ser	10
	15
	20
Ser Leu Lys Gln Ser Arg Pro Gly Arg Ser Ala Ala Ala Pro Ser Thr	25
	30
Val Ala Ala Arg Gln Ala Ala Pro Leu Leu Ala Ala Ala Leu Val Leu	35
	40
	45
Val Ala Ala Pro Pro Gly Leu Pro Ala Ala Ile Ser Pro Ala Phe Ala	50
	55
	60
65	70
Gln Pro Val Ser Glu Gly Ala Ala Leu Phe Arg Lys Ala Cys Ile Gly	75
	80
	85
Cys His Asp Met Gly Gly Asn Ile Leu Gln Pro Gly Ala Thr Leu Phe	90
	95
	100
Leu Lys Asp Leu Glu Arg Asn Gly Val Ala Thr Glu Glu Leu Tyr	105
	110
	115
Asn Ile Thr Tyr Tyr Gly Lys Gly Arg Met Pro Gly Phe Gly Glu Lys	120
	125
	130
Cys Thr Pro Arg Gly Gln Cys Thr Phe Gly Pro Arg Leu Ser Glu Asp	135
	140
	145
Asp Ile Lys Ile Leu Ala Leu Phe Val Lys Ser Gln Ala Gln Asn Gly	150
	155
	160
	165
Trp Pro Lys Ile Glu Gly Asp Gly Asp	170
	175
	180
	185

(2) INFORMATION FOR SEQ ID NO:3683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 923 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..923

(D) OTHER INFORMATION: / Ceres Seq. ID 1577787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3683:

atacgccttt	tctgcwgcgc	ctgcattctt	cactcgcgtc	aagaaacgaa	accagctgc	60
accagcaact	tctgccagca	gacccaacga	cogaagcttt	tttttccctt	tcttttcac	120
gccgccgctc	gggggttcaag	gttcagcgcg	tcccgaatg	acgggcacgt	acgargctc	180
cgaccgtctc	ctctctccca	actcgcgcgc	ccaccggacc	gacaaagtc	ggcggaagcg	240


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gtcgcggcgc cagaagagga aagagatcaa ggaggcgttc gacctcttcg acatcgacgg 300
ctccgcgacc atcgatgcaa gggagctgaa cgtcgcgatg agagcccttg gattcgagat 360
gacacgggag caaatcgggc agatgatcgc ggaggtggac aaggacggca gcggcaccat 420
cgactctgac gagtctgtgc acatgatgac ggacaagatg ggcgagcggg acgcccggga 480
cgagctgcac aaggCgttcc gcacatcaga ccaggacgcc aacggaaaaga tctcggacat 540
ggacatccag cggctggcca tcgagaccgg cgagcacttc acgctcgacg aggtccggga 600
gatgatagag gcgcgcgacg aggacggcga cggcgagatc gacctggagg agttcatgaa 660
gatgatgaag cggacagact ttggctctgg gttctagtag tcacaggcaa gccaatccca 720
acatacatcc ccatcggtga aaaatacata tcacctacgc tacatatgac tggagtattg 780
ggatttattt gagaaataat ggcgtacaca caccatacat catagtgtac taactactgt 840
aatatatgtg tagtgctgtc catgtacatc ctagctagct acggcttgtg tatttacctt 900
cacgtaataa aacacataatt act

```

(2) INFORMATION FOR SEQ ID NO:3684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..263
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3684:

```

Ile Arg Leu Phe Cys Xaa Arg Cys Ile Phe His Ser Arg Gln Glu Thr
1      5      10      15
Lys Pro Ser Cys Thr Ser Asn Phe Cys Gln Gln Thr Gln Arg Pro Lys
20      25      30
Leu Phe Phe Pro Phe Leu Phe Ile Ala Ala Ala Arg Gly Ser Arg Phe
35      40      45
Ser Ala Ser Pro Asn Asp Gly His Val Arg Xaa Leu Arg Pro Ser Ser
50      55      60
Ser Ser Gln Leu Arg Arg Pro Pro Asp Arg Gln Ser Pro Ala Glu Ala
65      70      75      80
Ala Asp Gly Ala Glu Glu Glu Arg Asp Gln Gly Gly Val Arg Pro Leu
85      90      95
Arg His Arg Arg Leu Arg His His Arg Cys Lys Gly Ala Glu Arg Arg
100      105      110
Asp Glu Ser Pro Trp Ile Arg Asp Asp Thr Gly Ala Asn Arg Ala Asp
115      120      125
Asp Arg Gly Gly Gly Gln Gly Arg Gln Arg His His Arg Leu Arg Arg
130      135      140
Val Arg Ala His Asp Asp Gly Gln Asp Gly Arg Ala Gly Arg Pro Gly
145      150      155      160
Arg Ala Ala Gln Gly Val Pro His His Arg Pro Gly Arg Gln Arg Lys
165      170      175
Asp Leu Gly His Gly His Pro Ala Ala Gly His Arg Asp Arg Arg Ala
180      185      190
Leu His Ala Arg Arg Gly Pro Gly Asp Asp Arg Gly Arg Arg Arg Gly
195      200      205
Arg Arg Arg Arg Asp Arg Pro Gly Gly Val His Glu Asp Asp Glu Ala
210      215      220
Asp Arg Leu Trp Leu Trp Val Leu Val Val Thr Gly Lys Pro Ile Pro
225      230      235      240
Thr Tyr Ile Pro Ile Gly Glu Lys Tyr Ile Ser Pro Thr Leu His Met
245      250      255
Thr Gly Val Leu Gly Phe Ile
260

```

(2) INFORMATION FOR SEQ ID NO:3685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..231
(D) OTHER INFORMATION: / Ceres Seq. ID 1577789
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3685:

Tyr Ala Phe Ser Xaa Ala Ala Ala Ser Ser Thr Arg Val Lys Lys Arg
1 5 10 15
Asn Pro Ala Ala Pro Ala Thr Ser Ala Ser Arg Pro Asn Asp Arg Ser
20 25 30
Phe Phe Phe Phe Ser Ser Pro Pro Leu Gly Val Gln Gln Ser
35 40 45
Ala Arg Pro Arg Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro
50 55 60
Pro Pro Asn Ser Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg
65 70 75 80
Leu Thr Ala Gln Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe
85 90 95
Asp Ile Asp Gly Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala
100 105 110
Met Arg Ala Leu Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met
115 120 125
Ile Ala Glu Val Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu
130 135 140
Phe Val His Met Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp
145 150 155 160
Glu Leu His Lys Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys
165 170 175
Ile Ser Asp Met Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His
180 185 190
Phe Thr Leu Asp Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp
195 200 205
Gly Asp Gly Glu Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg
210 215 220
Thr Asp Phe Gly Ser Gly Phe
225 230

(2) INFORMATION FOR SEQ ID NO:3686:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1577790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3686:

Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro Pro Asn Ser
1 5 10 15
Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg Leu Thr Ala Gln
20 25 30
Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe Asp Ile Asp Gly
35 40 45
Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala Met Arg Ala Leu
50 55 60
Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met Ile Ala Glu Val
65 70 75 80

Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu Phe Val His Met
85 90 95
Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp Glu Leu His Lys
100 105 110
Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys Ile Ser Asp Met
115 120 125
Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His Phe Thr Leu Asp
130 135 140
Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp Gly Asp Gly Glu
145 150 155 160
Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg Thr Asp Phe Gly
165 170 175
Ser Gly Phe

(2) INFORMATION FOR SEQ ID NO:3687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..729

(D) OTHER INFORMATION: / Ceres Seq. ID 1577807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3687:

accaggcagc	ccagcctcac	tcgccagacc	acctcacacg	cacgaagcat	cagcagtgga	60
ctggactagc	tctaggtggg	caacatgaag	cttcagacca	ccgtcacccg	tgtctggcctc	120
ctcctctctc	tcctctctct	ggcgtgcctc	tcctcccgsg	tctccatggc	tggatcaggg	180
ttctgcgagm	gctgcaagga	cgagttcgct	gcgtggggaga	agtgcgtgga	ggagacggat	240
gccgcggatg	ccagcattga	cgtcgtggag	cggtgccaa	acgtcacggc	Cgcgctcgcg	300
aagGtgGcat	ggagcgcGca	cgccgcctac	tacagcgcta	tcctccgggc	cgagcgcgcc	360
atggctgcgg	acctcgnagc	tttcaggccc	aagaagccgc	ctccgactcc	gcggcgctcgg	420
aggaagacca	gaaggaggcg	gcagcggcgg	ccgagggcag	gccgcgtccg	tcagacgaag	480
gccagaataa	gcagggtggc	gagggcggcag	ttgcggaggga	gagcagagat	cctgcacgct	540
gattggggcga	aaaaaggcag	cggcgtcttc	aattttttgt	gagggatttg	aggatatgaa	600
ttccgtttgt	accttaggag	agcatcaatt	aacattttgt	gagggggata	gattttctgtc	660
ctttctctct	tacatgaaac	atgtgattct	attgattgaa	aacccaaatt	gtccactttt	720
gccagatgc						

(2) INFORMATION FOR SEQ ID NO:3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1577808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3688:

Gln	Ala	Arg	Gln	Pro	His	Ser	Pro	Asp	His	Leu	Thr	Arg	Thr	Lys	His
1			5				10							15	
Gln	Gln	Trp	Thr	Gly	Leu	Ala	Leu	Gly	Gln	His	Glu	Ala	Ser	Asp	
			20				25					30			
His	Arg	His	Arg	Cys	Trp	Pro	Pro	Leu	Pro	Pro	Pro	Gly	Ala		
			35			40					45				
Ala	Phe	Pro	Pro	Xaa	Leu	His	Gly	Trp	Ile	Arg	Val	Leu	Arg	Xaa	Leu
			50		55						60				
Gln	Gly	Arg	Val	Arg	Arg	Val	Gly	Glu	Val	Arg	Gly	Gly	Asp	Gly	Cys
65			70					75						80	

Arg Gly Cys Gln His
85

(2) INFORMATION FOR SEQ ID NO:3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1577809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3689:

```
Met Lys Leu Gln Thr Thr Val Thr Val Ala Gly Leu Leu Leu Phe Leu
1      5      10      15
Leu Leu Leu Ala Leu Pro Ser Leu Xaa Val Ser Met Ala Gly Ser Gly
      20      25      30
Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala Trp Glu Lys Cys Val
      35      40      45
Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp Val Val Glu Arg Cys
      50      55      60
Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala Trp Thr Arg His Ala
65      70      75      80
Xaa Tyr Tyr Glu Pro Ile Leu Arg Ala Glu Arg Ala Met Ala Ala Asp
      85      90      95
Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Thr Pro Arg Arg Arg
      100      105      110
Arg Lys Ala Arg Arg Arg Arg Gln Arg Arg Pro Arg Gln Arg Arg Val
      115      120      125
Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu Arg Arg Gln Leu Arg
      130      135      140
Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala Lys Lys Gly Ser Gly
145      150      155      160
Val Phe Asn Phe Leu
      165
```

(2) INFORMATION FOR SEQ ID NO:3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1577810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3690:

```
Met Ala Gly Ser Gly Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala
1      5      10      15
Trp Glu Lys Cys Val Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp
      20      25      30
Val Val Glu Arg Cys Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala
      35      40      45
Trp Thr Arg His Ala Xaa Tyr Tyr Glu Pro Ile Leu Arg Ala Glu Arg
      50      55      60
Ala Met Ala Ala Asp Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Pro
65      70      75      80
Thr Pro Arg Arg Arg Arg Lys Ala Arg Arg Arg Gln Arg Arg Pro
      85      90      95
Arg Gln Arg Arg Val Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu
```

100 105 110
Arg Arg Gln Leu Arg Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala
115 120 125
Lys Lys Gly Ser Gly Val Phe Asn Phe Leu
130 135

(2) INFORMATION FOR SEQ ID NO:3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..440

(D) OTHER INFORMATION: / Ceres Seq. ID 1577813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3691:

aactcgagcc	aaacccctc	aactcaactg	ctgaacgcag	agttcgatct	agcacgcgc	60
gCGgcggNcc	gtgccccaca	atggcgctccc	ttttcaagga	cccgagcaag	ctctcagcgt	120
acagggaccg	ccgattcaag	ggcacacagg	aggagtatga	ggcaacgcgt	catgctgcga	180
caacgctgtta	cattgggaat	atgtccttct	acaccacgga	ggagcaggcc	ttgcttgacg	240
cgaatgctt	caagtgcgtg	tgcttgcctg	gagacagaac	tgtttagccc	ttgaatttgc	300
ctatgggaaga	gtttgccctt	ttactagtgt	cgatgttgat	ctggtatacc	ttgctatgaa	360
ctggttaaag	tttgtctgg	tttgggattt	ttttgtgcat	cttgtgatac	ctcaagtctt	420
catcatttaa	atgtttagcc					

(2) INFORMATION FOR SEQ ID NO:3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1577814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3692:

Asn	Ser	Ser	Gln	Thr	Pro	Ser	Thr	Gln	Leu	Asn	Ala	Glu	Phe	Asp
1			5					10				15		
Leu	Ala	Arg	Ala	Ala	Ala	Xaa	Arg	Cys	Pro	Gln	Trp	Arg	Pro	Phe
			20				25				30			
Arg	Thr	Arg	Ala	Ser	Ser	Gln	Arg	Thr	Gly	Thr	Ala	Asp	Ser	Arg
			35				40				45			
His	Arg	Arg	Ser	Met	Arg	Gln	Arg	Cys	Met	Arg	Arg	Gln	Arg	Cys
			50				55				60			
Leu	Gly	Ile	Cys	Pro	Ser	Thr	Pro	Arg	Arg	Ser	Arg	Pro	Cys	Leu
			65				70				75			80
Arg	Asn	Ala	Ser	Ser	Glu	Cys	Ala	Cys	Leu	Glu	Thr	Glu	Leu	Phe
							85				90			95

Pro

(2) INFORMATION FOR SEQ ID NO:3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3693:

(2) INFORMATION FOR SEQ ID NO:3694:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1577816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3694:

(2) INFORMATION FOR SEQ ID NO:3695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1577817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3695:

(X1) SEQUENCE DESCRIPTION: SL2						
agacactgac	accggttcgaa	gcacaaaagag	gcacacacgag	cacgaacaca	aggcgagagc	60
agccgaagac	cacacacacgc	ccgcagcgaa	ccaaccaacc	agctggtagt	aggttcgcgc	120
cgtgacgact	gatgcctcgc	cgccgcctct	ttcttcgcgc	ggtgctctct	ggcgctctgc	180
ctccgcgcgct	ctccgggttc	cacctgggag	gggacgagag	cggtctcgtg	aggggtgtgc	240
cctgcGcgct	ccgcgacgca	gcggaggcgc	aggcagccgc	gtccttcgcg	gtgcgccact	300
acacacaagaa	ccaggggcgc	gctttggagt	ttactaaggt	gctcaaatcc	aagcggcagg	360
tgtgtgacgg	gacctctgat	gacgtcgatc	tggaggcagc	tgatgctgga	tgatgctgga	420
tgtacagagc	aaaggtttgg	gtgaaagatt	gggaagatt	acaagtctgc	gttgagtctc	480
gccttttgct	agactctgaa	tctgaacgcg	agcctctctg	tgcctttgat	gttagctctg	540
ggcaagcaat	tgccaaactc	ttctcttgag	cagatatgtg	acaaagagat	gctgcctcgc	600
acaccattga	gaatgatggg	cttttcgcgc	atttcacatc	atcatcttag	gattccagcg	660
aagggatgaa	ccgtgtaaag	tttaaaatga	agatttaggt	atttagagta	gttcaagctg	720
aaatgcttga	cctgtgttat	tggaaatagt	atggtttcgt	tcaaacctgg	gagcatagaa	780
ctgtatattt	cggtatttca	cactgttcat	tccatgtctc	tgatataagg	aggtttctct	840
ggc						

(2) INFORMATION FOR SEQ ID NO:3696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1577818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3696:

```
Thr Leu Thr Pro Phe Glu Ala Lys Arg Ala Asn Thr Ser Thr Asn Thr
1      5      10      15
Ser Ala Glu Gln Pro Ser Ala Thr His Thr Pro Thr Arg Thr Asn Gln
20      25      30
Pro Ala Gly Ser Arg Phe Ala Ala Leu Thr Met Met Pro Arg Arg Ala
35      40      45
Leu Leu Phe Ala Ala Val Leu Leu Ala Ala Ser Ala Ala Ala Val Ser
50      55      60
Gly Phe His Leu Gly Gly Asp Glu Ser Gly Leu Val Arg Gly Val Leu
65      70      75      80
Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu Asp Ala Ala Arg Phe Ala
85      90      95
Val Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu Phe Thr Arg
100      105      110
Val Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu His Asp Leu
115      120      125
Ile Leu Glu Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala Lys
130      135      140
Val Trp Val Lys Pro Trp Glu Asp Phe Lys Ser Val Val Glu Phe Arg
145      150      155      160
Leu Val Gly Asp Ser Glu Ser Glu Pro Glu Pro Ser Val Ala Ser Asp
165      170      175
Val Ser Ser Gly Gln Ala Ile Ala Lys Leu Ser Leu Glu Ala Asp Ile
180      185      190
Val Gln Glu Glu Ala Arg Leu His Thr Ile Glu Asn Asp Gly Leu Ser
195      200      205
Gly Asp Phe Thr Ser Ser Ser
210      215
```

(2) INFORMATION FOR SEQ ID NO:3697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1577819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3697:

```
Met Met Pro Arg Arg Ala Leu Leu Phe Ala Ala Val Leu Leu Ala Ala
1      5      10      15
Ser Ala Ala Ala Val Ser Gly Phe His Leu Gly Gly Asp Glu Ser Gly
20      25      30
Leu Val Arg Gly Val Leu Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu
35      40      45
Asp Ala Ala Arg Phe Ala Val Ala His Tyr Asn Lys Asn Gln Gly Ala
50      55      60
Ala Leu Glu Phe Thr Arg Val Leu Lys Ser Lys Arg Gln Val Val Thr
```

aaggagagag agagaggcag agggagagat tggaggggagg cccctgccca aggcaagaga
aacGcgcgcg cgcggagaga gggtaggggt gagttctcag aagcccgtag ggacttggct

60
120

gctcttgaga aggactatga ggaagtcggt gcagaggggt cggatgacga gggtagcagag 180
ggagacgact attgagtacg tggctaataa gtatgtctct ggtgggtaat ggttgggta 240
ttttgagtat atactctatg gttccactcc attgatact gctgctgtgt gtgtttccat 300
tttgactat gtatgaaatt gttcgtgacc cctattggc catgattgtt catatcatcc 360
ttctttggtt tgcaacgcta ttcgtccaat ttcggtgtat atgtcataat gctattatgt 420
tg

(2) INFORMATION FOR SEQ ID NO:3700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3700:

Lys Glu Arg Glu Arg Gly Arg Gly Arg Asp Trp Arg Glu Ala Pro Ala
1 5 10 15
Gln Gly Lys Arg Asn Arg Gly Ala Arg Arg Glu Gly Glu Gly Glu Phe
20 25 30
Ser Glu Ala Arg Glu Asp Leu Ala Ala Leu Glu Lys Asp Tyr Glu Glu
35 40 45
Val Gly Ala Glu Gly Ala Asp Asp Glu Gly Asp Glu Gly Asp Asp Tyr
50 55 60

(2) INFORMATION FOR SEQ ID NO:3701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3701:

Arg Arg Glu Arg Glu Glu Ala Glu Gly Glu Ile Gly Gly Arg Pro Leu Pro
1 5 10 15
Lys Ala Arg Glu Thr Ala Ala Arg Gly Glu Arg Val Arg Val Ser Ser
20 25 30
Gln Lys Pro Val Arg Thr Trp Leu Leu Arg Arg Thr Met Arg Lys
35 40 45
Ser Val Gln Arg Val Pro Met Thr Arg Val Thr Arg Glu Thr Thr Ile
50 55 60

Glu
65

(2) INFORMATION FOR SEQ ID NO:3702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..822
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3702:

attccacggc	ctgtcgaccc	acaaaccacg	caaccgatat	attccccagc	acccccagtc	60
cagcccgcca	accgagacac	cgcgtgcgaa	ccaagcagac	cacagcaaga	agcgtagtcg	120
tcgcccgaag	gaaaggccgc	gasaagatgt	cgtggcaggc	gtacgctgat	gagcacctra	180
tgtgcgarat	ggaaggacaa	catctcagcg	ccgccgscat	cgtcggtcac	gaggncagcg	240
cttggggcgca	gtccgagagc	ttccccgart	taaagcctga	ggaggttgct	ggtatcataa	300
aggactttga	tgaacctggt	actcttgcac	caactggctc	tttctgttga	ggtacaaaagt	360
acatggtgat	ccaagggtgaa	cctggagttg	tcattccgag	aaagaagggc	actgggggcca	420
ttactataca	gaaaaccggc	atgtccttga	ttattggtGt	ctacgcagag	ccaatgactc	480
cagggcaatg	caacatggtg	gtggagaggg	tcggcgatta	cctgatcgag	caggggtctc	540
aaaagtctgt	catgyyctgt	tttggctcatt	tgggccaccaa	agtttgcgcc	ycatttggtt	600
ctgtaatccg	tgaagctcgt	catgtactttg	gcgtatttga	tgcagtgaaat	aatttagctt	660
gggtttgttt	gttgggggca	gtgttggggga	cggatttggga	ttggggttta	tgcttggcat	720
cgcgctogtat	cgaaaactcag	ctgctgttttc	gctgagtaat	gtacatttcc	ctggtaatgg	780
tacttttgga	ctctgatgct	tttaygggaa	cgagtgcatt	tt		

(2) INFORMATION FOR SEQ ID NO:3703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3703:

Ser	Thr	Ala	Cys	Arg	Pro	Thr	Asn	His	Ala	Thr	Asp	Ile	Phe	Pro	Ser	
1				5						10				15		
Thr	Pro	Ser	Pro	Ala	Val	Gln	Pro	Arg	His	Arg	Val	Arg	Thr	Lys	Gln	
			20					25					30			
Thr	Thr	Ala	Arg	Ser	Val	Val	Val	Ala	Gly	Arg	Lys	Gly	Ala	Xaa	Lys	
			35				40					45				
Met	Ser	Trp	Gln	Ala	Tyr	Val	Asp	Glu	His	Xaa	Met	Cys	Xaa	Ile	Glu	
		50				55					60					
Gly	Gln	His	Leu	Ser	Ala	Ala	Xaa	Ile	Val	Gly	His	Glu	Xaa	Ser	Ala	
		65			70				75					80		
Trp	Ala	Gln	Ser	Glu	Ser	Phe	Pro	Xaa	Leu	Lys	Pro	Glu	Glu	Val	Ala	
			85					90						95		
Gly	Ile	Ile	Lys	Asp	Phe	Asp	Glu	Pro	Gly	Thr	Leu	Ala	Pro	Thr	Gly	
			100				105						110			
Leu	Phe	Val	Gly	Gly	Thr	Lys	Tyr	Met	Val	Ile	Gln	Gly	Glu	Pro	Gly	
		115					120					125				
Val	Val	Ile	Arg	Gly	Lys	Lys	Gly	Thr	Gly	Gly	Ile	Thr	Ile	Lys	Lys	
		130				135					140					
Thr	Gly	Met	Ser	Leu	Ile	Ile	Gly	Val	Tyr	Asp	Glu	Pro	Met	Thr	Pro	
		145			150				155					160		
Gly	Gln	Cys	Asn	Met	Val	Val	Glu	Arg	Leu	Gly	Asp	Tyr	Leu	Ile	Glu	
			165					170					175			
Gln	Gly	Phe														

(2) INFORMATION FOR SEQ ID NO:3704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

{D} OTHER INFORMATION: / Ceres Seq. ID 1577868

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:3704:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Xaa Met Cys Xaa Ile Glu
1 5 10 15
Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly His Glu Xaa Ser Ala
20 25 30
Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys Pro Glu Val Ala
35 40 45
Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly
50 55 60
Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65 70 75 80
Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly Ile Thr Ile Lys Lys
85 90 95
Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp Glu Pro Met Thr Pro
100 105 110
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu
115 120 125
Gln Gly Phe
130

(2) INFORMATION FOR SEQ ID NO:3705:

{i} SEQUENCE CHARACTERISTICS:

{A} LENGTH: 120 amino acids

{B} TYPE: amino acid

{C} STRANDEDNESS:

{D} TOPOLOGY: linear

{ii} MOLECULE TYPE: peptide

{ix} FEATURE:

{A} NAME/KEY: peptide

{B} LOCATION: 1..120

{D} OTHER INFORMATION: / Ceres Seq. ID 1577869

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:3705:

Met Cys Xaa Ile Glu Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly
1 5 10 15
His Glu Xaa Ser Ala Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys
20 25 30
Pro Glu Glu Val Ala Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr
35 40 45
Leu Ala Pro Thr Gly Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile
50 55 60
Gln Gly Glu Pro Gly Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly
65 70 75 80
Ile Thr Ile Lys Lys Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp
85 90 95
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly
100 105 110
Asp Tyr Leu Ile Glu Gln Gly Phe
115 120

(2) INFORMATION FOR SEQ ID NO:3706:

{i} SEQUENCE CHARACTERISTICS:

{A} LENGTH: 371 base pairs

{B} TYPE: nucleic acid

{C} STRANDEDNESS: single

{D} TOPOLOGY: linear

{ii} MOLECULE TYPE: DNA (genomic)

{ix} FEATURE:

{A} NAME/KEY: -

{B} LOCATION: 1..371

{D} OTHER INFORMATION: / Ceres Seq. ID 1577881

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:3706:

atataaaaagg atcgccctcc gcgcgcgcgc gctccttcgc aaacctctct accccattcc

gccgccgccgcc gccgccgccgcc gccccccgcga ccccgaggag gaggcaagat gaagacgatc 120
ctggcgctcgg agacGatgga catccccggag gGcgtcacgg tgacgggtggc ggccaagctg 180
gtgacgggtgg agggccccccct ggcttcggcc gagttatctt atctatctat agtatcgtgt 240
tacccgttcgc ttctgtcacc gtgttatgtt ccgtttctacc ttgtgattag gtgttggtac 300
ccctgtttgtt ccctttgtgt gctcccgccta tgaacgaga cgagagaaga atgagcaag 360
ttttgttcg c

(2) INFORMATION FOR SEQ ID NO:3707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1577882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3707:

Ile	Lys	Gly	Ser	Pro	Ser	Ala	Arg	Arg	Arg	Ser	Phe	Ala	Asn	Pro	Pro	
1				5					10				15			
Thr	Pro	Phe	Arg	Arg	Pro	Pro	Pro	Ala	Ala	Arg	Pro	Ala	Thr	Pro	Arg	
			20					25				30				
Arg	Arg	Gln	Asp	Glu	Asp	Asp	Pro	Gly	Val	Gly	Asp	Asp	Gly	His	Pro	
		35					40				45					
Gly	Gly	Arg	His	Gly	Asp	Gly	Gly	Gly	Gln	Ala	Gly	Asp	Gly	Gly	Gly	
		50				55					60					
Pro	Pro	Gly	Phe	Gly	Arg	Val	Ile	Leu	Ser	Ile	Tyr	Ser	Ile	Val	Leu	
		65			70				75					80		
Pro	Phe	Ala	Ser	Val	Thr	Val	Leu	Val	Ser	Val	Leu	Pro	Leu	Asp		
			85					90					95			

(2) INFORMATION FOR SEQ ID NO:3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1577883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3708:

Met	Lys	Thr	Ile	Leu	Ala	Ser	Glu	Thr	Met	Asp	Ile	Pro	Glu	Gly	Val	
1				5				10					15			
Thr	Val	Thr	Val	Ala	Ala	Lys	Leu	Val	Thr	Val	Glu	Gly	Pro	Leu	Ala	
			20					25				30				
Ser	Ala	Glu	Leu	Ser	Tyr	Leu	Ser	Ile	Val	Ser	Cys	Tyr	Arg	Ser	Leu	
		35				40					45					
Leu	Ser	Pro	Cys													
			50													

(2) INFORMATION FOR SEQ ID NO:3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..800
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3709:

ttttgatgaa	aacgtcgact	cttttttgtc	gaatgatgat	gtagacggaa	gaggcatgtt	60
tgcagcaact	gaaaaaggtt	cttcagagca	caatacagag	tccttaaaag	gtctctcttt	120
gagtgaagtt	ggtaacaacc	gtacaaagtaa	caacaaagtt	gtttgtctgc	actctctctc	180
agatgggaag	ttactogcta	gtgcccggcca	tgagaagaag	gtcttctctc	ggaatatgga	240
caatttttaag	atgggatacca	aaatagaaga	ccatacaaac	tttatcacag	acataagatt	300
cagaactaat	tcaactcagt	tggctacatc	atcttctgtc	ggaactgttc	gactttggaa	360
tgctgctgat	gaaagtggcg	ctttacaac	ttttcatggg	cataggtctc	atgtaacatc	420
agtagatttt	caccocaagt	tgacagaggt	tctttgtctc	tgcgacgaca	atggagAaaa	480
ttctctctctg	gacagtttgt	cagactacat	ctactcatgt	tttgccgggtg	aagcagggtg	540
gaacttggaa	agtcagggtt	gaacctcgaa	gtgggcagct	cctcgctgtg	gcagctggaa	600
gcactgttgaa	catttttgat	gttgaaaagc	aatccagctt	accctgcttc	gtgattcaga	660
tgctgctttc	tttcaagtga	tatgtcgatg	tagtgtgcga	gcaatgtatt	tggtttggct	720
acagctgttc	tgtcgtctgt	gcgtaaaaca	ttagctatgt	atctatccat	atctgcata	780
ttgaatgtat	ggctgttttc					

(2) INFORMATION FOR SEQ ID NO:3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3710:

Ph	Asp	Glu	Asn	Val	Asp	Ser	Phe	Leu	Ser	Asn	Asp	Val	Asp	Gly	
1			5					10					15		
Arg	Gly	Met	Phe	Ala	Ala	Leu	Glu	Lys	Gly	Ser	Ser	Glu	His	Asn	Thr
			20				25					30			
Glu	Ser	Leu	Lys	Gly	Leu	Ser	Leu	Ser	Glu	Val	Gly	Asn	Asn	Arg	Thr
		35				40					45				
Ser	Asn	Asn	Lys	Val	Val	Cys	Cys	His	Phe	Ser	Ser	Asp	Gly	Lys	Leu
	50				55					60					
Leu	Ala	Ser	Ala	Gly	His	Glu	Lys	Lys	Val	Phe	Leu	Trp	Asn	Met	Asp
65				70					75				80		
Asn	Phe	Lys	Met	Asp	Thr	Lys	Ile	Glu	Asp	His	Thr	Asn	Phe	Ile	Thr
			85					90					95		
Asp	Ile	Arg	Phe	Arg	Thr	Asn	Ser	Thr	Gln	Leu	Ala	Thr	Ser	Ser	Ser
		100				105						110			
Asp	Gly	Thr	Val	Arg	Leu	Trp	Asn	Ala	Ala	Asp	Glu	Ser	Gly	Ala	Leu
		115				120					125				
Gln	Thr	Phe	His	Gly	His	Arg	Ser	His	Val	Thr	Ser	Val	Asp	Phe	His
	130				135						140				
Pro	Arg	Leu	Thr	Glu	Val	Leu	Cys	Ser	Cys	Asp	Asp	Asn	Gly	Glu	Asn
145				150					155						160
Ser	Leu	Leu	Asp	Ser	Trp	Ser	Asp	Tyr	Ile	Tyr	Ser	Cys	Phe	Ala	Gly
			165					170					175		
Glu	Ala	Gly	Trp	Asn	Trp	Lys	Ser	Gln	Val						
		180				185									

(2) INFORMATION FOR SEQ ID NO:3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1577907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3711:

Met	Phe	Ala	Ala	Leu	Glu	Lys	Gly	Ser	Ser	Glu	His	Asn	Thr	Glu	Ser	
1				5						10				15		
Leu	Lys	Gly	Leu	Ser	Leu	Ser	Glu	Val	Gly	Asn	Asn	Arg	Thr	Ser	Asn	
			20					25					30			
Asn	Lys	Val	Val	Cys	Cys	His	Phe	Ser	Ser	Asp	Gly	Lys	Leu	Leu	Ala	
			35				40					45				
Ser	Ala	Gly	His	Glu	Lys	Lys	Val	Phe	Leu	Trp	Asn	Met	Asp	Asn	Phe	
			50				55				60					
Lys	Met	Asp	Thr	Lys	Ile	Glu	Asp	His	Thr	Asn	Phe	Ile	Thr	Asp	Ile	
65					70					75					80	
Arg	Phe	Arg	Thr	Asn	Ser	Thr	Gln	Leu	Ala	Thr	Ser	Ser	Ser	Asp	Gly	
				85						90				95		
Thr	Val	Arg	Leu	Trp	Asn	Ala	Ala	Asp	Glu	Ser	Gly	Ala	Leu	Gln	Thr	
			100					105					110			
Phe	His	Gly	His	Arg	Ser	His	Val	Thr	Ser	Val	Asp	Phe	His	Pro	Arg	
			115				120					125				
Leu	Thr	Glu	Val	Leu	Cys	Ser	Cys	Asp	Asp	Asn	Gly	Glu	Asn	Ser	Leu	
			130				135				140					
Leu	Asp	Ser	Trp	Ser	Asp	Tyr	Ile	Tyr	Ser	Cys	Phe	Ala	Gly	Glu	Ala	
145					150					155					160	
Gly	Trp	Asn	Trp	Lys	Ser	Gln	Val									
					165											

(2) INFORMATION FOR SEQ ID NO:3712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3712:

Met	Asp	Asn	Phe	Lys	Met	Asp	Thr	Lys	Ile	Glu	Asp	His	Thr	Asn	Phe	
1				5					10					15		
Ile	Thr	Asp	Ile	Arg	Phe	Arg	Thr	Asn	Ser	Thr	Gln	Leu	Ala	Thr	Ser	
			20					25					30			
Ser	Ser	Asp	Gly	Thr	Val	Arg	Leu	Trp	Asn	Ala	Ala	Asp	Glu	Ser	Gly	
			35				40					45				
Ala	Leu	Gln	Thr	Phe	His	Gly	His	Arg	Ser	His	Val	Thr	Ser	Val	Asp	
			50				55				60					
Phe	His	Pro	Arg	Leu	Thr	Glu	Val	Leu	Cys	Ser	Cys	Asp	Asp	Asn	Gly	
65					70					75					80	
Glu	Asn	Ser	Leu	Leu	Asp	Ser	Trp	Ser	Asp	Tyr	Ile	Tyr	Ser	Cys	Phe	
			85						90					95		
Ala	Gly	Glu	Ala	Gly	Trp	Asn	Trp	Lys	Ser	Gln	Val					
			100				105									

(2) INFORMATION FOR SEQ ID NO:3713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..774

(D) OTHER INFORMATION: / Ceres Seq. ID 1577940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3713:

atatatttcaa	gcgcgcgcgat	cagcgctgcc	cccaaatagt	acatctccct	ccatgatgct	60
cgcaactcct	cctagcatca	ctcacgcgca	ccttcacagc	ggcatcatcc	cgccaccggg	120
tccggggccac	cgagaggac	tgtctccac	tgacgcggcc	gccgtgaagc	gagatggctg	180
caccacggag	gtagcaggcg	atgaggggcg	gtcgtcgtcg	tcgtcgtcgc	cgccgCccgc	240
cggaagctc	gaggggtgact	aaggctgcgc	cgacggcgac	cccgcgcgcg	ttttcgttgc	300
ccaaggacta	cagccatagc	ctgttccact	ccgagttcct	ggaggtgctg	ggcctgatcg	360
acctcagagtc	gctgcgggaag	cgcccgaggc	tcaccgtagg	ggtagcgggt	aaggcgctccc	420
tgccgctccc	gggtgctcgtg	gtcctggcgg	ccctgtacct	cgcggaagctg	accagcGggt	480
ctttgtgact	ggacgcacatca	tcacctggag	ggcgacgcgc	acgacgtagg	ggactagtga	540
agaaggagc	ccctcactgc	cgtgccctgc	catgccccgg	ctctccattg	tagcggatgc	600
aggcatgcag	cagcctcaac	ttgcttgtgt	aaacaatcag	cttcaggaca	taaaactgact	660
tttagtttag	tggtgtgctt	tgtaaacctc	gcttttatct	tactcgctct	attcttaact	720
attagatata	atgtatttcaa	acacatcttt	gaataagaaa	cgattttagt	ctct	

(2) INFORMATION FOR SEQ ID NO:3714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3714:

Tyr	Ile	Gln	Ala	Arg	Ala	Ser	Ala	Leu	Pro	Pro	Asn	Ser	Thr	Ser	Pro	
1		5						10						15		
Ser	Met	Met	Leu	Ala	Thr	Pro	Pro	Ser	Ile	Thr	His	Arg	His	Leu	His	
			20					25					30			
Ser	Gly	Ile	Ile	Pro	Pro	Pro	Gly	Pro	Gly	His	Arg	Arg	Arg	Leu	Val	
		35					40					45				
Ser	Thr	Ala	Arg	Ala	Ala	Val	Lys	Arg	Asp	Gly	Ala	Thr	Thr	Glu	Val	
		50				55						60				
Ala	Gly	Asp	Glu	Gly	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Ala	
		65				70				75				80		
Gly	Lys	Leu	Glu	Gly	Asp											
						85										

(2) INFORMATION FOR SEQ ID NO:3715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3715:

Met	Met	Leu	Ala	Thr	Pro	Pro	Ser	Ile	Thr	His	Arg	His	Leu	His	Ser	
1		5						10					15			
Gly	Ile	Ile	Pro	Pro	Pro	Gly	Pro	Gly	His	Arg	Arg	Arg	Leu	Val	Ser	
			20					25					30			
Thr	Ala	Arg	Ala	Ala	Val	Lys	Arg	Asp	Gly	Ala	Thr	Thr	Glu	Val	Ala	
		35				40						45				
Gly	Asp	Glu	Gly	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Ala	Gly
		50				55						60				
Lys	Leu	Glu	Gly	Asp												

(2) INFORMATION FOR SEQ ID NO:3716:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1577943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3716:

Met	Arg	Ala	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Pro	Pro	Glu	Ser		
1			5					10				15			
Ser	Arg	Val	Thr	Lys	Ala	Ala	Ala	Thr	Ala	Thr	Pro	Ala	Phe	Ser	
			20					25				30			
Leu	Pro	Lys	Asp	Tyr	Ser	His	Thr	Leu	Phe	His	Ser	Glu	Phe	Leu	Glu
			35				40					45			
Val	Leu	Gly	Leu	Ile	Asp	Leu	Glu	Ser	Leu	Arg	Lys	Arg	Pro	Arg	Leu
			50				55				60				
Thr	Val	Gly	Val	Thr	Val	Lys	Ala	Ser	Leu	Pro	Leu	Pro	Val	Leu	Val
			65			70				75					80
Val	Leu	Ala	Ala	Leu	Tyr	Leu	Ala	Asp	Val	Thr	Ser	Gly	Ser	Cys	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:3717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1577969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3717:

ctcgctataa	aacatgcgcc	cwccctgcact	accactacta	caaccagcgg	tagtgccgg	60
catcatccgt	ctcgtctcgt	ctcgtctcgc	ctctctctc	cttttcccc	ctccctgcac	120
agcgccgctc	accgtcaccc	taccacagca	gcgatcgatg	gctgagggtac	acaacgagcg	180
gccgctgatg	gtggcgacg	tccgggacgc	gccggtgggc	cgcgagaacg	acctcgaggc	240
catcgagctc	Gcgcgcttcg	Cggtcgccga	gcacaacagc	aagaccaacg	cgatgctgga	300
attcgagagg	ctggtgaagg	tgaggcaacca	ggtcgtggcc	gggaccctgc	accacttcac	360
cgtcgaggtg	aaggaggcgc	gcggcgccga	aaagaagctg	tacgaggcca	agggtggtgg	420
agaaggcgctg	ggagaacttc	aagcagctgc	agagcttcga	gctcgtcgga	gaNcgccgcg	480
ctgcgctgag	gcgcacagcg	ttttcgtctg	aggctggagc	acaacaatga	aagaatttaa	540
ctgtcatccc	actggaaaaa	tatgatataa	tgaataaac	agcgtcttac	ccacatgtat	600
tgtaacctaa	tgagatattt	gaccatgta	atagaatgag	atgtgctaag	gaatctgaaa	660
gcctctctgc	tttt					

(2) INFORMATION FOR SEQ ID NO:3718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1577970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3718:

Met	Pro	Xaa	Pro	Ala	Leu	Pro	Leu	Leu	Gln	Pro	Ala	Val	Val	Ala	Gly
1			5					10				15			

Ile	Ile	Arg	Leu	Val	Ser	Ser	Arg	Leu	Ala	Ser	Pro	Leu	Leu	Phe	Pro
			20					25					30		
Pro	Pro	Cys	Thr	Ala	Pro	Leu	Thr	Val	Thr	Val	Pro	Gln	Gln	Arg	Ser
		35				40						45			
Met	Ala	Glu	Val	His	Asn	Glu	Arg	Pro	Val	Met	Val	Gly	Asp	Val	Arg
	50				55					60					
Asp	Ala	Pro	Val	Gly	Arg	Glu	Asn	Asp	Leu	Glu	Ala	Ile	Glu	Leu	Ala
65				70					75					80	
Arg	Phe	Ala	Val	Ala	Glu	His	Asn	Ser	Lys	Thr	Asn	Ala	Met	Leu	Glu
			85						90				95		
Phe	Glu	Arg	Leu	Val	Lys	Val	Arg	His	Gln	Val	Val	Ala	Gly	Thr	Leu
			100					105					110		
His	His	Phe	Thr	Val	Glu	Val	Lys	Glu	Ala	Gly	Gly	Gly	Glu	Lys	Lys
	115						120					125			
Leu	Tyr	Glu	Ala	Lys	Val	Val	Gly	Glu	Gly	Val	Gly	Glu	Leu	Gln	Ala
	130					135					140				
Ala	Ala	Glu	Leu	Arg	Ala	Arg	Arg	Arg	Xaa	Pro	Arg	Ser	Pro	Glu	Ala
145					150				155					160	
His	Arg	Leu	Phe	Ala	Gly	Gly	Trp	Ser	Thr	Thr	Met	Lys	Glu	Phe	Asn
				165					170					175	
Cys	His	Pro	Thr	Gly	Lys	Val									
				180											

(2) INFORMATION FOR SEQ ID NO:3719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3719:

Met	Ala	Glu	Val	His	Asn	Glu	Arg	Pro	Val	Met	Val	Gly	Asp	Val	Arg
1				5					10				15		
Asp	Ala	Pro	Val	Gly	Arg	Glu	Asn	Asp	Leu	Glu	Ala	Ile	Glu	Leu	Ala
			20					25				30			
Arg	Phe	Ala	Val	Ala	Glu	His	Asn	Ser	Lys	Thr	Asn	Ala	Met	Leu	Glu
	35					40					45				
Phe	Glu	Arg	Leu	Val	Lys	Val	Arg	His	Gln	Val	Val	Ala	Gly	Thr	Leu
	50				55				60						
His	His	Phe	Thr	Val	Glu	Val	Lys	Glu	Ala	Gly	Gly	Gly	Glu	Lys	Lys
65				70					75					80	
Leu	Tyr	Glu	Ala	Lys	Val	Val	Gly	Glu	Gly	Val	Gly	Glu	Leu	Gln	Ala
			85					90				95			
Ala	Ala	Glu	Leu	Arg	Ala	Arg	Arg	Arg	Xaa	Pro	Arg	Ser	Pro	Glu	Ala
			100				105					110			
His	Arg	Leu	Phe	Ala	Gly	Gly	Trp	Ser	Thr	Thr	Met	Lys	Glu	Phe	Asn
			115				120					125			
Cys	His	Pro	Thr	Gly	Lys	Val									
				130		135									

(2) INFORMATION FOR SEQ ID NO:3720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1577972
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3720:
Met Val Gly Asp Val Arg Asp Ala Pro Val Gly Arg Glu Asn Asp Leu
1 5 10 15
Glu Ala Ile Glu Leu Ala Arg Phe Ala Val Ala Glu His Asn Ser Lys
20 25 30
Thr Asn Ala Met Leu Glu Phe Glu Arg Leu Val Lys Val Arg His Gln
35 40 45
Val Val Ala Gly Thr Leu His His Phe Thr Val Glu Val Lys Glu Ala
50 55 60
Gly Gly Gly Glu Lys Lys Leu Tyr Glu Ala Lys Val Val Gly Glu Gly
65 70 75 80
Val Gly Glu Leu Gln Ala Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa
85 90 95
Pro Arg Ser Pro Glu Ala His Arg Leu Phe Ala Gly Gly Trp Ser Thr
100 105 110
Thr Met Lys Glu Phe Asn Cys His Pro Thr Gly Lys Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:3721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..800

(D) OTHER INFORMATION: / Ceres Seq. ID 1577981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3721:

aaaaaacctc	ctgcagtcgt	tttcacctcc	tcctctctc	acggcggtt	ttctggcgac	60
ggcgccggcg	gcgacgacga	gcagccacct	ggggaagagc	aggtagcagg	aaatggcggc	120
gttctcgagg	tcaaaatggt	caccagttgg	acgtactttg	atgggaagcc	ttggaatatg	180
tttgtttggg	gctgccaaat	cttctgttgg	ggcaataaca	aggcctcttc	attgcatgat	240
tatcagtcag	cAaaatcaga	acattcatcc	agatgaggac	taacctgaag	gtggctcgata	300
actccggggc	caagcgggtg	atgtgcatcc	agtcctctag	ggggaagaaa	ggagcaaggc	360
tcggggacat	gatcatcgga	tccgtaaaag	aggccccagc	tcgtggcaag	gtcaagaaga	420
gagacgtagt	ctacggcggt	gtcgtcgtg	ccgccatgaa	gaaaggagcg	agcgatggca	480
gcgaggtcca	gttcgacgac	aacgcggtgg	tcctcgtgaa	caagaagggc	gagctgatcg	540
gcaccccgct	ctttggcccc	gtccccacg	agctgaggaa	gaagaagcac	ctcaagatcc	600
tgccctctgc	tgaacacatt	gtttgaggtg	tgctgcatag	ccaagtgttt	gtgggaaatg	660
ttttttttgt	gtgttctctg	tttgaataat	gcattgtgaa	acgatagcat	ggaccctttg	720
aactattttg	atgacattgc	tcgtccattt	ggatggccaa	tacgtgtcgt	gatcgattct	780
ggagttccat	ttttttgtt					

(2) INFORMATION FOR SEQ ID NO:3722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1577982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3722:

Met	Leu	Ser	Val	Ser	Lys	Ile	Arg	Thr	Phe	Ile	Gln	Met	Arg	Thr	Asn
1		5					10					15			
Leu	Lys	Val	Val	Asp	Asn	Ser	Gly	Ala	Lys	Arg	Val	Met	Cys	Ile	Gln
		20					25					30			

```

Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp Met Ile Ile Gly
      35              40              45
Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys Lys Gly Asp Val
      50              55              60
Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys Gly Arg Ser Asp
      65              70              75              80
Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val Leu Val Asn Lys
      85              90              95
Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro Val Pro His Glu
      100             105             110
Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu Ala Glu His Ile
      115             120             125
Val

```

(2) INFORMATION FOR SEQ ID NO:3723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3723:

```

Met Arg Thr Asn Leu Lys Val Val Asp Asn Ser Gly Ala Lys Arg Val
1      5              10              15
Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp
      20              25              30
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys
      35              40              45
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys
      50              55              60
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val
      65              70              75              80
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro
      85              90              95
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu
      100             105             110
Ala Glu His Ile Val
      115

```

(2) INFORMATION FOR SEQ ID NO:3724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3724:

```

Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp
1      5              10              15
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys
      20              25              30
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys
      35              40              45
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val

```

50 55 60
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro
65 70 75 80
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu
85 90 95
Ala Glu His Ile Val
100

(2) INFORMATION FOR SEQ ID NO:3725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..747

(D) OTHER INFORMATION: / Ceres Seq. ID 1577999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3725:

acc	aaacacacc	gtg	gcccccg	caa	attactc	aa	attgccc	ttc	ctgtctc	ggt	ccctct	60
tcc	cgcgcca	cc	agctacc	tc	gccgacgc	cag	gccgcca	cg	ccgccga	gac	atgaacc	120
agc	ccgtgca	ga	agaacacc	ct	ctacgtcg	gt	gggctggc	gg	agaggtg	gac	gagaaga	180
tcc	tgcaacg	cg	cttcgtg	cc	cttgggtg	agg	tcaagg	cg	taagacg	cc	gtcgatc	240
agt	ccacgca	ga	agcaccgc	t	Ccttgccgt	tc	gtcacctt	cc	tgagcgc	gag	gacgcgc	300
ccg	ctgccat	gg	acaacatg	g	acggcgccg	ag	ctcttcgg	cc	gctgtctt	acc	gtcaact	360
acg	cccttcc	cg	agcgcac	ta	aaggagggg	ag	caggggatg	gg	ctgcccg	cca	atctggg	420
ccg	atgcgga	ca	cttggttc	ga	gagggcagc	ag	caggaaga	gg	agatgcag	cg	gtgcagg	480
cag	agcacgc	tg	cagcgatg	ca	ggcagcag	aga	agctgcga	ca	ggggagaaa	cg	gtcccgctg	540
aa	agggaaag	cg	agaagaag	ga	gatgccca	tg	gtgcgcgc	ag	agggcccg	gct	gtgaacc	600
aa	gttcttta	aga	accgggat	at	caactcat	aac	tcattgtg	ct	acgttgtg	gcc	gttttgt	660
cag	atatgac	taa	acgaatc	tt	gcgaatgc	tg	tttgtttt	gct	gaaagaa	cc	ctatttct	720
cac	ctgacgt	gg	gattctta	tt	ggtttt							

(2) INFORMATION FOR SEQ ID NO:3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1578000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3726:

Gln	Pro	Pro	Trp	Pro	Arg	Gln	Ile	Thr	Gln	Ile	Cys	Pro	Ser	Cys	Leu
1			5					10						15	
Gly	Ser	Leu	Phe	Pro	Ala	His	Gln	Pro	Thr	Ser	Pro	Thr	Pro	Gly	Arg
			20					25						30	
His	Ala	Ala	Gly	Asp	Met	Asn	Gln	Pro	Val	Gln	Lys	Asn	Thr	Leu	Tyr
			35				40					45			
Val	Gly	Gly	Leu	Ala	Glu	Glu	Val	Asp	Glu	Lys	Ile	Leu	His	Ala	Ala
			50			55				60					
Phe	Val	Pro	Phe	Gly	Glu	Val	Lys	Asp	Val	Lys	Thr	Pro	Leu	Asp	Gln
65				70				75						80	
Ser	Thr	Gln	Lys	His	Arg	Ser	Phe	Gly	Phe	Val	Thr	Phe	Leu	Glu	Arg
			85					90					95		
Glu	Asp	Ala	Ala	Ala	Ala	Met	Asp	Asn	Met	Asp	Gly	Ala	Glu	Leu	Phe
			100				105						110		
Gly	Arg	Val	Leu	Thr	Val	Asn	Tyr	Ala	Phe	Pro	Glu	Arg	Ile	Lys	Gly
			115				120					125			
Gly	Glu	Gln	Gly	Trp	Ala	Ala	Gln	Pro	Ile	Trp	Ala	Asp	Ala	Asp	Thr

130	135	140	
Trp Phe Glu Arg Gln Gln Gln Glu Glu Glu Met Gln Arg Leu Gln Ala			
145	150	155	160
Glu His Arg Ala Ala Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys			
	165	170	175
Leu Ala Ala Glu Arg Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala			
	180	185	190
Ala Glu Ala Gln Ala Val Lys Gln Ser Ser			
	195	200	

(2) INFORMATION FOR SEQ ID NO:3727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1578001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3727:

Met Asn Gln Pro Val Gln Lys Asn Thr Leu Tyr Val Gly Gly Leu Ala	
1	5
Glu Glu Val Asp Glu Lys Ile Leu His Ala Ala Phe Val Pro Phe Gly	15
	20
Glu Val Lys Asp Val Lys Thr Pro Leu Asp Gln Ser Thr Gln Lys His	25
	30
Arg Ser Phe Gly Phe Val Thr Phe Leu Glu Arg Glu Asp Ala Ala Ala	35
	40
Ala Met Asp Asn Met Asp Gly Ala Glu Leu Phe Gly Arg Val Leu Thr	45
	50
65	70
Val Asn Tyr Ala Phe Pro Glu Arg Ile Lys Gly Gly Glu Gln Gly Trp	75
	80
	85
Ala Ala Gln Pro Ile Trp Ala Asp Ala Asp Thr Trp Phe Glu Arg Gln	90
	95
Gln Gln Glu Glu Glu Met Gln Arg Leu Gln Ala Glu His Arg Ala Ala	100
	105
Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys Leu Ala Ala Glu Arg	110
	115
	120
Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala Glu Ala Gln Ala	125
	130
	135
145	150
Val Lys Gln Ser Ser	155
	160
	165

(2) INFORMATION FOR SEQ ID NO:3728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 967 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..967

(D) OTHER INFORMATION: / Ceres Seq. ID 1578004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3728:

aaaaactaacc ccaaaccccca atccacccca tcccctctc atccactccg ggcggccatg	60
gcctgctctc tctccgcccgc catcacccgtc tcttccgccc ctaccgccgc cgccagaccc	120
ctcgctgctg ccccgcaagtc cgtctgcatc gctcgctccg cggctgccac cactgccagg	180
ccgctccgccc tcgcgcgctc aaggctccgc cgggctacca gactcgttgc ccgcccagg	240
tangtcgatg acttgccgct ggctcggaac aaggccgcag acttagaagc cgaggctgtg	300
ttcgaccagg agttcatcaa cgtgaagctc tctgattaca ttgggaagaa gtacgtcatt	360

ctgttcttct	accctcttga	tttcaccttc	gtctgcmcga	cgcagattAc	tcggtttagt	420
gacagatagc	aggaatttga	gaagttgaac	actgaggttc	ttggtgttcc	cattgacagt	480
gtgtttctcc	acctctcatg	ggtgcagaca	gacaggaagt	cgggtgggct	cggcgatctt	540
aaatacccca	ttgtttctga	tgtagccaaa	tcaatttcaa	aggcctttgg	tggtctgac	600
cctgaccagg	gtattgtctt	gagaggactg	ttcatcattg	acaaggaggg	agtgtattca	660
caactctacca	ttacaacact	tgccatttgt	cgtagtgttg	atgagaccat	gaggaccctt	720
caggcattgc	agtagctcca	ggagaaccca	gacgaggtgt	gcccgccggg	atggaaacca	780
ggggagaggt	cgatgaagcc	cgaccccaag	ggaagcaaa	agtagctcgc	ggccatctag	840
attcgtcgtc	attgagaagc	aggtgcccg	taagtgtctc	agcagtaggt	tctcgtgttc	900
agcggagctc	gcgttttgac	aagtgtattg	tgctgatgtg	catcccgatt	tgagtgtctg	960
ctctttgc						

(2) INFORMATION FOR SEQ ID NO:3729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1578005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3729:

Lys	Thr	Asn	Pro	Lys	Pro	Gln	Ser	Thr	Pro	Ser	Pro	Pro	His	Pro	Leu
1			5					10					15		
Arg	Ala	Ala	Met	Ala	Cys	Ser	Phe	Ser	Ala	Ala	Ile	Thr	Val	Ser	Ser
			20					25					30		
Ala	Pro	Thr	Pro	Ala	Ala	Arg	Pro	Leu	Ala	Ala	Ala	Pro	Gln	Ser	Val
			35				40					45			
Cys	Ile	Ala	Arg	Ser	Ala	Val	Ala	Thr	Thr	Ala	Arg	Pro	Leu	Arg	Leu
			50			55				60					
Ala	Ala	Ser	Arg	Ser	Ala	Arg	Ala	Thr	Arg	Leu	Val	Ala	Arg	Ala	Arg
			65			70			75				80		
Xaa	Val	Asp	Asp	Leu	Pro	Leu	Val	Gly	Asn	Lys	Ala	Pro	Asp	Leu	Glu
			85					90					95		
Ala	Glu	Ala	Val	Phe	Asp	Gln	Glu	Phe	Ile	Asn	Val	Lys	Leu	Ser	Asp
			100				105						110		
Tyr	Ile	Gly	Lys	Lys	Tyr	Val	Ile	Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe
			115				120						125		
Thr	Phe	Val	Cys	Xaa	Thr	Glu	Ile	Thr	Ala	Phe	Ser	Asp	Arg	Tyr	Glu
			130			135					140				
Glu	Phe	Glu	Lys	Leu	Asn	Thr	Glu	Val	Leu	Gly	Val	Ser	Ile	Asp	Ser
			145			150				155				160	
Val	Phe	Ser	His	Leu	Ala	Trp	Val	Gln	Thr	Asp	Arg	Lys	Ser	Gly	Gly
			165					170					175		
Leu	Gly	Asp	Leu	Lys	Tyr	Pro	Leu	Val	Ser	Asp	Val	Thr	Lys	Ser	Ile
			180					185					190		
Ser	Lys	Ala	Phe	Gly	Val	Leu	Ile	Pro	Asp	Gln	Gly	Ile	Ala	Leu	Arg
			195			200						205			
Gly	Leu	Phe	Ile	Ile	Asp	Lys	Glu	Gly	Val	Ile	Gln	His	Ser	Thr	Ile
			210			215				220					
Asn	Asn	Leu	Ala	Ile	Gly	Arg	Ser	Val	Asp	Glu	Thr	Met	Arg	Thr	Leu
			225			230				235				240	
Gln	Ala	Leu	Gln	Tyr	Val	Gln	Glu	Asn	Pro	Asp	Glu	Val	Cys	Pro	Ala
			245					250					255		
Gly	Trp	Lys	Pro	Gly	Glu	Arg	Ser	Met	Lys	Pro	Asp	Pro	Lys	Gly	Ser
			260				265						270		
Lys	Glu	Tyr	Phe	Ala	Ala	Ile									
			275												

(2) INFORMATION FOR SEQ ID NO:3730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..260
(D) OTHER INFORMATION: / Ceres Seq. ID 1578006
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3730:

Met Ala Cys Ser Phe Ser Ala Ala Ile Thr Val Ser Ser Ala Pro Thr
1 5 10 15
Pro Ala Ala Arg Pro Leu Ala Ala Ala Pro Gln Ser Val Cys Ile Ala
20 25 30
Arg Ser Ala Val Ala Thr Thr Ala Arg Pro Leu Arg Leu Ala Ala Ser
35 40 45
Arg Ser Ala Arg Ala Thr Arg Leu Val Ala Arg Ala Arg Xaa Val Asp
50 55 60
Asp Leu Pro Leu Val Gly Asn Lys Ala Pro Asp Leu Glu Ala Glu Ala
65 70 75 80
Val Phe Asp Gln Glu Phe Ile Asn Val Lys Leu Ser Asp Tyr Ile Gly
85 90 95
Lys Lys Tyr Val Ile Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val
100 105 110
Cys Xaa Thr Glu Ile Thr Ala Phe Ser Asp Arg Tyr Glu Glu Phe Glu
115 120 125
Lys Leu Asn Thr Glu Val Leu Gly Val Ser Ile Asp Ser Val Phe Ser
130 135 140
His Leu Ala Trp Val Gln Thr Asp Arg Lys Ser Gly Gly Leu Gly Asp
145 150 155 160
Leu Lys Tyr Pro Leu Val Ser Asp Val Thr Lys Ser Ile Ser Lys Ala
165 170 175
Phe Gly Val Leu Ile Pro Asp Gln Gly Ile Ala Leu Arg Gly Leu Phe
180 185 190
Ile Ile Asp Lys Glu Gly Val Ile Gln His Ser Thr Ile Asn Asn Leu
195 200 205
Ala Ile Gly Arg Ser Val Asp Glu Thr Met Arg Thr Leu Gln Ala Leu
210 215 220
Gln Tyr Val Gln Glu Asn Pro Asp Glu Val Cys Pro Ala Gly Trp Lys
225 230 235 240
Pro Gly Glu Arg Ser Met Lys Pro Asp Pro Lys Gly Ser Lys Glu Tyr
245 250 255
Phe Ala Ala Ile
260

(2) INFORMATION FOR SEQ ID NO:3731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..828
(D) OTHER INFORMATION: / Ceres Seq. ID 1578007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3731:

agaaacagac ctgcacggct ccactccaac tccctcccaa gccccaagcc ggcaagcccc 60
caaccacacct ccttttccac atccacacccg ccccggtttt cctcacgcct cgcgcctccc 120
accgcgtcac tcccgctccct atccacccgc atggcctccc gctcgcgt cgccgctcgc 180
gtcgccgcgc ccgcgtcgtc tccttccccg gtcggcacccg tcgccccgcm ccgcgtcgcg 240
ctccgcgcgag gctcccgccg gacgtggcac gctctccgcg ccctccctcg atcccgctggc 300

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ggcgccgctg tgtgccaggc ccaggcgccg caggacaccg ccattccaagt tctgtgatgtg 360
agcaaatcca catggcaatc acttgtgggt gagagcgagc ttcccggtCcc tctgtcagtt 420
ctgggcctca tgggtgtggac cgtgtaagat gatagacccc atcggttgga agctctcgaa 480
ggagtacgaa ggaagctga agtgttacc gataaacacc gacgagaaac ctgacatcgc 540
gacccaattc ggcattccga gcatccccc catgatgata ttcaagaatg gtgagaagaa 600
ggacgcggtg attggagccg tgccagagag caccctgttc acctgcatcg acaagtacgt 660
tggtgggagg tgaatatcca acttggggcca ctgacctgtg acttccatag gtgacggat 720
gggtatgtgt ataccgttca taccgaactg ctgttgagta gttgtatga gataataatg 780
tgatgctcac tccaataaat gcatgccaag gatgggcaag tcatctgtg

```

(2) INFORMATION FOR SEQ ID NO:3732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1578008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3732:

```

Arg Asn Arg Pro Ala Arg Leu His Ser Asn Ser Leu Pro Ser Pro Lys
1      5      10      15
Pro Ala Ser Pro Gln Pro Pro Ser Phe Ser Thr Ser Thr Pro Pro Arg
20      25      30
Val Ser Ser Arg Leu Arg Pro Pro Thr Arg Ser Leu Pro Ser Leu Ser
35      40      45
Thr Ala Met Ala Ser Arg Leu Ala Val Ala Val Ala Val Ala Ala Pro
50      55      60
Ala Ser Ser Pro Ser Pro Val Gly Thr Val Ala Pro Xaa Arg Val Ala
65      70      75      80
Leu Arg Arg Gly Leu Pro Pro Thr Trp His Ala Leu Arg Ala Leu Pro
85      90      95
Arg Ser Arg Gly Ala Ala Val Val Cys Gln Ala Gln Gly Gly Gln Asp
100      105      110
Thr Ala Ile Gln Val Pro Asp Val Ser Lys Ser Thr Trp Gln Ser Leu
115      120      125
Val Val Glu Ser Glu Leu Pro Val Pro Arg Ser Val Leu Gly Leu Met
130      135      140
Val Trp Thr Val
145

```

(2) INFORMATION FOR SEQ ID NO:3733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1578009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3733:

```

Glu Thr Asp Leu His Gly Ser Thr Pro Thr Pro Ser Gln Ala Pro Ser
1      5      10      15
Arg Gln Ala Pro Asn His Leu Pro Phe Pro His Pro His Arg Pro Gly
20      25      30
Phe Pro His Ala Ser Ala Leu Pro Pro Ala His Ser Arg Pro Tyr Pro
35      40      45
Pro Arg Trp Pro Pro Ala Ser Pro Ser Pro Ser Pro Ser Pro Arg Pro
50      55      60

```


Arg Arg Leu Leu Pro Arg Ser Ala Pro Ser Pro Arg Xaa Ala Ser Pro
65 70 75 80
Ser Ala Glu Ala Ser Arg Arg Gly Thr Leu Ser Ala Pro Ser Leu
85 90 95
Asp Pro Val Ala Arg Pro Ser Cys Ala Arg Pro Arg Ala Ala Arg Thr
100 105 110
Pro Pro Ser Lys Phe Leu Met
115

(2) INFORMATION FOR SEQ ID NO:3734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1578010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3734:

Lys Gln Thr Cys Thr Ala Pro Leu Gln Leu Pro Pro Lys Pro Gln Ala
1 5 10 15
Gly Lys Pro Pro Thr Thr Phe Leu Phe His Ile His Thr Ala Pro Gly
20 25 30
Phe Leu Thr Pro Pro Pro Ser His Pro Leu Thr Pro Val Pro Ile His
35 40 45
Arg Asp Gly Leu Pro Pro Arg Arg Arg Arg Arg Arg Ala Arg
50 55 60
Val Val Ser Phe Pro Gly Arg His Arg Arg Pro Xaa Pro Arg Arg Pro
65 70 75 80
Pro Pro Arg Pro Pro Ala Asp Val Ala Arg Ser Pro Arg Pro Pro Ser
85 90 95
Ile Pro Trp Arg Gly Arg Arg Val Pro Gly Pro Gly Arg Pro Gly His
100 105 110
Arg His Pro Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:3735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..628

(D) OTHER INFORMATION: / Ceres Seq. ID 1578015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3735:

atatatttga ttgtgaagga aaataactta agactcgtaa aggtcgtgga ggacgaggtg 60
tttcccgacg ggacgggtgct gaagaaggcg accaaggtgg tctacgccat gtactccatg 120
grgcggatgg agagcatctg gggcgacgac tgccggggagt acaggccggga gcggtggctc 180
cgggacggcc gcttcattgag cgagtccgcc tacaagttca Cgcgccttcaa cggcgggccg 240
cgccgtgtgc tcggcaagga ctctgcctac taccagatga agttcgccgc cgccctccatc 300
ctNccgCegy tacocgcgtcg acgtcgtcga gggccacccc gtcgcgcctca agatggcgct 360
caccatgtac atgaagcaag gctcaagggt cacgctgacc aagagagaca agaccaagct 420
ctgaactggt ggtgcggagc cgagcttggc agagcttggc tgagactgaa gagagatata 480
cagtatgaaa gaagcagggc tcttcatttg ttctcattac atctagtata gaacttttat 540
atatatgtat agatacatat gtatatgtgt tggcaaaaag cttgaccttc aggtgatgta 600
accggttaata ttgtagcagt atattttc

(2) INFORMATION FOR SEQ ID NO:3736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..176
(D) OTHER INFORMATION: / Ceres Seq. ID 1578016
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3736:

Ile Tyr Leu Ile Trp Lys Glu Asn Asn Leu Arg Leu Val Lys Val Val
1 5 10 15
Glu Asp Glu Val Phe Pro Asp Gly Thr Val Leu Lys Lys Gly Thr Lys
20 25 30
Val Val Tyr Ala Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly
35 40 45
Asp Asp Cys Arg Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg
50 55 60
Phe Met Ser Glu Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro
65 70 75 80
Arg Leu Cys Leu Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala
85 90 95
Ala Ala Ser Ile Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Gly Pro
100 105 110
Pro Arg Arg Ala Gln Asp Gly Ala His His Val His Glu Ala Arg Pro
115 120 125
Gln Gly His Ala Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp
130 135 140
Cys Arg Ala Glu Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile
145 150 155 160
Gln Tyr Glu Arg Ser Arg Ala Leu His Leu Phe His Leu His Leu Val
165 170 175

(2) INFORMATION FOR SEQ ID NO:3737:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..140
(D) OTHER INFORMATION: / Ceres Seq. ID 1578017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3737:

Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg
1 5 10 15
Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu
20 25 30
Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu
35 40 45
Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ser Ile
50 55 60
Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala
65 70 75 80
Gln Asp Gly Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala
85 90 95
Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu
100 105 110
Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg

115 120 125
Ser Arg Ala Leu His Leu Phe His Leu His Leu Val
130 135 140
(2) INFORMATION FOR SEQ ID NO:3738:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1578018
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3738:
Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg Glu Tyr Arg
1 5 10 15
Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu Ser Ala Tyr
20 25 30
Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu Gly Lys Asp
35 40 45
Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ala Ser Ile Xaa Pro Pro
50 55 60
Xaa Pro Arg Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala Gln Asp Gly
65 70 75 80
Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala Asp Gln Glu
85 90 95
Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu Leu Ala Asn
100 105 110
Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg Ser Arg Ala
115 120 125
Leu His Leu Phe His Leu His Leu Val
130 135

(2) INFORMATION FOR SEQ ID NO:3739:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..922
(D) OTHER INFORMATION: / Ceres Seq. ID 1578031
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3739:
ctttccctcc ccattccgtg aggcgtgagc gccacaccca cacgaagatg ccgaagccg 60
aagagaaccc taccgaggag gcagaaaatc cgtatagcgcc ctcatacagt tccagatcc 120
gtgcctcttta tcggcagcca tgatgctgcg cgcngcgggc aggcgaactcc tcggcgtagg 180
aggcgcgcat ccagcgcccg cggtcgctgc tgctgtggcg gcgagcagga gcagaggata 240
ccacgagcgg gtgggtggacc actacaacaa cccgcgcaac gtggggtcct tggacaagga 300
cgacacggag gtcggaacgg ggatgctcgg cgcgcggcgc tgcggggagc tcatgaagct 360
gcagatccgc gtccgacgag ggctcggcag gatcgctcgc gcgcgcttca agaCcttcgg 420
ctgcRgtccc gccatcgctg cctcctccgt cgtctccgaa tgggtcaagg gcaagcaagt 480
ggaggaaagt gtggccatca agaacaccca gattgcgaag cacctgtctc ttcaccagt 540
gaagctccac tgcagcatgc tcgctgagga cgcaatcaag gccgccgtga aggattacga 600
ggcaagaaga ggggaagaaga tggccaaggc agaggagcag gacaccccat gcccgtaaga 660
gcgacagcta gtaaaactga gcgagcagag agtactgtat gtagtatgta acggctaacg 720
agcgaggtae tcgtgtcgtg tgtgccaaaa gaagcatgta tgtaaatgaa agctaggttaa 780
caacgatgtt tgggtttcat agaataagcg aacttcgcgc agtgtgtttt ttatctgttc 840
tgacatgaa taaggtctgc ccattgtctt ttatctgttt agtcggagca tgtagtctta 900
gtttgatcaa gcaatgctgt tg

(2) INFORMATION FOR SEQ ID NO:3740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1578032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3740:

Met Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Gly
1 5 10 15
Asp Pro Ala Pro Ala Val Ala Ala Ala Val Ala Ala Ser Arg Ser Arg
20 25 30
Gly Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val
35 40 45
Gly Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly
50 55 60
Ala Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu
65 70 75 80
Gly Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa
85 90 95
Ser Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys
100 105 110
Gln Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His
115 120 125
Leu Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp
130 135 140
Ala Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys
145 150 155 160
Met Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1578033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3741:

Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Asp
1 5 10 15
Pro Ala Pro Ala Val Ala Ala Val Ala Ala Ser Arg Ser Arg Gly
20 25 30
Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val Gly
35 40 45
Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly Ala
50 55 60
Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu Gly
65 70 75 80
Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser
85 90 95
Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys Gln
100 105 110
Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His Leu

115 120 125
Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp Ala
130 135 140
Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met
145 150 155
Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1578034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3742:

Met Lys Leu Gln Ile Arg Val Asp Glu Gly Ser Gly Arg Ile Val Asp
1 5 10 15
Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser Ala Ile Ala Ser Ser Ser
20 25 30
Val Ala Ser Glu Trp Val Lys Gly Lys Gln Val Glu Glu Val Val Ala
35 40 45
Ile Lys Asn Thr Glu Ile Ala Lys His Leu Ser Leu Pro Pro Val Lys
50 55 60
Leu His Cys Ser Met Leu Ala Glu Asp Ala Ile Lys Ala Ala Val Lys
65 70 75 80
Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met Ala Lys Ala Glu Glu Gln
85 90 95
Asp Thr Pro Cys Pro
100

(2) INFORMATION FOR SEQ ID NO:3743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..753
(D) OTHER INFORMATION: / Ceres Seq. ID 1578035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3743:

aatgacgcc atgcgcggcgc caccgagggc gaaagctgtc cagatcgtgt gattttgcat 60
cccatccgcg agcgcgacac gsstgacctc ctcgacggcc tcacactccg tcttgaggcg 120
aacgtangtg cgaaggacca actcttttga agggaaatta tatctcaggt gcttaggagt 180
ctgcatggc cagcgagaat aaggtattta ggttcgagga agtcgccaag cacaacgtca 240
ccaaggactg ctggatcatc atcgccggca aggtgtatga tgtcactcct tttatggatg 300
agcatcctgg tggagatgag gttttgctag ctgttaactg gaaagatgct acagctgatt 360
ttgaagatat tggccacagt gattccgcaa gggacatgat ggagaagtac cacatcgggc 420
agatagatgc ttcaacaatc ccagcaaaagc gaacttatgt gcacccccag caagcgccca 480
gccactcaga caagaataat gatctcctca tcaagatcct gcagttcctt gtgCccatta 540
tgatcctggg ccttgcatctt ggtatagctc agtacagcaa atcagatgag tactgttctt 600
gaagacttgc ctttgagtc tggtttatgg taatggtttg gatgagaaca gttcagtaat 660
tgcttagtgt atttgcagtg tggatgttat ctcatgggtc atatactatg tattatggag 720
atccatgtgt tgccgaatat tgctcttttc ccc

(2) INFORMATION FOR SEQ ID NO:3744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1578036
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3744:

Met Ala Ser Glu Asn Lys Val Phe Arg Phe Glu Glu Val Ala Lys His
1 5 10 15
Asn Val Thr Lys Asp Cys Trp Ile Ile Ala Gly Lys Val Tyr Asp
20 25 30
Val Thr Pro Phe Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu
35 40 45
Ala Val Thr Gly Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His
50 55 60
Ser Asp Ser Ala Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile
65 70 75 80
Asp Ala Ser Thr Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln
85 90 95
Ala Pro Ser His Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu
100 105 110
Gln Phe Leu Val Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg
115 120 125
Gln Tyr Ser Lys Ser Glu
130

(2) INFORMATION FOR SEQ ID NO:3745:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1578037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3745:

Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu Ala Val Thr Gly
1 5 10 15
Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His Ser Asp Ser Ala
20 25 30
Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile Asp Ala Ser Thr
35 40 45
Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln Ala Pro Ser His
50 55 60
Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu Gln Phe Leu Val
65 70 75 80
Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg Gln Tyr Ser Lys
85 90 95
Ser Glu

(2) INFORMATION FOR SEQ ID NO:3746:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..803
(D) OTHER INFORMATION: / Ceres Seq. ID 1578042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3746:

aatccccaca	acaccagaat	cgcggaatca	cagacgcgtc	tatctcagct	tgctgcactg	60
cactaccctg	ccctgccatc	atatcgtacg	tgagcccgcc	cgagcgagag	crnnggagag	120
gcattggctg	tcgcgaagctc	gcgacgctgg	cgctggcgct	gctcctggcg	gcgacogtgg	180
tggtccccc	ggccgcggtg	cgcgcggcga	tgctgtgctc	cacogtgtac	agcacgctga	240
tgccgtgcct	gcgcttcgtc	cagatggggc	gggccatgcc	gccccagccg	tgctgcggcg	300
gcattccgag	cctgctgcag	cagccaacaa	cacccccgac	cgccgcacta	tctgcggctg	360
cctcaagaac	gcgcgcaacg	cgcgcaacgg	gagcgccacc	tacatcagcc	scgcccggcg	420
gctgcccgag	aagtgcggcg	tcgCctcgcc	gtacaagatc	agcaccacag	ttaactgcaa	480
cacgattaat	taagtgtatg	ggcgtcctgt	gcgcgtcccg	gcgaggaatg	catgcattgc	540
gctggcgagg	agtaataaaa	taagtctact	ggatatttaa	gctatatcga	gggtgcctcg	600
tctctagcta	tttattatgg	tgtttaggaa	tggtctacac	agtttgtaac	gggtgatcgt	660
ggatgcattg	tgccgcgagc	agagtacgta	ggcatgaacc	gatgtgtgcg	cttctgtctg	720
tttactctct	ctatgtagta	atgtgtgggt	gctttgatcc	agatgtattc	gctcgtgagt	780
cgtaggaagta	gatcggttca	gtg				

(2) INFORMATION FOR SEQ ID NO:3747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1578043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3747:

Ile	Pro	Thr	Thr	Pro	Glu	Ser	Ala	Asn	His	Arg	Arg	Val	Tyr	Leu	Ser
1				5					10					15	
Leu	Leu	His	Cys	Thr	Thr	Leu	Pro	Cys	His	His	Ile	Val	Arg	Glu	Pro
				20					25					30	
Gly	Arg	Ala	Arg	Xaa	Xaa	Glu	Arg	His	Gly	Cys	Ser	Glu	Ala	Arg	Asp
				35					40					45	
Ala	Gly	Ala	Gly	Arg	Ala	Pro	Gly	Gly	Asp	Arg	Gly	Gly	Ser	Pro	Gly
				50					55					60	
Arg	Gly	Ala	Arg	Gly	Asp	Val	Val	Leu	His	Arg	Val	Gln	His	Ala	Asp
				65					70					75	
Ala	Val	Pro	Ala	Val	Arg	Pro	Asp	Gly	Arg	Gly	His	Ala	Ala	Pro	Ala
				85					90					95	
Val	Leu	Arg	Arg	His	Pro	Gln	Pro	Ala	Ala	Ala	Asn	Asn	Thr	Pro	
				100					105					110	
Asp	Arg	Arg	Thr	Ile	Cys	Gly	Cys	Leu	Lys	Asn	Val	Ala	Asn	Gly	Ala
				115					120					125	
Asn	Gly	Ser	Gly	Thr	Tyr	Ile	Ser	Xaa	Ala	Ala	Ala	Leu	Pro	Ser	Lys
				130					135					140	
Cys	Gly	Val	Ala	Leu	Pro	Tyr	Lys	Ile	Ser	Thr	Asn	Val	Asn	Cys	Asn
				145					150					155	
Thr	Ile	Asn													

(2) INFORMATION FOR SEQ ID NO:3748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1578044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3748:

```
Ser Pro Gln His Gln Asn Pro Arg Ile Thr Asp Ala Ser Ile Ser Ala
1      5      10      15
Cys Cys Thr Ala Leu Pro Cys Pro Ala Ile Ile Ser Tyr Val Ser Pro
20      25      30
Ala Glu Arg Glu Xaa Gly Arg Gly Met Ala Ala Pro Lys Leu Ala Thr
35      40      45
Leu Ala Leu Ala Val Leu Leu Ala Ala Thr Val Val Ala Pro Pro Ala
50      55      60
Ala Val Arg Ala Ala Met Ser Cys Ser Thr Val Tyr Ser Thr Leu Met
65      70      75      80
Pro Cys Leu Pro Phe Val Gln Met Gly Gly Ala Met Pro Pro Gln Pro
85      90      95
Cys Cys Gly Gly Ile Arg Ser Leu Leu Gln Gln Pro Thr Thr Pro Pro
100      105      110
Thr Ala Ala Leu Ser Ala Ala Ala Ser Arg Thr Ser Pro Thr Ala Pro
115      120      125
Thr Gly Ala Ala Pro Thr Ser Ala Xaa Pro Pro Arg Cys Pro Ala Ser
130      135      140
Ala Ala Ser Pro Cys Arg Thr Arg Ser Ala Pro Thr Leu Thr Ala Thr
145      150      155      160
Arg Leu Ile Lys
```

(2) INFORMATION FOR SEQ ID NO:3749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1578045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3749:

```
Met Ala Ala Pro Lys Leu Ala Thr Leu Ala Leu Ala Val Leu Leu Ala
1      5      10      15
Ala Thr Val Val Ala Pro Pro Ala Ala Val Arg Ala Ala Met Ser Cys
20      25      30
Ser Thr Val Tyr Ser Thr Leu Met Pro Cys Leu Pro Phe Val Gln Met
35      40      45
Gly Gly Ala Met Pro Pro Gln Pro Cys Cys Gly Gly Ile Arg Ser Leu
50      55      60
Leu Gln Gln Pro Thr Thr Pro Pro Thr Ala Ala Leu Ser Ala Ala Ala
65      70      75      80
Ser Arg Thr Ser Pro Thr Ala Pro Thr Gly Ala Ala Pro Thr Ser Ala
85      90      95
Xaa Pro Pro Arg Cys Pro Ala Ser Ala Ala Ser Pro Cys Arg Thr Arg
100      105      110
Ser Ala Pro Thr Leu Thr Ala Thr Arg Leu Ile Lys
115      120
```

(2) INFORMATION FOR SEQ ID NO:3750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..667
(D) OTHER INFORMATION: / Ceres Seq. ID 1578056
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3750:
aatcgctccat ccgtattttcc gtcaacaactc acaaccccgag ccccccaaac ccgaagcagc 60
aggagctccc ctgacotttgc tccgcctccg atcaaggaaa aggaagatga gctactacgg 120
ccagcagccc cccgtcggcg tccgcgccga gcaaggctac ccgggggaag acggctaccc 180
gccagcGggg tacccGCGcg gccggctacc ccccgccggc gcaggggctac ccgcagcagg 240
gttaccacaca gcagggtctac ccgcgcgagt acgcgcGcc gccctccacag cagcagcaga 300
gcagcggggc ttcttctcatg gaaggatgct tggctgccct ctgctgctgc tncctctgg 360
acgcctgctt ctgacggatc catcggtccg ggttcaacac ggctgcaagt gaagcaacaa 420
gcttacggaa gagctggaa tgggcctgct tattctagct ttgtcctgcg ttatcgccct 480
cttttctttt tttttcttt tttttctct ctctctctct ctctgttata agactactgg 540
tactctgtcg atgtcgattg gattagacta gggctgggtg gtattctgtg gatgctcctg 600
gtttctggtg ggattcaagt tcaaacctgg gattattgta tttcttctac ctgttactct 660
gttgcg

(2) INFORMATION FOR SEQ ID NO:3751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..176
(D) OTHER INFORMATION: / Ceres Seq. ID 1578057
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3751:
Asn Arg Pro Ser Val Phe Pro Ser Gln Leu Thr Thr Arg Ala Pro Gln
1 5 10 15
Thr Arg Ser Ser Arg Ser Ser Pro Asp Leu Ala Pro Pro Pro Ile Lys
20 25 30
Glu Lys Glu Asp Glu Leu Leu Arg Pro Ala Ala Pro Arg Arg Arg Pro
35 40 45
Ala Ala Ala Arg Leu Pro Gly Glu Gly Arg Leu Pro Ala Ser Gly Val
50 55 60
Pro Arg Arg Pro Ala Thr Pro Arg Arg Arg Arg Ala Thr Arg Ser Arg
65 70 75 80
Val Thr His Ser Arg Ala Thr Arg Arg Ser Thr Arg Ser Arg Leu His
85 90 95
Ser Ser Ser Arg Ala Ala Gly Leu Pro Ser Trp Lys Asp Ala Trp Leu
100 105 110
Pro Ser Ala Ala Xaa Ser Trp Thr Pro Ala Ser Asp Gly Ser Ile
115 120 125
Val Pro Gly Ser Thr Arg Leu Gln Val Lys Gln Gln Ala Tyr Gly Arg
130 135 140
Ala Gly Thr Gly Pro Cys Tyr Ser Ser Phe Val Leu Arg Tyr Arg Pro
145 150 155 160
Leu Phe Phe Ser Phe Leu Phe Phe Phe Ser Leu Ser Leu Ser Leu Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:3752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1578058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3752:

Ile Val His Pro Tyr Phe Arg His Asn Ser Gln Pro Glu Pro Pro Lys
1 5 10 15
Pro Glu Ala Ala Gly Ala Pro Leu Thr Leu Leu Arg Leu Arg Ser Arg
20 25 30
Lys Arg Lys Met Ser Tyr Tyr Gly Gln Gln Pro Pro Val Gly Val Pro
35 40 45
Pro Gln Gln Gly Tyr Pro Gly Lys Asp Gly Tyr Pro Pro Ala Gly Tyr
50 55 60
Pro Ala Gly Arg Leu Pro Pro Ala Gly Ala Gly Leu Pro Ala Ala Gly
65 70 75 80
Leu Pro Thr Ala Gly Leu Pro Ala Ala Val Arg Ala Ala Ala Ser Thr
85 90 95
Ala Ala Ala Glu Gln Arg Ala Phe Leu His Gly Arg Met Leu Gly Cys
100 105 110
Pro Leu Leu Leu Xaa Pro Pro Gly Arg Leu Leu Thr Asp Pro Ser
115 120 125
Cys Arg Val Gln His Gly Cys Lys
130 135

(2) INFORMATION FOR SEQ ID NO:3753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1578059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3753:

Met Ser Tyr Tyr Gly Gln Gln Pro Pro Val Gly Val Pro Pro Gln Gln
1 5 10 15
Gly Tyr Pro Gly Lys Asp Gly Tyr Pro Pro Ala Gly Tyr Pro Ala Gly
20 25 30
Arg Leu Pro Pro Ala Gly Ala Gly Leu Pro Ala Ala Gly Leu Pro Thr
35 40 45
Ala Gly Leu Pro Ala Ala Val Arg Ala Ala Ala Ser Thr Ala Ala Ala
50 55 60
Glu Gln Arg Ala Phe Leu His Gly Arg Met Leu Gly Cys Pro Leu Leu
65 70 75 80
Leu Xaa Pro Pro Gly Arg Leu Leu Leu Thr Asp Pro Ser Cys Arg Val
85 90 95
Gln His Gly Cys Lys
100

(2) INFORMATION FOR SEQ ID NO:3754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1578070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3754:

atgccacaac aagaccaga acccacaatc tttctttgtg cacagaaga agaaagaacc 60
tatggcacag tcgtgtccg cctccgtcaa gctgctgggt ctggtgtgcc tccctgcgct 120

cctcctgttc ctcgtccaag cgcaargrc tcggccagcg gcggcgaaca cgacgacccc 180
gacccccgcc accaccaccg ggtgcgcggc gtcgagcgtg acggtgtcgc agtcccaacac 240
gggacgacag gccgggtacg acccggtgtt cgaggtgacg gtgagcaacg cctgcccCtg 300
cgccgtcgcc gccgtgcgcc tccgctccga GGccttcgcc agctcgggtg cctgaggacc 360
gcgcctgttc gcgcgcgccg gccgcgacta cctcgtcgcc gacggccgcc ggatcgagcc 420
cGgcgcgcgac gcgcgcttcc gCTacgcctg ggaccgcgcc ttccggatga ccgcgcgcgc 480
cgtgcgcgac gactgctcct gatggagtga gtgagtgcgg tagctcctgc ctgcaacgag 540
tgaattgcag tagctcctgt ccttcgtgag agagagagac tcgctctgtc gtgatccaca 600
gggaatttac ctcggtttta cgtctgttta ttacgccttc ttcttaacgt attggctagt 660
tcgctggatc atacttcg

(2) INFORMATION FOR SEQ ID NO:3755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1578071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3755:

Met	Pro	Gln	Gln	Asp	Pro	Glu	Pro	Thr	Ile	Phe	Leu	Cys	Ala	Gln	Lys
1			5						10					15	
Glu	Glu	Arg	Thr	Tyr	Gly	Thr	Val	Val	Arg	Leu	Arg	Gln	Ala	Ala	
			20				25					30			
Gly	Ser	Gly	Cys	Pro	Pro	Cys	Ala	Pro	Pro	Val	Pro	Arg	Pro	Ser	Ala
			35				40					45			
Xaa	Xaa	Ser	Ala	Ser	Gly	Gly	Glu	His	Asp	Asp	Pro	Asp	Pro	Arg	His
			50				55				60				
His	His	Arg	Val	Arg	Gly	Val	Glu	Arg	Asp	Gly	Val	Ala	Val	Gln	His
			65				70				75			80	
Gly	Arg	Gln	Gly	Arg	Val	Arg	Pro	Gly	Val	Arg	Gly	Asp	Gly	Glu	Gln
			85						90					95	
Arg	Leu	Pro	Leu	Arg	Arg	Pro	Arg	Arg	Ala	Pro	Pro	Leu	Arg	Gly	Leu
			100						105				110		
Arg	Gln	Leu	Gly	Ala	Arg	Gly	Pro	Ala	Pro	Val	Pro	Pro	Arg	Arg	Pro
			115				120					125			
Arg	Leu	Pro	Arg	Arg	Arg	Arg	Pro	Pro	Asp	Arg	Ala	Arg	Arg	Arg	Arg
			130				135				140				
Ala	Leu	Pro	Leu	Arg	Leu	Gly	Pro	Arg	Leu	Pro	Asp	Arg	Arg	Arg	Arg
			145				150				155			160	
Arg	Ala	Arg	Arg	Leu	Leu	Leu	Met	Glu							
							165								

(2) INFORMATION FOR SEQ ID NO:3756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1578073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3756:

Cys	His	Asn	Lys	Thr	Gln	Asn	Pro	Gln	Ser	Phe	Phe	Val	His	Arg	Lys
1			5						10				15		
Lys	Lys	Glu	Pro	Met	Ala	Gln	Ser	Ser	Ser	Ala	Ser	Val	Lys	Leu	Leu
			20						25			30			
Val	Leu	Val	Val	Leu	Pro	Ala	Leu	Leu	Phe	Leu	Val	Gln	Ala	Gln	

(2) INFORMATION FOR SEQ ID NO:3757:

(A) LENGTH: 878 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..878

(D) OTHER INFORMATION: / Ceres Seq. ID 1578083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3757:

(X1) SEQUENCE DESCRIPTION: SEQ ID:1973:						
aaggcagcgcg	ccgagcgagc	acgcgcatcaa	cgggcgccagc	tacgccctcg	agctgcagat	60
gggtgcacagc	acgacgaccca	acagcagtcg	cgtaggtctcg	cagctctcga	ggatctccgg	120
cgggcgctctc	gacgagaccca	ttcaccgtagc	ggagcggtagc	atccggagga	tcattcgccag	180
gaggaagaac	cacgagggagc	ctatcgacga	ggaggtggac	ccgcggcgcc	cggtgacgcg	240
gagcagcggc	tactacaagt	acacgggtctc	cttcacgaca	cgccctcgca	cgaggggcgt	300
gcagctgggtc	gttgccgcacc	agacacggcg	ggtgacgcgg	cgccaggtca	ggctgctgcg	360
gaacscgtcc	acgacggcac	cagcggcaac	agggagggcac	tcgcaggaac	caacggcCag	420
ggccatcacc	tttctactaca	cytcggcgac	gcacggcgca	ggcgccgaac	gggactagca	480
cgcatctgca	ggagacggcc	ggcggaatct	tggcgctccc	gtgctctctt	ttctgcgcag	540
gcacagccagc	catggccaac	caaacctctc	catgtgatcg	atctcgacga	gtgttagctg	600
agagtcgaca	ccaatttttt	tttctctcca	gcgatcatca	atctggttgc	gagtaatgtc	660
tgatgtcgat	tgcgaatttg	catctggcaag	tgagtttgtg	gcacaaaaaa	ggacatcaaa	720
ttagttagaac	gtttgcggtt	tacactcctt	gttcogtgac	tgagtgcgag	aattgcaatc	780
tcgaaaaatc	tgtgattcta	aggatagcac	gtctcgccaca	tgtgaagggt	aaaacgatcg	840
gtaacgctgc	gaaaaaaatc	ctaccggctt	ttactcgc			

(2) INFORMATION FOR SEQ ID NO:3758:

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amin

(B) TYPE: amino a

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE

FEATURE:

(A) NAME/KEY: peptid

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1578084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3758:

(xi) SEQUENCE DESCRIPTION: SEQ. 1															
Arg	His	Ala	Pro	Ser	Glu	His	Ala	Ile	Asn	Gly	Arg	Arg	Tyr	Ala	Leu
1				5				10						15	
Glu	His	Gln	Met	Val	His	Gln	Ser	Asp	Thr	Asn	Arg	Tyr	Ala	Val	Val
			20					25					30		
Ser	Gln	Leu	Tyr	Arg	Ile	Ser	Arg	Arg	Arg	Pro	Asp	Arg	Thr	Ile	His

35	40	45
Arg Leu Glu Arg Tyr Ile	Arg Arg Ile Ile Ala Arg	Arg Arg Lys Asn His
50	55	60
Glu Glu Leu Ile Asp Glu	Glu Val Asp Pro Arg Arg	Pro Val Ser Arg
65	70	75
Ser Thr Ala Tyr Tyr Lys	Tyr Thr Gly Ser Phe Thr	Thr Pro Pro Cys
85	90	95
Thr Glu Gly Val Thr Trp	Val Val Ala His Gln Thr	Arg Arg Val Thr
100	105	110
Arg Arg Gln Val Arg Leu	Leu Arg Asn Xaa Ser Thr	Thr Ala Pro Gly
115	120	125
Ala Thr Gly Gly His Ser	Arg Lys Pro Thr Ala Arg	Ala Ile Thr Phe
130	135	140
Tyr Tyr Xaa Ser Pro Ala	His Gly Arg Gly Ala Asn	Gly Asp
145	150	155

(2) INFORMATION FOR SEQ ID NO:3759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3759:

Met Val His Gln Ser Asp Thr Asn Arg Tyr Ala Val Val Ser Gln Leu	
1	5 10 15
Tyr Arg Ile Ser Arg Arg Arg Pro Asp Arg Thr Ile His Arg Leu Glu	
	20 25 30
Arg Tyr Ile Arg Arg Ile Ile Ala Arg Arg Lys Asn His Glu Leu	
	35 40 45
Ile Asp Glu Glu Val Asp Pro Arg Arg Pro Val Ser Arg Ser Thr Ala	
50	55 60
Tyr Tyr Lys Tyr Thr Gly Ser Phe Thr Thr Pro Cys Thr Glu Gly	
65	70 75
Val Thr Trp Val Val Ala His Gln Thr Arg Arg Val Thr Arg Gln	
	85 90 95
Val Arg Leu Leu Arg Asn Xaa Ser Thr Thr Ala Pro Gly Ala Thr Gly	
	100 105 110
Gly His Ser Arg Lys Pro Thr Ala Arg Ala Ile Thr Phe Tyr Tyr Xaa	
	115 120 125
Ser Pro Ala His Gly Arg Gly Ala Asn Gly Asp	
130	135

(2) INFORMATION FOR SEQ ID NO:3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..951

(D) OTHER INFORMATION: / Ceres Seq. ID 1578086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3760:

acccatgttc ctgttccac actcgactgt catcctgtga tatccgctcg ccagtcgcga	60
ctccgtttcg gcattccgac tcctcccgac acacactcttt aactcgcttc cgtttccaaa	120
aaaatgctcc agttaattta atccagacga ggaatcgctc cgccgcggat ctctccgctc	180
gcgcacaaga ccgcgtatcg gctccggcgg gaagactcgc actacggtgg ggcgcgtcgc	240

```
cgccgcctcgg caccgtggctc gtcgggttcga cgttcgcttg tggaggtcgt cggggccagc 300
gggtgcgggg caatgcggctc agtttttgga gccgtctgar gcgcttggtt gggatctgag 360
ggtgtcaggt argggggcgc asragctctg tcgggtggga rttggttggt gttgtagcgt 420
agggcgcgtc gcgtgttttg ctgcggggat ggagcacgta gttgggggca agttcaagct 480
tggggaagaag atcgggaagcg gatcatttgg ggagctctac ctccggctga acatgcagag 540
tgacgaggag gtggctgtca aactggtatt ccacgaacat ctccacgtg atttttgtgt 600
ccactatcca tgccttggtg aacagttctg tgttagacct tctccaacgc caccocccaa 660
accctccctc acccttgcta ttgctacgca cctactgtgt actatggggg gaagtattct 720
ttaggatgat gtagtaaaat ataatagaaa atacagatat gaggaaaaaa tatgggggaa 780
atggttgag atggtcttag gagttaacct tagtcggagt cactgaaatc tatagttagc 840
ctaattgctt gcaggagcta atgagcctgt agcactctga agtgagggta tcaatgctga 900
aaagcaccca ctggaaactc atctctgttt tgttctgatt ggattattct c
```

(2) INFORMATION FOR SEQ ID NO:3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3761:

```
Pro Cys Ser Cys Ser His Thr Arg Leu Ser Ser Cys Asp Ile Arg Ser
1      5      10      15
Pro Val Ala Thr Pro Phe Arg His Ser Ala Ser Ser Arg His Thr Ser
      20      25      30
Leu Thr Arg Phe Arg Phe Gln Lys Asn Ala Pro Val Asn Leu Ile Gln
      35      40      45
Thr Arg Asn Arg Leu Ala Ala Asp Leu Ser Ala Arg Arg Gln Asp Pro
      50      55      60
Leu Ser Ala Pro Ala Gly Arg Leu Ala Leu Arg Trp Gly Ala Ser Pro
65      70      75      80
Pro Leu Gly Thr Trp Leu Val Gly Ser Thr Phe Ala Cys Gly Gly Arg
      85      90      95
Arg Gly Gln Arg Cys Arg Gly Asn Ala Val Ser Leu Trp Ser Arg Leu
      100     105     110
Xaa Arg Leu Ala Gly Ile
      115
```

(2) INFORMATION FOR SEQ ID NO:3762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3762:

```
Met Glu His Val Val Gly Gly Lys Phe Lys Leu Gly Lys Lys Ile Gly
1      5      10      15
Ser Gly Ser Phe Gly Glu Leu Tyr Leu Gly Val Asn Met Gln Ser Asp
      20      25      30
Glu Glu Val Ala Val Lys Leu Val Phe His Glu His Leu Pro Arg Asp
      35      40      45
Phe Cys Val His Tyr Pro Cys Leu Gly Glu Gln Phe Cys Val Arg Pro
      50      55      60
Ser Pro Thr Ala Pro Pro Lys Pro Pro Leu Thr Leu Ala Ile Ala Thr
```

65 70 75
Asp Leu Leu Cys Thr Met Gly Gly Ser Ile Phe
 85 90

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1578089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3763:

Met	Glu	Arg	Pro	Asp	Glu	Glu	Val	Ala	Val	Lys	Leu	Val	Phe	His	Glu	His
1				5					10						15	
Leu	Pro	Arg	Arg	Phe	Cys	Val	His	Tyr	Pro	Cys	Leu	Gly	Glu	Gln	Phe	
			20					25					30			
Cys	Val	Arg	Pro	Ser	Pro	Thr	Ala	Pro	Pro	Lys	Pro	Pro	Leu	Thr	Leu	
			35				40					45				
Ala	Ile	Ala	Thr	Asp	Leu	Cys	Thr	Met	Gly	Gly	Ser	Ile	Phe			
	50					55			60							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..802
(D) OTHER INFORMATION: / Ceres Seq. ID 1578090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3764:

(A12) Sub						
ataccctgaa	cttcactgcc	ttttgttcag	gcaogctggt	caggaaaatca	gtatcgctgt	60
ttgctgctgt	ttgtctaata	ctgtgggagc	ggggagatgg	ccggaggagaa	catcgcgatc	120
cgagtgctgt	ttctgtctgt	cagcaaaagc	gctttcgctg	ccgtgcgcag	gaaccttgcg	180
aggaaacggc	acagcgtctat	actactccac	gtgaacagct	ctctgccaaag	cgagcggggc	240
cgcgctctac	ctgtggagca	gacgggtttc	ccattgatcc	cttctggcca	gttttcagac	300
gtcgccagga	catacggtgt	gtccaccgac	aaggagacaa	tcgagatctc	catctaaagc	360
gcaaatcata	gagggatcga	agtctttgca	aaggtgtttc	accggcacct	ggcaaaagaa	420
ctgtacgaag	cagccgcacat	ggtcccgctt	agctgcattg	tgtgtcggga	cacaggaacta	480
agcaacgtca	agagggtctc	gtgggggaac	gtgaacacgt	attgttgtga	ccacgcggcc	540
tgcccgctca	cggttgtgaa	ggatgaggtg	tagcgtgttg	aacaccgcgt	gttacaagct	600
tcaccctagc	cagattgaat	aagcgtgctt	gataagcaat	gaccggggag	gatcttgcta	660
ctatacagca	attttgtgct	tgaattttgt	gttaactagg	ccgggcgcga	catatctatg	720
tcttgggctc	atggcactga	catctgaaca	tatgcctcaa	gtctgtgtga	atcgcaaaat	780
atttttgtct	ataaaatcag	tt				

(2) INFORMATION FOR SEQ ID NO:3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1X) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1578091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3765:

Met Ala Arg Arg Asn Ile Gly Val Ala Val Asp Phe Ser Ser Cys Ser
1 5 10 15
Lys Ala Ala Leu Arg Trp Ala Ser Thr Asn Leu Ala Arg Asn Gly Asp
20 25 30
Arg Leu Ile Leu Ile His Val Asn Ser Ser Cys Gln Asn Glu Arg Gly
35 40 45
Ala Val His Leu Trp Glu Gln Ser Gly Ser Pro Leu Ile Pro Leu Ala
50 55 60
Glu Phe Ser Asp Val Ala Arg Thr Tyr Gly Val Ser Pro Asp Lys Glu
65 70 75 80
Thr Ile Glu Ile Leu Thr Gln Ala Ala Asn His Arg Gly Ile Glu Val
85 90 95
Phe Ala Lys Val Phe Tyr Gly Asp Pro Ala Lys Lys Leu Tyr Glu Ala
100 105 110
Ala Asp Met Val Pro Leu Ser Cys Met Val Val Gly Ser Arg Gly Leu
115 120 125
Ser Thr Leu Lys Arg Ala Leu Met Gly Ser Val Ser Thr Tyr Val Val
130 135 140
Asn His Ala Ala Cys Pro Val Thr Val Val Lys Glu Met Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..630
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3766:

atgatgggtg	caagcitttg	gatcttcgga	aattaagaaa	ttttaggacc	ttctctccct	60
atgattcaga	tacgccaaca	aatactgtgg	aatttgattt	tagtggAaaa	ctatcttgcc	120
attgggtggt	cagatataag	ggctaccaa	gtagctaagt	tttagggcga	atggaatctc	180
atcaagacat	taccagattt	atctggaaca	gggaaagtaa	cttcggtaaa	gttcggagca	240
gatgctaagt	acatagccgt	aggttctatg	gaccgcgaatc	tacggatatt	tggcctccct	300
ggagacgacc	aaatggagga	atcaaccaca	gcggcagagt	gaggaaaaatc	catgggttatc	360
agcattcatt	gtctatttgg	ccactgtcga	gaggtaatcc	acggagacac	accgctggcg	420
cccgtagacac	ttggcctggt	tggttacttg	ctaaaaattg	ctacacattt	ttgtgccaca	480
cttggtttaag	cacactgtgt	taagggtgtt	aagggttatac	gtctcaaatc	cgcttcacag	540
cttgtttgtc	actcataaga	gaatattgccc	tgtaaaatga	gagttctgaac	gacttgcgccg	600
taaaatgaga	tggaaaaatca	gttagctgct				

(2) INFORMATION FOR SEQ ID NO:3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3767:

Asp Gly Val Lys Leu Trp Asp Leu Arg Lys Leu Arg Asn Phe Arg Thr	
1 5 10 15	
Phe Ser Pro Tyr Asp Ser Asp Thr Pro Thr Asn Thr Val Glu Phe Asp	
20 25 30	
Phe Ser Gly Lys Leu Ser Cys His Trp Trp Phe Arg Tyr Lys Gly Leu	
35 40 45	

Pro Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3768:

```
Met Ile Gln Ile Arg Gln Gln Ile Leu Trp Asn Leu Ile Leu Val Glu
1      5      10      15
Asn Tyr Leu Ala Ile Gly Gly Ser Asp Ile Arg Val Tyr Gln Val Ala
20      25      30
Asn Val Lys Ala Glu Trp Asn Leu Ile Lys Thr Leu Pro Asp Leu Ser
35      40      45
Gly Thr Gly Lys Val Thr Ser Val Lys Phe Gly Ala Asp Ala Lys Tyr
50      55      60
Ile Ala Val Gly Ser Met Asp Arg Asn Leu Arg Ile Phe Gly Leu Pro
65      70      75      80
Gly Asp Asp Gln Met Glu Glu Ser Thr Thr Ala Ala Glu
85      90
```

(2) INFORMATION FOR SEQ ID NO:3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3769:

```
atcagccctc acgcatgtgg caccgatgg gccgatctg aggttgagtg tgcgatcccg 60
ttggcatatc gacaaagtgt ggtgggtccc accgcagatc ccggcccggg aggtactagt 120
tccgcgctcc cccctcccta gtctccgggg aggaccgtct cggcgcgcgag agtgcgctcg 180
tcgactccac tcagctctct cgctccctct cctcccccaa gggcccagag acaggcgagcc 240
ggcgaggccc ccgcgcgcga aGcaatgga ttcaagggtt tctgggagtc cagattccggg 300
ggcaagaagg aaccagagcc ggagcagaac gggcacgccca acgggggtcca gaaccagaag 360
aggacctccg atctggcggg ctacgagcag ttcgagcagc aggccaggca gacccaggtc 420
cgagcccgcg cgattcgcca cggagacgct gatgtcataa gccctttcta ccttctattg 480
agtgcagctga aatgcgtaat ctgcgcagaga cattgttgag ggaattattt cgcgggagcc 540
cagatgtgaa atgggagagc atcaaaaggc tggaaaatgc aaaaacgcct ctaaaaaggg 600
ctgtttgcat gcccataaag tacccaaaat acttcaactg tctcctttct ccattggaag 660
gcattcttact ttttggcccc ccagggcacag gaaagacaat gctgggcaaaa gcggtcgcta 720
ctgagtgcaa aaccaccttc ttcaacattt cagcatcatc aattgtcagc aaatggcgtg 780
gagattcaga gaagcttgtc aaagtcttgt ttgagcttgc taggcatcat gcaccatcca 840
caatattcct tgaatgaata gatgtatca tcagcc
```

(2) INFORMATION FOR SEQ ID NO:3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1578151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3770:

Met	Asp	Phe	Lys	Gly	Phe	Trp	Glu	Ser	Arg	Phe	Gly	Gly	Lys	Lys	Glu
1			5					10					15		
Pro	Glu	Pro	Glu	Gln	Asn	Gly	His	Ala	Asn	Gly	Val	Gln	Asn	Gln	Lys
			20				25					30			
Arg	Thr	Ser	Asp	Leu	Ala	Val	Tyr	Glu	Gln	Phe	Glu	Gln	Gln	Ala	Arg
			35				40					45			
Gln	Thr	Gln	Val	Arg	Ala	Ala	Ala	Ile	Arg	Asp	Gly	Asp	Ala	Asp	Val
			50				55				60				
Ile	Ser	Pro	Phe	Tyr	Leu	His	Leu	Ser	Gln	Leu	Lys	Cys	Val	Ile	Ser
65					70					75				80	
Gln	Arg	His	Cys												

(2) INFORMATION FOR SEQ ID NO:3771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1578152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3771:

Met	Arg	Asn	Leu	Ala	Glu	Thr	Leu	Leu	Arg	Asp	Ile	Ile	Arg	Gly	Ser
1			5					10					15		
Pro	Asp	Val	Lys	Trp	Glu	Ser	Ile	Lys	Gly	Leu	Glu	Asn	Ala	Lys	Arg
			20				25					30			
Leu	Leu	Lys	Glu	Ala	Val	Val	Met	Pro	Ile	Lys	Tyr	Pro	Lys	Tyr	Phe
			35				40				45				
Thr	Gly	Leu	Leu	Ser	Pro	Trp	Lys	Gly	Ile	Leu	Leu	Phe	Gly	Pro	Pro
			50				55				60				
Gly	Thr	Gly	Lys	Thr	Met	Leu	Ala	Lys	Ala	Val	Ala	Thr	Glu	Cys	Lys
65					70				75					80	
Thr	Thr	Phe	Phe	Asn	Ile	Ser	Ala	Ser	Ser	Ile	Val	Ser	Lys	Trp	Arg
				85				90					95		
Gly	Asp	Ser	Glu	Lys	Leu	Val	Lys	Val	Leu	Phe	Glu	Leu	Ala	Arg	His
			100				105				110				
His	Ala	Pro	Ser	Thr	Ile	Phe	Leu	Asp	Glu	Ile	Asp	Ala	Ile	Ile	Ser
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1578153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3772:

Met	Pro	Ile	Lys	Tyr	Pro	Lys	Tyr	Phe	Thr	Gly	Leu	Leu	Ser	Pro	Trp
1			5					10					15		
Lys	Gly	Ile	Leu	Leu	Phe	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Met	Leu

20	25	30
Ala Lys Ala Val Ala Thr	Glu Cys Lys Thr Thr Phe Phe Asn Ile Ser	
35	40	45
Ala Ser Ser Ile Val Ser	Lys Trp Arg Gly Asp Ser Glu Lys Leu Val	
50	55	60
Lys Val Leu Phe Glu Leu Ala Arg His His	Ala Pro Ser Thr Ile Phe	
65	70	75
Leu Asp Glu Ile Asp Ala Ile Ile Ser		80
	85	

(2) INFORMATION FOR SEQ ID NO:3773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..776
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3773:

aaaagaatat	ttagttgaag	caaaattcaa	gaaacttgaa	gaagaggcct	gcaatatatt	60
gtccctcgagt	tctggtgaaa	caatgaaaaa	caacattgat	gttttggttt	gcaaaagctga	120
atactaccac	cagagtggag	agtacacaaa	gtgttttAaa	actcacatcc	tcgttacttg	180
agagagaccc	tttccatcta	aattgcacat	tagttcattt	ggcaactgca	atggagcttg	240
gtcattccaa	tgatctttat	cttttagcat	gcaacttagt	gaaggattat	cctgaaaaag	300
ctctttcatg	gtttgctgtc	ggttgctatt	actactgtat	taagaagat	gatcaagcgc	360
gaagataact	cggaagaagct	acaggtttag	atgggacgtt	tcctcctgct	tggattggta	420
caggcattgc	ctatgctgct	caagaggaag	gtgaccaaac	aatggctgca	tttcggacgg	480
cagctcggtt	atttctctga	tGgtcatctg	ccaactttat	acatgggcac	gcaatatgtg	540
cgaatgcama	atttcaaacT	ttgcagagca	gttcttcaca	caagcAaaat	ccatctgccc	600
atctgatcca	cttattttaca	atgagtggg	ggttggttgc	tataatatga	aggagaccg	660
aaaagcagtt	cagttgtttg	agttaacatt	ggaccatact	tcactctctc	tgaatgaat	720
gtgggaacca	acattgttga	atcttgggca	tgcacttcgg	aaactcaagg	aatatc	

(2) INFORMATION FOR SEQ ID NO:3774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3774:

Met Phe Trp Phe Ala Lys Leu Asn Thr Thr Thr Arg Val Glu Ser Thr	
1	5 10 15
Lys Ser Val Leu Lys Leu Thr Ser Ser Leu Leu Glu Arg Asp Pro Phe	
	20 25 30
His Leu Lys Cys Thr Leu Val His Leu Ala Thr Ala Met Glu Leu Gly	
	35 40 45
His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu Val Lys Asp Tyr	
	50 55 60
Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys Tyr Tyr Tyr Cys	
	65 70 75 80
Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly Lys Ala Thr Gly	
	85 90 95
Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr Gly Ile Ala Tyr	
	100 105 110
Ala Ala Gln Glu Glu Gly Asp Gln Ala Met Ala Ala Phe Arg Thr Ala	

115 120 125
Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe Ile His Gly His
130 135 140
Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln Ser Ser Ser Ser
145 150 155 160
His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu Phe Thr Met Ser
165 170 175
Trp Gly Leu Leu Arg Ile Ile
180

(2) INFORMATION FOR SEQ ID NO:3775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3775:

Met Glu Leu Gly His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu
1 5 10 15
Val Lys Asp Tyr Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys
20 25 30
Tyr Tyr Tyr Cys Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly
35 40 45
Lys Ala Thr Gly Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr
50 55 60
Gly Ile Ala Tyr Ala Ala Gln Glu Glu Gly Asp Gln Ala Met Ala Ala
65 70 75 80
Phe Arg Thr Ala Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe
85 90 95
Ile His Gly His Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln
100 105 110
Ser Ser Ser Ser His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu
115 120 125
Phe Thr Met Ser Trp Gly Leu Leu Arg Ile Ile
130 135

(2) INFORMATION FOR SEQ ID NO:3776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1578157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3776:

Met Val Ile Cys Gln Leu Tyr Thr Trp Ala Cys Asn Met Cys Glu Cys
1 5 10 15
Xaa Ile Ser Asn Phe Ala Glu Gln Phe Phe Thr Gln Ala Lys Ser Ile
20 25 30
Cys Pro Ser Asp Pro Leu Ile Tyr Asn Glu Leu Gly Val Val Ala Tyr
35 40 45
Asn Met Lys Glu Tyr Arg Lys Ala Val Gln Leu Phe Glu Leu Thr Leu
50 55 60
Asp His Thr Ser Ser Ser Leu Asn Glu Met Trp Glu Pro Thr Leu Val
65 70 75 80

Asn Leu Gly His Ala Leu Arg Lys Leu Lys Glu Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:3777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..654

(D) OTHER INFORMATION: / Ceres Seq. ID 1578185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3777:

tyatgctgat	acagttggag	acttggggata	tgcatcagag	cttggaaact	atgcagagta	60
tagtggtgct	cctaagtggg	aggaggttct	gaattattct	agagttgttc	ttgattgtgc	120
aactgctgat	cctgatggcc	gcaagagagc	ctctctcatt	ggaggtggca	tagctaaact	180
cactgatgtt	gctaccacat	tcaatggcat	catccgagcc	ttaaaggaga	aggaatccaa	240
gttgaaggct	tcaagaatgc	acatttatgt	ccgccgaggt	ggtccaaatt	accaatctgg	300
actggctaaa	atgcgtaaGc	ttgtgtcaga	actcggcggt	ccaattgagg	tgtatggggc	360
agaagcgact	atgactggaa	tctgcaaaaca	agcaattgaa	tgcatcatgg	ctgcagcgta	420
atcagagcgt	aGcTctNgg	tagtttggga	tctgcaaaaca	cgcgaattgaa	tgtgtcatgg	480
actcagcata	aatgagagat	ggatagtagt	tgcatatatat	agttcacaca	tggtgtttct	540
gtttttgtt	tcagatatgt	tgtagcgtgt	tgtttgaacg	aaaccttcac	agatcattac	600
tgcaaaagaaa	ttgtgtgtgt	ttaaaataaa	ttcaagtct	agtttgtgc	cttt	

(2) INFORMATION FOR SEQ ID NO:3778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3778:

Xaa	Ala	Asp	Thr	Val	Gly	Asp	Leu	Gly	Tyr	Ala	Ser	Glu	Leu	Gly	Asn	
1				5					10						15	
Tyr	Ala	Glu	Tyr	Ser	Gly	Ala	Pro	Asn	Glu	Glu	Glu	Val	Leu	Asn	Tyr	
				20				25					30			
Ser	Arg	Val	Val	Leu	Asp	Cys	Ala	Thr	Ala	Asp	Pro	Asp	Gly	Arg	Lys	
				35			40					45				
Arg	Ala	Leu	Leu	Ile	Gly	Gly	Gly	Ile	Ala	Asn	Phe	Thr	Asp	Val	Ala	
				50			55				60					
Thr	Thr	Phe	Asn	Gly	Ile	Ile	Arg	Ala	Leu	Arg	Glu	Lys	Glu	Ser	Lys	
				65			70			75					80	
Leu	Lys	Ala	Ser	Arg	Met	His	Ile	Tyr	Val	Arg	Arg	Gly	Gly	Pro	Asn	
				85			90						95			
Tyr	Gln	Ser	Gly	Leu	Ala	Lys	Met	Arg	Lys	Leu	Gly	Ala	Glu	Leu	Gly	
				100			105						110			
Val	Pro	Ile	Glu	Val	Tyr	Gly	Pro	Glu	Ala	Thr	Met	Thr	Gly	Ile	Cys	
				115			120					125				
Lys	Gln	Ala	Ile	Glu	Cys	Ile	Met	Ala	Ala	Ala						
				130			135									

(2) INFORMATION FOR SEQ ID NO:3779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1578190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3779:

gaggacgaag	gttcgttcag	ttcaagacca	gacgargagg	aagagaggcg	cgcaaggntc	60
cggttcctatg	gcgcctctcc	ccgcctcccg	ctcatcgctg	ccggtngccg	ccgcccgcggc	120
gccgtcgctgc	ggtcgcggtgt	ccggccacgc	atctgcggcg	cccagcaaga	ggcgcgctcgt	180
ctcctgcagg	gccgtcagca	gcaggtcgct	gtccatcatc	aggtgcgagc	agagcgcgaa	240
gaagggcgccg	gggcccggaca	catggctggg	ccgcgcggcc	atGGtbnngcG	ttcgctcccg	300
cgaatcgctc	cgaggtggcc	accggcaagg	gcttctctca	ggtagggacc	gtcgtagagt	360
atgagtatca	acgtaacatc	gacagcagcg	aggaacgcgc	aaacgcgtgc	gtaacaaaaa	420
taccacagat	ttgttggtga	tggcgtgcag	aacttgggcg	tgggtactcc	ggcgccgaAS	480
STGGcgctgg	ccgtgtcggg	gctcgtcgct	ggcctcgccg	tctttctcct	gctccagtcg	540
ggaggaggca	cgcgagactg	acggctgatg	gaaccccatg	agctgagagc	acgcgcacgt	600
cgaacatcgt	ctccccactc	gacatcagtt	gctgtaatgg	ttggtgaagt	gaggatgaaa	660
accaggcgca	tatatcatca	tcatcatgtc	atgtgtaaca	aagacgataa	ctctcatgtg	720

tt

(2) INFORMATION FOR SEQ ID NO:3780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1578191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3780:

Glu	Asp	Glu	Gly	Ser	Phe	Ser	Ser	Arg	Pro	Asp	Xaa	Glu	Glu	Glu	Arg	
1				5				10					15			
Arg	Ala	Arg	Xaa	Arg	Ser	His	Gly	Ala	Leu	Pro	Arg	Pro	Pro	Leu	Ile	
			20				25					30				
Val	Ala	Gly	Xaa	Arg	Arg	Arg	Gly	Ala	Val	Ala	Arg	Ser	Arg	Val	Arg	
			35				40					45				
Pro	Arg	Ile	Cys	Gly	Ala	Gln	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Gln	Gly	
			50			55					60					
Arg	Gln	Gln	Gln	Val	Ala	Val	His	His	Gln	Val	Arg	Ala	Glu	Arg	Glu	
			65			70			75					80		
Glu	Gly	Arg	Arg	Ala	Gly	His	Met	Ala	Gly	Pro	Arg	Gly	His	Gly	Xaa	
			85			90			95							
Arg	Ser	Pro	Pro	Arg	Ser	Pro	Ser	Arg	Trp	Pro	Pro	Ala	Arg	Ala	Ser	
			100					105					110			

Ser Arg

(2) INFORMATION FOR SEQ ID NO:3781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1578192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3781:

Arg	Thr	Lys	Val	Arg	Ser	Val	Gln	Asp	Gln	Thr	Xaa	Arg	Lys	Arg	Gly	
1				5				10					15			

Ala Gln Xaa Ser Gly Leu Met Ala Pro Phe Pro Ala Leu Arg Ser Ser
20 25 30
Ser Pro Xaa Ala Ala Ala Ala Pro Ser Leu Gly Arg Val Ser Gly
35 40 45
His Ala Ser Ala Ala Pro Ser Lys Arg Arg Val Val Ser Cys Arg Ala
50 55 60
Val Ser Ser Arg Ser Leu Ser Ile Ile Arg Cys Glu Gln Ser Ala Lys
65 70 75 80
Lys Gly Gly Gly Pro Asp Thr Trp Leu Gly Arg Ala Ala Met Xaa Xaa
85 90 95
Val Arg Leu Arg Asp Arg Arg Arg Gly Gly His Arg Gln Gly Leu Pro
100 105 110
Pro Gly Arg Asp Arg Arg Arg Val
115 120

(2) INFORMATION FOR SEQ ID NO:3782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3782:

Gly Arg Arg Phe Val Gln Phe Lys Thr Arg Arg Xaa Gly Arg Glu Ala
1 5 10 15
Arg Lys Xaa Pro Val Ser Trp Arg Pro Ser Pro Pro Ser Ala His Arg
20 25 30
Arg Arg Xaa Pro Pro Pro Arg Arg Arg Ser Val Ala Cys Pro Ala
35 40 45
Thr His Leu Arg Arg Pro Ala Arg Gly Ala Ser Ser Pro Ala Gly Pro
50 55 60
Ser Ala Ala Gly Arg Cys Pro Ser Ser Gly Ala Ser Arg Ala Arg Arg
65 70 75 80
Arg Ala Ala Gly Arg Thr His Gly Trp Ala Ala Arg Pro Trp Xaa Ala
85 90 95
Phe Ala Ser Ala Ile Ala Val Glu Val Ala Thr Gly Lys Gly Phe Leu
100 105 110
Gln Val Gly Thr Val Val Glu Tyr Glu Tyr Gln Arg Asn Ile Asp Ser
115 120 125
Ser Glu Glu Arg Arg Asn Ala Cys Val Thr Asn Ile Pro Arg Val Cys
130 135 140
Cys Gly Trp Arg Ala Glu Leu Gly Arg Gly Tyr Ser Gly Ala Glu Xaa
145 150 155 160
Gly Ala Gly Arg Val Gly Ala Arg Arg Arg Pro Arg Arg Leu Leu Pro
165 170 175
Ala Pro Val Gly Arg Arg His Ala Arg Leu Thr Ala Asp Gly Thr Pro
180 185 190

(2) INFORMATION FOR SEQ ID NO:3783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1578201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3783:

atgagtcctat	ttcagcggtc	tgcggttc	tgtattttca	tattatcgaa	accctcgctc	60
acatctccgt	ttcgacgaag	ccaaatctgt	ctgtttttat	aatcccaaaa	gtctccacct	120
aagtccacga	ctcgatacgg	caagatcgac	agagagaccg	acgcgcgcgc	agatcccaag	180
ctcaccggag	aggggggaaga	ggcgacacga	agcggcgatg	ggtttcata	tggacttcgc	240
ggagaatctg	atcctccgtc	tgatggagga	cccgacaaga	cgcgaccCag	gttcggcggg	300
agcatgtcta	caagatgaag	gagcgggtgc	agcgacacta	ggcgccgtgg	agcctccctc	360
tgcgcccCta	cggcttcggg	accttcgacc	gcttcaactc	gcagctctcc	tgggatcccc	420
agatcagcca	ggcgccgggc	Cgtcgggacc	cctacgcaga	cctcatcgcc	cgcaactctg	480
gctcgccgcc	gtcttcctga	acaaccgttc	cgatctttgc	ccagaaggtc	tacttggggc	540
atcaataaga	aactctttcc	cctcaaacgt	attgtggttc	catcctcttc	tgtctggaaa	600
atgttgatcc	caaaactacc	tattctctgt	tccagtttgg	catggaagta	taagtgtgtg	660
acttctattc	tcaagttgtt	gtctttgtat	tatgaaatgt	ttccaataat	cagcagtttt	720
tgatgtatgg	tcgtggatcc	g				

(2) INFORMATION FOR SEQ ID NO:3784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3784:

Met	Gly	Phe	Ile	Met	Asp	Phe	Ala	Glu	Asn	Leu	Ile	Leu	Arg	Leu	Met	
1			5						10					15		
Glu	Asp	Pro	Asp	Lys	Arg	Asp	Pro	Gly	Ser	Ala	Gly	Ala	Cys	Leu	Gln	
			20					25					30			
Asp	Glu	Gly	Ala	Val	Arg	Ala	His									
			35				40									

(2) INFORMATION FOR SEQ ID NO:3785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3785:

Met	Lys	Glu	Arg	Cys	Glu	Arg	Thr	Lys	Ala	Ala	Trp	Ser	Leu	Pro	Leu	
1				5					10					15		
Arg	Pro	Tyr	Gly	Phe	Trp	Thr	Phe	Asp	Arg	Phe	Asn	Ser	Gln	Leu	Ser	
			20					25					30			
Trp	Asp	Pro	Gln	Ile	Ser	Gln	Ala	Ala	Gly	Arg	Arg	Asp	Pro	Tyr	Asp	
			35				40					45				
Asp	Leu	Ile	Ala	Arg	His	Ser	Gly	Ser	Pro	Pro	Ser	Ser				
			50			55					60					

(2) INFORMATION FOR SEQ ID NO:3786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1578204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3786:

Met Leu Ser Pro Asn Tyr Pro Ile Ser Cys Ser Ser Leu Ala Trp Lys
1 5 10 15
Tyr Lys Leu Cys Thr Ser Ile Leu Lys Leu Leu Ser Leu Tyr Tyr Glu
20 25 30
Met Phe Pro Ile Ile Ser Ser Phe
35 40

(2) INFORMATION FOR SEQ ID NO:3787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..765
(D) OTHER INFORMATION: / Ceres Seq. ID 1578239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3787:

gacaagcaag aacagctgtc gatccaattg tcaattgtct tccctccaac aagctaatta 60
aggccgggtca tccctcttct agctcgtttc attatccatg gcggaggaga agcaccacca 120
ccaccacctg ttccaccaca agaaggacga ggagcaggag gagcagctcg ccgccgsgsg 180
tacgGcgagt ccgccgagta cacggaggcc acggtgacgg aggtcgtgtc cacggcgag 240
aacgagtacg acgagtacaa gaaggaggag aagcagcaca agcacaagca gcacctcgcg 300
gaggccggcg ccatGccgcg cggcgccctc gcaactctac agaagcacga ggcaagaaga 360
gaccggagac acgcgccacg ccacaagatc gaggaggagg tcgcggcgcg ggccggcgct 420
ggctccggcg gCttcgcCtt ccacgagcac caccagaaga agaaggacca caaggacgcc 480
gaggaggccg cggcgagaaa gaagcaccac ttcttcggct gattgatcct ccggtatcgt 540
cgtcccCtcc ccgtgtgCta cgcgtgcCgt gtgtgagagt gatatcgagc gccCgcgctg 600
ttgtgcgcgc gtacgtatgt atgcgctcgt gtgatgcacg aataagcgtg gctacgtaat 660
ctatcgatg tatacgtgtg tgtatgcatt tgctttgtga tgatcgtggt acgaggaccg 720
aaaaaaatgta tgcaactctg attacttac atggttagtt gtttc

(2) INFORMATION FOR SEQ ID NO:3788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..218
(D) OTHER INFORMATION: / Ceres Seq. ID 1578240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3788:

Gln Ala Arg Thr Ala Val Asp Pro Ile Val Thr Cys Ser Pro Ser Asn
1 5 10 15
Lys Leu Ile Lys Ala Gly His Pro Ser Ser Ser Ser Phe His Tyr Pro
20 25 30
Trp Arg Arg Arg Ser Thr Thr Thr Thr Cys Ser Thr Thr Arg Arg
35 40 45
Thr Arg Ser Arg Arg Ser Ser Ser Pro Ala Xaa Val Arg Arg Val Arg
50 55 60
Arg Val His Gly Gly His Gly Asp Gly Gly Arg Val His Gly Arg Glu
65 70 75 80
Arg Val Arg Arg Val Gln Glu Gly Gly Glu Ala Ala Gln Ala Gln Ala
85 90 95
Ala Pro Arg Arg Gly Arg Arg His Arg Arg Arg Arg Leu Arg Thr Leu

100 105 110
Arg Glu Ala Arg Gly Lys Glu Gly Pro Gly Ala Arg Ala Pro Pro Gln
115 120 125
Asp Arg Gly Gly Gly Arg Gly Gly Gly Gly Arg Arg Leu Arg Arg Leu
130 135 140
Arg Leu Pro Arg Ala Pro Arg Glu Glu Glu Gly Pro Gln Gly Arg Arg
145 150 155 160
Gly Gly Arg Arg Arg Glu Ala Pro Leu Leu Arg Arg Leu Ile Asp Pro
165 170 175
Pro Val Ser Ser Ser Pro Pro Arg Val Leu Arg Val Pro Cys Val Arg
180 185 190
Val Ile Ser Ser Ala Arg Arg Val Val Arg Ala Tyr Val Cys Met Arg
195 200 205
Ser Cys Asp Ala Arg Ile Ser Val Ala Thr
210 215

(2) INFORMATION FOR SEQ ID NO:3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..822
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3789:

arggtccctg	gctatcgaga	gaactcgacg	agttcatctc	catcgtttgt	gagagtttgc	60
gttgggccaag	attgtcatatc	tcacgcgtct	gcctcggtct	caggcccagg	gtgtactgaa	120
agccagctct	tgcccgcac	tacacggccc	cattttcagc	ttgcccctcc	agaaccgggt	180
cctatctgtg	gtgtgccaga	cttcaagatg	aggggaaaaga	agagtgatga	gctcgaacct	240
gtcgatgctk	gcgatgaaga	tgatgatggt	ggtgacgatg	gggacgagga	tggtgacttt	300
ggggaggagg	gtgaagagga	cgtctcagaa	ggggagggat	atgacaaccc	aaagggccaat	360
gagaccaaga	agcaaaagg	tgatcctgag	gaaaatgggt	aggaagatga	ggaagaacca	420
gaagatcagg	aggggtggcg	cgacgcacat	gatgacgacg	atgacgatga	tgagaacggg	480
gatgacgagg	acgacgacaa	tDggggatga	cgatgaggag	ggtgtagatg	aagaagacga	540
tgaccaggac	gaggatgagg	aggaagatga	tgatgaagac	tcgtccacgc	ccccaagaa	600
gaggaagaag	tgaagatctt	ctgcgcgttt	agttaccgtg	cgctgagttc	tgcttggtct	660
ttcgtcatat	cctcgcatct	caactttccc	atagagagtt	aagaaggatc	cacacgttca	720
cgagcacgtg	tgggcttgta	ggagctttat	gatttgaggc	aattagggac	aactcttatg	780
tcattgttgc	ttgcttctgt	ggagtcgaac	agatgtttcg	ct		

(2) INFORMATION FOR SEQ ID NO:3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3790:

Xaa	Val	Pro	Gly	Tyr	Arg	Glu	Asn	Ser	Thr	Ser	Ser	Pro	Ser	Phe
1				5					10				15	
Val	Arg	Val	Ser	Val	Gly	Pro	Asp	Cys	His	Thr	Gln	Arg	Pro	Ala
				20					25				30	Ser
Val	Ser	Gly	Pro	Gly	Cys	Thr	Glu	Ser	Gln	Leu	Leu	Pro	Ala	Ser
				35					40				45	Thr
Arg	Pro	His	Phe	Gln	Leu	Ala	Pro	Pro	Glu	Pro	Gly	Pro	Ile	Cys
				50				55					60	Gly

```

Val Pro Asp Phe Lys Met Arg Gly Lys Lys Ser Asp Glu Leu Glu Pro
65              70              75              80
Val Asp Ala Xaa Asp Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu
85              90              95
Asp Gly Asp Phe Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu
100             105             110
Gly Tyr Asp Asn Pro Lys Gly Asn Glu Thr Lys Lys Gln Arg Gly Asp
115             120             125
Pro Glu Glu Asn Gly Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu
130             135             140
Gly Gly Gly Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly
145             150             155             160
Asp Asp Glu Asp Asp Asp Asn Xaa Gly
165

```

(2) INFORMATION FOR SEQ ID NO:3791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3791:

```

Met Ser Ser Asn Leu Ser Met Xaa Ala Met Lys Met Met Met Val Val
1      5      10      15
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr
20     25     30
Ser Gln Lys Gly Arg Asp Met Thr Thr Gln Arg Ala Met Arg Pro Arg
35     40     45
Ser Lys Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn
50     55     60
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr
65     70     75     80
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp
85     90     95
Glu Glu Gly Val Asp Glu Glu Asp Asp Asp Gln Asp Glu Asp Glu Glu
100    105    110
Glu Asp Asp Asp Glu Asp Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys
115    120    125

```

(2) INFORMATION FOR SEQ ID NO:3792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3792:

```

Met Xaa Ala Met Lys Met Met Met Val Val Thr Met Gly Thr Arg Met
1      5      10      15
Val Thr Leu Gly Arg Arg Val Lys Arg Thr Ser Gln Lys Gly Arg Asp
20     25     30
Met Thr Thr Gln Arg Ala Met Arg Pro Arg Ser Lys Glu Val Ile Leu

```

35	40	45
Arg Lys Met Val Arg Lys Met Arg Lys Asn Gln Lys Ile Arg Arg Val		
50	55	60
Ala Ala Thr Thr Met Met Thr Thr Met Thr Met Met Arg Thr Gly Met		
65	70	75
Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp Glu Glu Gly Val Asp Glu		80
	85	90
Glu Asp Asp Asp Glu Asp Glu Asp Glu Glu Asp Asp Asp Glu Asp		95
	100	105
Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys		110
	115	120

(2) INFORMATION FOR SEQ ID NO:3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3793:

aagacagcaa	ccacatgctc	accagtgcat	gccccgaag	caaaagactt	gctggatatc	60
accaagatt	aggttaagaa	gcagctcgag	cgcgccttcc	ttccagtc	atggccgcgcg	120
ccgcttcttc	ggttaacctcc	agaggcttgg	cactccgtag	cagtacctcc	gtgggttttc	180
atcgccacgc	cgggataaat	ccggtgatca	gccccgcgtc	ttctcgtcgc	cgacgaagcc	240
ttactggtgg	atcaacgatg	aactcctcgg	gcataaacgg	tgcccttccct	cctatacaag	300
gaagtacacg	aatcccccca	gttggtctcg	gccccgccag	tcctgcagga	ggaaaacctgc	360
cgatacccaa	catgcctcca	tgggccaaagt	ggctggtcgg	cgccgcata	gtcgcgatac	420
caatctacag	gaggttcaaga	acactagaag	ataagataga	gaagaacggcg	gaggtggcga	480
tcgaggtggt	ggacacgggtg	cgggggtcgg	cgagagaagg	ggcgccgagg	tcgcgcgcgc	540
gttccccggc	aacgagagcc	tcagggaggg	ggcgtcgcgg	atcaaggcgg	tcacggatga	600
gatcgaggag	gagcccgaga	gagccgaggg	cctgatcgag	aaggttgacg	agataaagga	660
acaagttgat	tcaatcgtcg	atcccttaat	cgacaagggt	gtcaaggata	aagaaacctta	720
gagagaagga	accaaggagg	aggcaatgac	atgatgtaga	ttattgaagg	tataaagatt	780
ggttaggcgg	tgccgcgggtg	gtaaccggaa	gaaaataacct	accgcattga	aaaaaatatca	840
ctaaatataa	atataagaag	cttttcagaa	aaaaaactct	tcttcaacag	ttatgtaaga	900
caagttctta	aatttacaaa	cttcttct				

(2) INFORMATION FOR SEQ ID NO:3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3794:

Met Ala Ala Pro Ala Ser Ser Val Thr Ser Arg Gly Leu Ala Leu Arg		
1	5	10
Ser Ser Thr Ser Val Gly Phe His Arg His Arg Gly Asn Asn Pro Val		15
	20	25
Ile Ser Pro Ala Ser Ser Arg Arg Arg Ser Leu Thr Gly Gly Ser		30
	35	40
Thr Met Asn Ser Ser Gly Met Asn Gly Ala Phe Pro Pro Ile Lys Gly		45
	50	55
Ser Thr Arg Ile Pro Ala Val Gly Pro Gly Pro Ala Ser Pro Ser Gly		60
	65	70
		75
		80

Gly Asn Leu Pro Ile Pro Asn Met Pro Pro Trp Ala Lys Trp Leu Val
85 90 95
Gly Ala Ala Ile Val Ala Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu
100 105 110
Glu Asp Lys Ile Glu Lys Thr Ala Glu Val Ala Ile Glu Val Val Asp
115 120 125
Thr Val Ala Gly Ser Ala Glu Lys Val Ala Ala Arg Ser Pro Ala Arg
130 135 140
Ser Pro Ala Thr Arg Ala Ser Gly Arg Arg Arg Arg Gly Ser Arg Arg
145 150 155 160
Ser Arg Met Arg Ser Arg Arg Thr Pro Arg Glu Pro Arg Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1578257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3795:

Met Asn Ser Ser Gly Met Asn Gly Ala Phe Pro Pro Ile Lys Gly Ser
1 5 10 15
Thr Arg Ile Pro Ala Val Gly Pro Gly Pro Ala Ser Pro Ser Gly Gly
20 25 30
Asn Leu Pro Ile Pro Asn Met Pro Pro Trp Ala Lys Trp Leu Val Gly
35 40 45
Ala Ala Ile Val Ala Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu Glu
50 55 60
Asp Lys Ile Glu Lys Thr Ala Glu Val Ala Ile Glu Val Val Asp Thr
65 70 75 80
Val Ala Gly Ser Ala Glu Lys Val Ala Ala Arg Ser Pro Ala Arg Ser
85 90 95
Pro Ala Thr Arg Ala Ser Gly Arg Arg Arg Arg Gly Ser Arg Arg Ser
100 105 110
Arg Met Arg Ser Arg Arg Thr Pro Arg Glu Pro Arg Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:3796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1578258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3796:

Met Asn Gly Ala Phe Pro Pro Ile Lys Gly Ser Thr Arg Ile Pro Ala
1 5 10 15
Val Gly Pro Gly Pro Ala Ser Pro Ser Gly Gly Asn Leu Pro Ile Pro
20 25 30
Asn Met Pro Pro Trp Ala Lys Trp Leu Val Gly Ala Ala Ile Val Ala
35 40 45
Ile Pro Ile Tyr Arg Arg Phe Arg Thr Leu Glu Asp Lys Ile Glu Lys
50 55 60
Thr Ala Glu Val Ala Ile Glu Val Val Asp Thr Val Ala Gly Ser Ala

(2) INFORMATION FOR SEQ ID NO:3797:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..611
(D) OTHER INFORMATION: / Ceres Seq. ID 1578317

(X17) SEQUENCE						
atcgccgtctc	agggttttga	cgcgcgcggc	gcttggtatc	ccttaaaagc	ttggcgtctc	60
gctcgtcctc	gctcgtcgtc	tctctctctc	cttcctatgc	cgcCaggttg	ttgagaagct	120
gcgtggcgct	ctcagatacc	tctgcctctc	tgcggttcga	ggcaggttag	cgcgccacct	180
gagccgcgtc	gggcagcctc	cggatctcaa	aaagtacatc	gacaaagaac	tcagatataa	240
gctgaatgca	aaccgctgtg	tatttgccac	ctcgcgggga	tctgcaccgt	tcatgaatct	300
ggtgacgcac	aacactgtgt	aggtcaatgt	aaatgacaa	acagatattg	gaatggctgt	360
ttcaggggga	aacagctgtg	gcctatgcga	ggcactggag	cagcttgcca	gaatcaggct	420
aatccttatt	tttcagcgac	tatagtgcga	gcctagaaa	tgatgtaaat	gctatgagtg	480
aaccctgttg	tacttcggca	tgctgctttt	ccacagcaac	attgactcgc	taccagcacc	540
ctgttttcaa	tggtgaactc	attactgcct	tggcgctaac	attggcaatg	catcatcttc	600
ctctattctc	t					

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..54
(D) OTHER INFORMATION: / Ceres Seq. ID 1578318

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..80
(D) OTHER INFORMATION: / Ceres Seq. ID 1578319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3799:

Met	Ser	Arg	Ser	Gly	Gln	Pro	Pro	Asp	Leu	Lys	Lys	Tyr	Met	Asp	Lys
1			5					10						15	
Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile	Gly	Thr	Leu
			20					25					30		
Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn	Thr	Val	Glu
			35				40					45			
Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val	Ile	Arg	Gly
			50				55				60				
Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala	Lys	Ser	Gln
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:3800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3800:

Met	Asp	Lys	Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile
1				5					10					15	
Gly	Thr	Leu	Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn
			20					25					30		
Thr	Val	Glu	Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val
			35				40					45			
Ile	Arg	Gly	Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala
			50				55				60				
Lys	Ser	Gln													
65															

(2) INFORMATION FOR SEQ ID NO:3801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..826
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3801:

cccatcgatt	ttctcttgga	atcgtaacct	cagaaaagcca	aattctattc	tccggcgctc	60
aggcccccac	aagcgtcgac	tctcccgcgt	caatcggtag	ctcctagtgc	ctcggccggc	120
gtagcggcgt	cggcgcaaca	cgggtgactt	ggcgaggggc	cttggccggc	gacaaatcac	180
cactaggatg	gaaggtgagg	cagagaccgt	ggttggttct	tgtttctaac	catgtggggc	240
ctctgagagc	tactacattc	cagattacat	tctgaagcca	gGtgcccaac	aagtacttgt	300
tgatcatgcg	gcaccctgcc	ccgttgtagt	gttcatcaac	tcaagatctg	gaggcccaact	360
tggaagtagt	ttaatcaaaa	catatcgtga	gcttctcaat	gaagcacagg	tttttgatct	420
ctcaaaaag	gtctcagata	aggtattgca	tcgtttatat	gccaaacctg	aaaggctgaa	480
gatggaagga	gacattctctg	cagttcaaat	ttKggaggac	actgaggcta	attgttgtag	540
gcgggtgattg	tacagctagc	tggtctgctt	gggtagtcag	tgaccttaag	ctttccacc	600
cacctccagt	ggcaactctg	ctctctggaa	ccggaaaata	ctctcccttt	tcatttgtag	660
ggggaaagaa	gaatcctctt	actgaccaag	aggctgtaaa	atcattcctc	gggctagtaa	720
agcatgcaaa	agaaattaag	attgatagtt	ggcacatcat	tttgagagat	cagagtccag	780
aggaagggtcc	atgtgatctc	attgctccac	tagatttgcc	tcattc		

(2) INFORMATION FOR SEQ ID NO:3802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3802:

Met	Glu	Gly	Glu	Ala	Glu	Thr	Val	Val	Gly	Ser	Cys	Ser	Lys	Pro	Cys
1			5						10					15	
Gly	Pro	Leu	Glu	Asp	Tyr	Tyr	Ile	Pro	Asp	Tyr	Ile	Leu	Lys	Pro	Gly
			20					25					30		
Ala	Gln	Gln	Val	Leu	Val	Asp	His	Ala	Ala	Pro	Cys	Pro	Val	Val	Val
			35				40					45			
Phe	Ile	Asn	Ser	Arg	Ser	Gly	Gly	Gln	Leu	Gly	Ser	Ser	Leu	Ile	Lys
			50			55				60					
Thr	Tyr	Arg	Glu	Leu	Leu	Asn	Glu	Ala	Gln	Val	Phe	Asp	Leu	Ser	Lys
			65			70				75				80	
Glu	Ala	Pro	Asp	Lys	Val	Leu	His	Arg	Leu	Tyr	Ala	Asn	Leu	Glu	Arg
			85					90					95		
Leu	Lys	Met	Glu	Gly	Asp	Ile	Leu	Ala	Val	Gln	Ile	Xaa	Glu	Asp	Thr
			100				105						110		
Glu	Ala	Asn	Cys	Cys	Arg	Arg									
			115												

(2) INFORMATION FOR SEQ ID NO:3803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..648
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3803:

aagcagcagc	agcagcagtc	tccacactaa	cgaacgaact	cttgctccga	tcacgagcta	60
gctgaggtcg	acgatggcgg	ctgtgctgaa	cagcaggaag	acggcgcagg	cggtggtggc	120
cgtgctgctg	gcggcggcgc	tgctggtctc	gtccacttcg	gcggcgatca	cCtgcgggca	180
gggtggggtcg	tcgCtggcgc	cgtgcatccc	gtacgcgcagc	gggagggcca	gcgcgctccc	240
cgcgctcgtcg	tgcagcggcg	tcaagagcct	caacagcgcg	gcgcggacca	gcgcggaccg	300
ccaggcgcgCg	tgccgctgcc	tcaagagcct	cgccaacagc	gtcaagagcg	tcaacatggg	360
caccgtcgcc	accatccccg	gcaagtcgcg	cgtctccgtc	ggattcccca	tcagcatgtc	420
caccgactgc	aacaagatca	gctaagttac	gacgaccaag	ctaataagcc	taccgaacgt	480
acacgaacgt	cccgcgcgct	gcacgagtga	tgaagccagg	ggagaaataa	aataaaagcc	540
ctgtattgcc	aggagcagca	tgcatatttt	atcgatctat	atatatactg	tactgtagta	600
ctctattata	tatgtatata	tgtgtggcct	gcagtcgcag	ttgccttcg		

(2) INFORMATION FOR SEQ ID NO:3804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1578336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3804:

Met Ala Ala Val Leu Asn Ser Arg Lys Thr Ala Gln Ala Val Val Ala
1 5 10 15
Val Leu Val Ala Ala Leu Leu Ala Ser Ser Thr Ser Ala Ala Ile
20 25 30
Thr Cys Gly Gln Val Gly Ser Ser Leu Ala Pro Cys Ile Pro Tyr Ala
35 40 45
Thr Gly Arg Ala Ser Ala Leu Pro Ala Ser Cys Cys Ser Gly Val Lys
50 55 60
Ser Leu Asn Ser Ala Ala Arg Thr Ser Ala Asp Arg Gln Ala Ala Cys
65 70 75 80
Arg Cys Leu Lys Ser Leu Ala Asn Ser Val Lys Ser Val Asn Met Gly
85 90 95
Thr Val Ala Thr Ile Pro Gly Lys Cys Gly Val Ser Val Gly Phe Pro
100 105 110
Ile Ser Met Ser Thr Asp Cys Asn Lys Ile Ser
115 120

(2) INFORMATION FOR SEQ ID NO:3805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..676

(D) OTHER INFORMATION: / Ceres Seq. ID 1578352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3805:

gacacacctc ccaaaccccta cactcccggc ggcggcggcg gcggcgccasa gcggcagcag 60
catccgaaga tggtagagtt cctcaagccc ggcaaggccg ttatcctcct ccagggcCGc 120
ttcgccggca ggaaggcagtt tatcgggcgc gtggcccttg tgaactacgg ggaggactat 180
ggcgctctcg ttgtcatcgt cgatgtgtgc gaccagaaca gggcacttgt ggaatgccctc 240
gatatggtca ggtgccaggt gaacttcaag cggctctcac ttactgacat caagattgac 300
atcaaaacgtg tccccaaagaa gacagccctg atcaaggcga tggaggaagc tgatgtgaag 360
accaagtggg agaacagctc atggggcagg aagctgattg tccagaagag gagagcatcg 420
ctcaatgact ttgataggtt caaagtcatg ctggcggaaga ttaagagggg cggtgtctatc 480
aggcaagagc tcgccaaagct gaagaaggcg tccacggctt aaggagcttc tttccgtgaa 540
tgtcatgtta gagttttttg ttatgagttg gatcagcaat tcatgttgagc gttgtcaaaag 600
ccagaattac caatatgttc cctgtaaac catttcaaac tttatcaagc acgggcgtgc 660
tcaggatact tttgcc

(2) INFORMATION FOR SEQ ID NO:3806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1578353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3806:

Asp Thr Pro Pro Lys Pro Tyr Thr Pro Gly Gly Gly Gly Gly Ala
1 5 10 15
Xaa Arg Gln Gln His Pro Lys Met Val Lys Phe Leu Lys Pro Gly Lys
20 25 30
Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly Arg Lys Ala Val Ile
35 40 45
Gly Arg Val Ala Leu Val Asn Tyr Gly Glu Asp Tyr Gly Arg Leu Val

(2) INFORMATION FOR SEQ ID NO:3807:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lip

MOLECULE TYPE: peptide

(1X) NAME: (A) NAME:

(B) LOCATION: 1..150

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:3807:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:30001:
Val Lys Phe Leu Lys Pro Gly Lys Ala Val Il

(2) INFORMATION FOR SEQ ID NO:3808:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1578355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3808:

Met Val Arg Cys Gln Val Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile
1 5 10 15

Lys Ile Asp Ile Lys Arg Val Pro Lys Lys Thr Ala Leu Ile Lys Ala
20 25 30
Met Glu Glu Ala Asp Val Lys Thr Lys Trp Glu Asn Ser Ser Trp Gly
35 40 45
Lys Lys Leu Ile Val Gln Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp
50 55 60
Arg Phe Lys Val Met Leu Ala Lys Ile Lys Arg Gly Gly Ala Ile Arg
65 70 75 80
Gln Glu Leu Ala Lys Leu Lys Lys Ala Ser Thr Ala
85 90

(2) INFORMATION FOR SEQ ID NO:3809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..730

(D) OTHER INFORMATION: / Ceres Seq. ID 1578379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3809:

tagtcgctgg	agatagagcc	gagaacaagg	gcaactgacg	cggtcaccct	cgcccccaac	60
acagagagaa	ggtctgctct	ccaccgggatg	gactccccacg	gcaagcccaa	gcccgcgggt	120
tcgacgcggc	cgacgcggcc	gaagccggcg	aagccggcga	cgccggcgaa	gcccgcggacg	180
cgccgcggc	cgacgcggcc	gagccggcg	gagccggcg	ggttcattcg	cgccatcttc	240
cctttctctc	tagccgcaaa	cctctttgtc	gtagcttalg	tcctcgtgcg	ggcccaaccaa	300
aaggactcag	caaagaagga	cccaacgact	gactctgcta	ctgcaactgc	tgggaagcct	360
gctgagccag	tctctatccc	cagaaaggag	ctcccaccaa	tccttgaaga	tgaccagcgc	420
aagCtctaca	aatggatgct	ggaagagaa	cggaagatca	agccacgcaa	tgctgcccag	480
aagaagaac	togatgagga	gaagccctt	ctaaaagagt	tcactccgagc	aggatccctc	540
ccaagcttct	aaaagagatc	aagccatttg	ggtctctgtg	gtctgatgtt	cagccaagaa	600
gatgattggg	cctgattgga	ttgtgtacaa	acacagtact	gtgctatctt	gtaaaactgat	660
gtctccatga	tgtagctccc	tcgagttcaa	aggttgtgtg	gatgcgaact	agtgttgtgt	720
gcattgtgtc						

(2) INFORMATION FOR SEQ ID NO:3810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1578380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3810:

Met Asp Ser His Gly Lys Pro Lys Pro Ala Gly Ser Thr Pro Pro Thr	
1 5 10 15	
Pro Pro Lys Pro Pro Lys Pro Pro Thr Pro Pro Lys Pro Pro Thr Pro	
20 25 30	
Pro Thr Pro Thr Pro Pro Thr Pro Glu Ala Arg Lys Gly Phe Met Arg	
35 40 45	
Arg Ile Phe Pro Phe Leu Leu Ala Ala Asn Leu Phe Val Val Ala Tyr	
50 55 60	
Val Leu Val Arg Ala Asn Gln Lys Asp Ser Ala Lys Lys Asp Pro Thr	
65 70 75 80	
Thr Asp Pro Ala Thr Ala Thr Ala Gly Lys Pro Ala Glu Pro Val Ser	
85 90 95	
Ile Pro Arg Lys Glu Leu Pro Pro Ile Pro Glu Asp Asp Gln Arg Lys	
100 105 110	

Leu Tyr Lys Trp Met Leu Glu Glu Lys Arg Lys Ile Lys Pro Arg Asn
115 120 125
Ala Ala Glu Lys Lys Lys Leu Asp Glu Glu Lys Ala Leu Leu Lys Glu
130 135 140
Phe Ile Arg Ala Gly Ser Leu Pro Ser Phe
145 150

(2) INFORMATION FOR SEQ ID NO:3811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3811:

Met Arg Arg Ile Phe Pro Phe Leu Leu Ala Ala Asn Leu Phe Val Val
1 5 10 15
Ala Tyr Val Leu Val Arg Ala Asn Gln Lys Asp Ser Ala Lys Lys Asp
20 25 30
Pro Thr Thr Asp Pro Ala Thr Ala Thr Ala Gly Lys Pro Ala Glu Pro
35 40 45
Val Ser Ile Pro Arg Lys Lys Glu Leu Pro Pro Ile Pro Glu Asp Asp Gln
50 55 60
Arg Lys Leu Tyr Lys Trp Met Leu Glu Glu Lys Arg Lys Ile Lys Pro
65 70 75 80
Arg Asn Ala Ala Glu Lys Lys Lys Leu Asp Glu Glu Lys Ala Leu Leu
85 90 95
Lys Glu Phe Ile Arg Ala Gly Ser Leu Pro Ser Phe
100 105

(2) INFORMATION FOR SEQ ID NO:3812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578382
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3812:

Met Ser Ser Cys Gly Pro Thr Lys Arg Thr Gln Gln Arg Arg Thr Gln
1 5 10 15
Arg Leu Ile Leu Leu Leu Gln Leu Leu Gly Ser Leu Leu Ser Gln Ser
20 25 30
Leu Ser Pro Glu Arg Ser Ser His Gln Ser Leu Lys Met Thr Ser Ala
35 40 45
Ser Ser Thr Asn Gly Cys Trp Lys Arg Ser Gly Arg Ser Ser His Ala
50 55 60
Met Leu Pro Arg Arg Arg Asn Ser Met Arg Arg Pro Phe
65 70 75

(2) INFORMATION FOR SEQ ID NO:3813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..831

(D) OTHER INFORMATION: / Ceres Seq. ID 1578386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3813:

aaacttgtaa	agcttttcca	agaaacctag	ctagctagct	agtaagaggc	acaggccggc	60
accatgtcgc	accaccattc	ccaccacaaa	tctcattctc	acaaccgtac	ccaccaccac	120
tctcactctc	actccggang	agntggaggc	ggcggcgggc	gtggcggtgc	cggtggaggc	180
ggaggcggag	tggtctaaatg	ccactgtgat	tgctcacacc	atgatcattc	accgccaaag	240
caaccgttct	tcccgccacc	gcagctttcca	ccaccacaaa	tctttcttcc	tgcaggacca	300
ccgctccctc	cgctcgggcc	gtccccattt	ccgccaccga	tattcttcgg	acctccgcgc	360
ccgccaccgc	cgcccccgc	accgttcacg	tgcccacgac	cgccaccatg	catgtaccgg	420
agGtggtaat	ggagataaaa	gttgatatac	acgggtgtgca	tgtgtttgtg	coaaagcttc	480
tcgtaactgg	tggttcagtt	tctgtcaccc	caaataagaa	ccgagctott	ctccgatatg	540
aactatcttc	acagggttcc	ctgttcaagt	taggatggca	cgcacatcaa	tatctcgtaa	600
ggaagccctc	ggggagtctt	ctccatgtat	gggtggagtt	ttgaaagaag	tcatttatatt	660
attgctagtt	cttgttccct	actagatggt	ctcgttgatg	cgtggatttt	atacgtgtac	720
ttgttctctt	gtgctttcca	cgggccctga	tgtcgtcccg	ttgtaaccga	tgttcggttg	780
tgtttcaatg	tgtcttttgt	ttaatgatat	gttgtgtgtc	tgctttccct	c	

(2) INFORMATION FOR SEQ ID NO:3814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1578387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3814:

Met	Ser	His	His	Ser	His	His	Lys	Ser	His	Ser	His	Asn	Arg	Thr
1				5				10					15	
His	His	His	Ser	Ser	His	Ser	Gly	Xaa	Xaa	Gly	Gly	Gly	Gly	Gly
				20				25					30	
Gly	Gly	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Val	Ala	Lys	Cys	His	Cys
				35				40					45	
Asp	Cys	Ser	His	His	Asp	His	Ser	Pro	Pro	Arg	Gln	Pro	Phe	Pro
				50				55					60	
Pro	Pro	Gln	Leu	Pro	Pro	Pro	Gln	Ile	Phe	Leu	Pro	Ala	Gly	Pro
				65				70					75	
Leu	Pro	Pro	Pro	Gly	Pro	Leu	Pro	Phe	Pro	Pro	Pro	Ile	Phe	Gly
				85				90					95	
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Phe	Met	Cys	Pro	Arg
				100				105					110	
Pro	Pro	Pro	Cys	Met	Tyr	Arg	Arg	Trp						
				115				120						

(2) INFORMATION FOR SEQ ID NO:3815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3815:

Met	Ile	Ile	His	Arg	Gln	Gly	Asn	Arg	Ser	Ser	Arg	His	Arg	Phe
1				5				10					15	

His His His Lys Ser Phe Phe Leu Gln Asp His Arg Ser Leu Arg Leu
20 25 30
Gly Arg Ser His Phe Arg His Arg Tyr Ser Ser Asp Leu Arg Arg Arg
35 40 45
His Pro Arg Pro Arg His Arg Ser Cys Ala His Asp Arg His His Ala
50 55 60
Cys Thr Gly Gly Gly Asn Gly Asp Lys Ser
65 70

(2) INFORMATION FOR SEQ ID NO:3816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3816:

Met His Val Pro Glu Val Val Met Glu Ile Lys Val Asp Ile His Gly
1 5 10 15
Val His Val Phe Val Pro Lys Leu Leu Val Arg Gly Val Arg Val Ser
20 25 30
Val Thr Pro Asn Lys Asn Arg Ala Leu Leu Arg Ile Glu Leu Ser Ser
35 40 45
Gln Gly Ser Leu Phe Lys Leu Gly Trp His Ala Ser Ser Tyr Leu Gly
50 55 60
Arg Lys Pro Ser Gly Ser Leu Leu His Val Trp Val Glu Phe
65 70 75

(2) INFORMATION FOR SEQ ID NO:3817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3817:

atctcttctt tccctctctc ctccctcgc cgtcgtgtc gtccgctcc gtgctagcca 60
tggatctagg cgtctccgcgt cgacggcgtc taccgatccg cctcttgAct ggtgtcgtc 120
gccgtctctca tggctctcac cgcgcgtctcc agtgccgaag tcataccct caccgaagag 180
accttctccg acaagataaa ggagaaggac acggtgtggt ttgtgcagtt ctgcgtcccc 240
tggtgttaac actgcaagaa ccttggaaca ctatgggagg acctgggaaa gggttatgaa 300
gggtcggatg aaattgagat tgggcaagtt gactgtggtg tcagcaaac agtatgctca 360
aaggtcgata tacactccta cccaacattc aaggtgtttt atgaaggcga agaagttaga 420
aaatataaag gacttaggaa tgtggaatcg ctgaagaact tcgtgttgaa tgaagctgag 480
aaagcagggt aggcacaagct tcaagctgat tgaggcaggg gagtttcagc aagcatgtgg 540
cgtagacaag gaacaatgct gtgcAacatt gtctctatc ctgtcattta caaagccaat 600
ttacagaaaa gaaatgatct tatgaccccg taticagata ttctctctcg aaagtaactc 660
ogaatcagtt catagaagct tactccatt ccatagtttt tatcacattg acaaacctcg 720
aatcagttaa tagaagctgt actccattcg

(2) INFORMATION FOR SEQ ID NO:3818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1578395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3818:

Leu	Phe	Phe	Pro	Leu	Ser	Leu	Pro	Ser	Pro	Ser	Leu	Ser	Ser	Pro	Ser
1			5						10					15	
Val	Leu	Ala	Met	Asp	Leu	Gly	Ala	Pro	Ala	Arg	Arg	Arg	Leu	Pro	Ile
			20					25					30		
Arg	Leu	Leu	Thr	Gly	Val	Ala	Arg	Arg	Pro	His	Gly	Pro	His	Arg	Ala
			35				40					45			
Phe	Gln	Cys	Arg	Ser	His	His	Pro	His	Arg	Arg	Asp	Leu	Leu	Arg	Gln
			50				55				60				
Asp	Lys	Gly	Glu	Gly	His	Gly	Val	Val	Cys	Ala	Val	Leu	Arg	Pro	Leu
65					70					75				80	
Val															

(2) INFORMATION FOR SEQ ID NO:3819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3819:

Met	Val	Leu	Thr	Ala	Arg	Ser	Ser	Ala	Glu	Val	Ile	Thr	Leu	Thr	Glu
1			5						10					15	
Glu	Thr	Phe	Ser	Asp	Lys	Ile	Lys	Glu	Lys	Asp	Thr	Val	Trp	Phe	Val
			20					25					30		
Gln	Phe	Cys	Val	Pro	Trp	Cys	Lys	His	Cys	Lys	Asn	Leu	Gly	Thr	Leu
			35				40				45				
Trp	Glu	Asp	Leu	Gly	Lys	Val	Met	Glu	Gly	Ala	Asp	Glu	Ile	Glu	Ile
			50				55				60				
Gly	Gln	Val	Asp	Cys	Gly	Val	Ser	Lys	Pro	Val	Cys	Ser	Lys	Val	Asp
65					70					75				80	
Ile	His	Ser	Tyr	Pro	Thr	Phe	Lys	Val	Phe	Tyr	Glu	Gly	Glu	Glu	Val
			85					90					95		
Val	Lys	Tyr	Lys	Gly	Pro	Arg	Asn	Val	Glu	Ser	Leu	Lys	Asn	Phe	Val
			100				105						110		
Leu	Asn	Glu	Ala	Glu	Lys	Ala	Gly	Glu	Ala	Lys	Leu	Gln	Ala	Ala	Asp
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1578397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3820:

Met	Glu	Gly	Ala	Asp	Glu	Ile	Glu	Ile	Gly	Gln	Val	Asp	Cys	Gly	Val
1			5						10					15	
Ser	Lys	Pro	Val	Cys	Ser	Lys	Val	Asp	Ile	His	Ser	Tyr	Pro	Thr	Phe

(2) INFORMATION FOR SEQ ID NO:3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1578418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3823:

Arg	Ser	Val	Pro	Gly	Ser	Ser	Ala	Pro	Ser	Val	Arg	Pro	Pro	Pro	Arg
1			5					10						15	
Met	Ser	Asp	Glu	Ala	Arg	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Val	Val
			20					25					30		
Leu	Arg	Ala	Ser	Ser	Glu	Asp	Arg	Lys	Pro	Val	Gly	Ser	Gly	Ser	Pro
			35					40				45			
Pro	Pro	Ala	Ala	Thr	Ala	Thr	Ala	Val	Ala	His	Lys	Ile	Gln	Leu	Lys
			50				55				60				
Ser	Ala	Asp	Met	Lys	Glu	Glu	Met	Arg	Gln	Glu	Ala	Phe	Glu	Ile	Ala
65				70					75					80	
Arg	Ile	Ala	Phe	Glu	Lys	His	Ser	Met	Glu	Lys	Asp	Ile	Ala	Glu	Tyr
				85					90					95	
Ile	Lys	Lys	Glu	Phe	Asp	Lys	Asn	His	Gly	Pro	Thr	Trp	His	Cys	Ile
			100					105					110		
Val	Gly	Arg	Asn	Phe	Gly	Ser	Tyr	Val	Thr	His	Glu	Thr	Asn	Tyr	Phe
			115				120					125			
Val	Tyr	Phe	Tyr	Ile	Asp	Ser	Lys	Ala	Val	Leu	Leu	Phe	Lys	Ser	Gly
			130			135					140				

(2) INFORMATION FOR SEQ ID NO:3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1578419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3824:

Met	Ser	Asp	Glu	Ala	Arg	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Val	Val
1			5					10					15		
Leu	Arg	Ala	Ser	Ser	Glu	Asp	Arg	Lys	Pro	Val	Gly	Ser	Gly	Ser	Pro
			20					25					30		
Pro	Pro	Ala	Ala	Thr	Ala	Thr	Ala	Val	Ala	His	Lys	Ile	Gln	Leu	Lys
			35				40					45			
Ser	Ala	Asp	Met	Lys	Glu	Glu	Met	Arg	Gln	Glu	Ala	Phe	Glu	Ile	Ala
			50				55				60				
Arg	Ile	Ala	Phe	Glu	Lys	His	Ser	Met	Glu	Lys	Asp	Ile	Ala	Glu	Tyr
65				70					75					80	
Ile	Lys	Lys	Glu	Phe	Asp	Lys	Asn	His	Gly	Pro	Thr	Trp	His	Cys	Ile
			85					90					95		
Val	Gly	Arg	Asn	Phe	Gly	Ser	Tyr	Val	Thr	His	Glu	Thr	Asn	Tyr	Phe
			100					105					110		
Val	Tyr	Phe	Tyr	Ile	Asp	Ser	Lys	Ala	Val	Leu	Leu	Phe	Lys	Ser	Gly
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:3825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..855

(D) OTHER INFORMATION: / Ceres Seq. ID 1578422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3825:

```
aactcactcg tcccttccca gttccgcttc cgaatcgcgc ttcatctccc ctcttcgcag      60
agggtgcttg gagcatgtat ctgctatgcaa acaaaagtgg aaagaagaaa gtgtatgtcg      120
attatatgaa tgtccctcta ccgctatgcca tcgaagagaa ttacggtggg cgcttctttg      180
acgacgacga cgaatcttgc caagttcttc aagatcagga aatattgtat catttaattc      240
aaggaaagtaa tgggtgtgga ggtttctacc tcaaagactg gtaagcatgg ccattgcccc      300
tgccactttg ttgccataga catattcaac gggaaaaaac ttgaagatat tgttccctta      360
tcacacaact gtgatattcc gcatgtgaac cgtactgagt accagctgat tgatatatca      420
gaggatggat ttgtgagcct tcttacttca gatggcaaca ctaaggatga tcttagactc      480
ccaactgatg agactcttgt gggccagatc aagggaaggg ttgaaagcgg caaggatctt      540
Ggttgtgact gtcacgtctg ctatggggga ggagcagatc tgcgcgctga aggatgttgg      600
ccccaagtaa cttactcgcc ttggaatact gtatctcaaa acctaaatcg aaaaaagaa      660
tgtatcaagg attgctacag agacatccat ctgggttgag ctggcttttg ctatggcaaa      720
cacaaagtga gggatcgctg ggtgttgca cgtgtctgca ttactctggt ttacattctg      780
gaccctgtat tttctatggt tttatgcccc ctactgttta gtattaatta tcaataaatt      840
tgtttgggac ggttg
```

(2) INFORMATION FOR SEQ ID NO:3826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1578423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3826:

```
Leu Thr Arg Pro Leu Pro Val Pro Leu Pro Ile Cys Ala Ser Ile Ser
1           5           10           15
Leu Phe Ala Glu Val Leu Val Ser Met Tyr Leu Leu Gly Asn Lys Ser
20           25           30
Gly Lys Lys Lys Val Tyr Val Asp Tyr Met Asn Val Pro Leu Pro Tyr
35           40           45
Ala Ile Glu Glu Asn Tyr Gly Gly Arg Phe Phe Asp Asp Asp Asp
50           55           60
Leu Ala Gln Val Leu Gln Asp Gln Glu Ile Leu Tyr His Leu Ile Gln
65           70           75           80
Gly Ser Asn Gly Gly Gly Gly Phe Tyr Leu Lys Asp Trp
85           90
```

(2) INFORMATION FOR SEQ ID NO:3827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1578424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3827:

Met Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys His Gly His Ala
1 5 10 15
Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu
20 25 30
Asp Ile Val Pro Ser Ser His Asn Cys Asp Ile Pro His Val Asn Arg
35 40 45
Thr Glu Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly Phe Val Ser Leu
50 55 60
Leu Thr Ser Asp Gly Asn Thr Lys Asp Asp Leu Arg Leu Pro Thr Asp
65 70 75 80
Glu Thr Leu Val Ala Gln Ile Lys Glu Gly Phe Glu Ser Gly Lys Asp
85 90 95
Leu Gly Cys Asp Cys Pro Val Cys Tyr Gly Gly Ala Asp Leu Arg
100 105 110
Ala Glu Gly Cys Trp Pro Gln Val Thr Tyr Leu Pro Trp Asn Thr Val
115 120 125
Ser Gln Asn Leu Asn Arg Lys Lys Lys Cys Ile Lys Asp Cys Tyr Arg
130 135 140
Asp Ile His Leu Ala
145

(2) INFORMATION FOR SEQ ID NO:3828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3828:

Met Leu Ala Pro Ser Asn Leu Pro Ala Leu Glu Tyr Cys Ile Ser Lys
1 5 10 15
Pro Lys Ser Lys Lys Glu Val Tyr Gln Gly Leu Leu Gln Arg His Pro
20 25 30
Ser Gly Leu Ser Trp Leu Leu Leu Trp Gln Thr Gln Val Gln Gly Ser
35 40 45
Leu Gly Val Ala Pro Cys Leu His Tyr Leu Trp Leu His Ser Gly Pro
50 55 60
Cys Ile Phe Tyr Gly Phe Met Pro Pro Thr Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:3829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 670 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..670

(D) OTHER INFORMATION: / Ceres Seq. ID 1578443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3829:

aaccggagaa caacgcacct gtgttgcgta cgtcggtcac atgcattgca tctgcatccg 60
gagtacgcag ttctagacac agcaggcaac agactgargt agcccagcga gcgagcgagc 120
aatggcaacc ctcagcgccg cccccctcgt cgGcgcgccc gccgtcgcca ggcctgttca 180
ggctcaaggt ttgccgcagc tgagggtgag agccgagaag gcgaggtgcg gcgccgccca 240

ctcgaggcgg ccgagccagc ggcggggacgc caacaacggc gcacgtcgct cgctttctggc 300
cgtrgccacc agcgcgggtga ccacgtcgcc cgsvctggcg ctgggtggagc agcggatgtc 360
gacggagggg accgggctca gctcggggct cagcaacaac ctgctggggg ggatcctgct 420
ggcgctcttc ggcctcatct ggtccctcta caccgtctac acctccacgc tcgacgagga 480
cgacgactcc ggcctctcgc tctgaactca tccgtcgatt attcctagct actgtatatt 540
ttgttcagcc tgaccggcta gttcgatoga tctatgcatt cggttggtgca gacgaagctt 600
aagaccgtgg ttgtatgcga ccgtaattca gttgttgcatt ctcagatggt aatgataatg 660
acgagtaacg

(2) INFORMATION FOR SEQ ID NO:3830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1578444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3830:

Pro Glu Asn Asn Ala Leu Val Leu Arg Thr Ser Val Thr Cys Ile Ala
1 5 10 15
Ser Ala Ser Gly Val Ala Ser Ser Arg His Ser Arg Gln Gln Thr Xaa
20 25 30
Val Ala Gln Arg Ala Ser Glu Gln Trp Gln Pro Ser Ala Pro Pro Pro
35 40 45
Ser Ser Ala Arg Pro Pro Ser Pro Gly Arg Val Arg Leu Lys Val Cys
50 55 60
Arg Ser
65

(2) INFORMATION FOR SEQ ID NO:3831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3831:

Met Ala Thr Leu Ser Ala Ala Pro Leu Val Gln Gly Ala Ala Val Ala
1 5 10 15
Arg Pro Cys Gln Ala Gln Gly Leu Pro Gln Leu Arg Val Arg Ala Glu
20 25 30
Lys Ala Arg Cys Gly Ala Ala His Ser Arg Arg Pro Ser Gln Arg Arg
35 40 45
Asp Gly Asn Asn Gly Ala Ser Ser Ser Leu Leu Ala Xaa Ala Thr Ser
50 55 60
Ala Val Thr Thr Ser Pro Xaa Leu Ala Leu Val Asp Glu Arg Met Ser
65 70 75 80
Thr Glu Gly Thr Gly Leu Ser Leu Gly Leu Ser Asn Asn Leu Leu Gly
85 90 95
Trp Ile Leu Leu Gly Val Phe Gly Leu Ile Trp Ser Leu Tyr Thr Val
100 105 110
Tyr Thr Ser Thr Leu Asp Glu Asp Asp Asp Ser Gly Leu Ser Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:3832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1027 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1027
(D) OTHER INFORMATION: / Ceres Seq. ID 1578448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3832:

ctcaataaaa	tatgtactcg	gaatcggaag	aagctgcctt	cottttccat	cgcggaacg	60
acgcacgcgg	acgcctcctt	gttcggggtc	ctaactccgc	cgcctagagg	cctgcgcctc	120
cccctcccg	cgaaaacgga	ttctctccgg	cgtttcctgg	tcccttagtg	caagcaagga	180
caccgctcct	ctagcgagct	ccgttctgaa	gcggcaagaa	agatgattaa	tcttttcaaa	240
ataaagggtc	aaaagaagaa	ggaggcagca	agtctgctgg	aaaggccctt	gttaagaaac	300
agttctgctg	ggagctccgt	cttcataaag	atattagtga	gctcaacctg	cogaagacca	360
cgtcaatttc	ttttcccaat	ggcaaggatg	atctgatgaa	ttttgagacc	accatccgac	420
ctgatgaagg	atattacatg	ggaggcactt	tctgtttcac	ctttcaagtg	tcccatcttt	480
atcctcatga	tcctccgaag	Gtcaaatgca	agaccaagGt	gtaccatcca	aattattgat	540
tggaaggcaa	tgtatgtctg	aacattctgc	gcgaagatgt	gaagcctggt	ctcaacatca	600
acactgttat	ttatggcctg	aatcttcttt	ttacgcgaacc	aaacgcagag	gatcctctga	660
accacgaagc	tgcagttgtc	cttcgtgaca	atccaaagat	gtttgaggca	aatgtgagaa	720
gagccatggc	tggaggctac	gtcggccaac	actattttcca	aagatgtgct	tgacttgatg	780
tgggtgtggc	ttgaaaacga	tcaacagagc	ccctcccccct	gtatcagcac	cagcgcgccc	840
agcttttgtt	gcgggaagta	cttctgggaag	caaaatccaa	accgttcatg	gtgtgatcat	900
gtgatgcatt	tgtttgcocg	ccctttgtgat	gtgtggtata	gtggtgtgtc	ataatgacat	960
ggaaatgctt	ctctaaactgt	atcattcatt	ccataaatcc	taaaacgagga	atgggaagtg	1020
gattgtt						

(2) INFORMATION FOR SEQ ID NO:3833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..74
(D) OTHER INFORMATION: / Ceres Seq. ID 1578449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3833:

Ser	Ile	Lys	Tyr	Val	Leu	Gly	Ile	Gly	Arg	Ser	Cys	Leu	Pro	Phe	Pro
1			5						10					15	
Ser	Ala	Glu	Arg	Arg	Thr	Arg	Thr	Pro	Pro	Cys	Ser	Gly	Ser	Tyr	Ser
			20					25					30		
Arg	Arg	Leu	Glu	Ala	Ser	Pro	Ser	Pro	Leu	Arg	Arg	Lys	Pro	Ile	Leu
			35				40					45			
Ser	Gly	Val	Ser	Trp	Ser	Leu	Ser	Ala	Ser	Lys	Asp	Thr	Ala	Pro	Leu
			50				55				60				
Ala	Ser	Ser	Val	Leu	Lys	Arg	Gln	Glu	Arg						
			65				70								

(2) INFORMATION FOR SEQ ID NO:3834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1578450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3834:

Met Asn Phe Glu Thr Thr Ile Arg Pro Asp Glu Gly Tyr Tyr Met Gly
1 5 10 15
Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro His Asp
20 25 30
Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn Ile Asp
35 40 45
Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp Lys Pro
50 55 60
Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu Phe Thr
65 70 75 80
Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val Val Leu
85 90 95
Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala Met Ala
100 105 110
Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala
115 120 125

(2) INFORMATION FOR SEQ ID NO:3835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3835:

Met Gly Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro
1 5 10 15
His Asp Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn
20 25 30
Ile Asp Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp
35 40 45
Lys Pro Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu
50 55 60
Phe Thr Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val
65 70 75 80
Val Leu Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala
85 90 95
Met Ala Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:3836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3836:

argccatggc tcgagcgccg ccttgagctcc tgcccccagg atgacgatga tccccctcgc 60
cggttcacc gccctatctg ccgcgcggcct cctgctcact ttctctcctc tctgctgca 120
aactcaagga ggagccagaa gcagcggaga ggagcggtag gtgccggtgc gcagggtggt 180
gtaccggtcc atgacaccgg crgcggcgag tgcrgcgagc acggcagagg cagcggcagc 240
gncggcatcg taagagccgt tcgaggtgtg cgaggggtgc cggtgCtgcc cgccgtcgtc 300
gtcgtcgtcc aacggcagca gcagctcgct ggacacgagc tgcgtCtgcc ccatcgactg 360
cgacctcccc ggcaagccCt tcggcacctg cgccttcacc ccgcaaacct gcggctcggg 420

```

cgggcgccagc agcaactgca ccccccctgt cctgatgatg actcctcttt cctgcaactt 480
ggctacttctt totgatcatc ccacgtgtctt acgttaacgtt acgattagat cgcagattag 540
atgactcacg tcaactactc catcatgatg gatagattat ccagttaatt ccagcttagc 600
gttctgcgtg aagttaataa tacaatgaat aataatgtgt gttcgtttca gagattgtga 660
ctgcagttgg ttccatgcac tttcagagtc ggcggcttct gttggcttga caactgttac 720
tgtcagggtc ggcggcctaa cctgttgtcg tcgtatacct actgtatgtt aggtatagat 780
tgaacatta ttttatactg tatgactatt aaaaactat aaagcaatac actcattat 840
tattgcc

```

(2) INFORMATION FOR SEQ ID NO:3837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3837:

```

Xaa Pro Trp Leu Asp Ala Ala Leu Glu Ser Cys Pro Gln Asp Asp Asp
1      5      10      15
Asp Pro Pro Arg Arg Leu His Arg Pro Ile Cys Arg Arg Pro Pro Ala
20     25     30
His Leu Leu Leu Leu Pro Ala Ala Asn Ser Arg Arg Ser Gln Lys Gln
35     40     45
Arg Gly Gly Ala Val Arg Ala Gly Ala Gln Gly Gly Val Pro Val His
50     55     60
Asp Thr Gly Xaa Gly Glu Cys Xaa Asp Asp Gly Arg Gly Ser Gly Ser
65     70     75     80
Xaa Gly Ile Val Arg Ala Val Arg Gly Val Arg Gly Val Pro Val Leu
85     90     95
Arg Ala Val Val Val Val Val Gln Arg Gln Gln Gln Leu Arg Gly His
100    105    110
Glu Leu Leu Leu Arg His Arg Leu Arg Pro Pro Arg Gln Ala Leu Arg
115    120    125
His Leu Arg Leu His Pro Ala Asn Leu Arg Leu Arg Arg Gln Gln
130    135    140
Gln Leu His Pro Pro Arg Pro Asp Asp Asp Ser Ser Phe Leu Gln Leu
145    150    155    160
Gly Tyr Phe Phe Trp Ile Ile His Arg Leu Thr Leu Arg Tyr Asp
165    170    175

```

(2) INFORMATION FOR SEQ ID NO:3838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1578454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3838:

```

Xaa His Gly Ser Thr Pro Pro Leu Ser Pro Ala Pro Lys Met Thr Met
1      5      10      15
Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly Leu Leu Leu
20     25     30
Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala Arg Ser Ser
35     40     45
Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr Arg Ser Met

```

50 55 60
Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala Ala Ala Ala
65 70 75 80
Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys Arg Cys Cys
85 90 95
Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys Val Asp Thr
100 105 110
Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys Pro Phe Gly
115 120 125
Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly Ala Ser Ser
130 135 140
Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser Cys Asn Leu
145 150 155 160
Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val Thr Ile Arg
165 170 175
Ser Gln Ile Arg
180

(2) INFORMATION FOR SEQ ID NO:3839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3839:

Met Thr Met Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly
1 5 10 15
Leu Leu Leu Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala
20 25 30
Arg Ser Ser Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr
35 40 45
Arg Ser Met Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala
50 55 60
Ala Ala Ala Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys
65 70 75 80
Arg Cys Cys Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys
85 90 95
Val Asp Thr Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys
100 105 110
Pro Phe Gly Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly
115 120 125
Ala Ser Ser Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser
130 135 140
Cys Asn Leu Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val
145 150 155 160
Thr Ile Arg Ser Gln Ile Arg
165

(2) INFORMATION FOR SEQ ID NO:3840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954

(D) OTHER INFORMATION: / Ceres Seq. ID 1578464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3840:

aaacatactc	cgtttccgaa	tccgttccac	cattgcctat	tgccccatcc	tccccgctag	60
gtttttgccag	catggccgcg	gccgccgcgc	ggaggctcct	ctccccgcgc	gcctcctcgt	120
cctccctctc	cgcgctctct	cgctcgccgg	ctgtccccga	gcagtcgctg	gtgttgcgcg	180
cggctgttgt	cgcggcgccg	tcccgcctcg	gcttcacgag	cgggatggcg	cggcgccctg	240
gcggggacg	ctacgtctcg	acgcggtctg	gcgcggcgcg	ggaccgcgcg	cmcatggaca	300
cggagatg	gccgctgttc	cccggtgcg	actacgagca	ttggctcatc	gtgatggaca	360
agccccgcg	ggaggcgccg	agCaagcagc	agatgattga	ctgtcatcatc	cagaccctcg	420
ccaaggtcct	tggaagcgag	gaggaggcga	agaagaagat	ctacaacgctc	tcgtgcgagc	480
gctacttcg	gtttgggtgc	gagatcgatg	aggagacatc	taacaagctc	gaggggctcc	540
ctggTgtgtc	tcctttgtct	cccgattcg	tatgttgatg	ctgaatacaa	ggactacgga	600
gctgaactct	tcgtcaacg	tgagattgtt	cagaggaccc	ccgagaggca	gaggagggtg	660
gagcccgctg	cacagagggc	agcagacagg	ccgaggtaca	atgacagaac	ccgtacgcac	720
gcaggagggg	gaaccagcga	tgaaacttgc	gataaaaata	taaaaaatac	cacagcaaca	780
agtcacaggt	ggtttcagct	ctggaattca	aggatcacgc	agtatcgctc	gtattaaatt	840
ggcaattcca	ctttacgtgc	agtcctagag	atcgcttcta	tggtctcagc	ttggacgtat	900
gtgattctgt	aattacagct	acttggagat	ttggaaggac	ctggcttgca	acgt	

(2) INFORMATION FOR SEQ ID NO:3841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1578465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3841:

Asn	Ile	Leu	Arg	Phe	Arg	Ile	Arg	Ser	Thr	Ile	Ala	Tyr	Cys	Pro	Ile	
1		5						10					15			
Leu	Pro	Ala	Arg	Phe	Cys	Gln	His	Gly	Arg	Arg	Arg	Arg	Pro	Glu	Ala	
		20						25					30			
Pro	Leu	Pro	Pro	Arg	Leu	Leu	Val	Leu	Pro	Leu	Arg	Ala	Pro	Pro	Ser	
		35					40					45				
Arg	Arg	Cys	Pro	Gly	Ala	Val	Ala	Gly	Val	Ala	Pro	Gly	Cys	Cys	Arg	
		50				55				60						
Gly	Gly	Leu	Pro	Pro	Arg	Leu	Pro	Ala	Arg	Asp	Gly	Ala	Ala	Ala	Trp	
		65			70				75				80			
Arg	Gly	Arg	Leu	Arg	Leu	Asp	Ala	Val	Trp	Arg	Gly	Arg	Gly	Pro	Arg	
		85					90					95				
Xaa	His	Gly	His	Gly	Asp	Gly	Ala	Ala	Val	Pro	Arg	Val	Arg	Leu	Arg	
		100					105					110				
Ala	Leu	Ala	His	Arg	Asp	Gly	Gln	Ala	Arg	Arg	Gly	Gly	Arg	Gln	Gln	
		115					120					125				
Ala	Ala	Asp	Asp													
		130														

(2) INFORMATION FOR SEQ ID NO:3842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1578466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3842:

Thr Thr Ser Val Ser Glu Ser Val Pro Pro Leu Pro Ile Ala Pro Ser

1	5	10	15
Ser Pro Leu Gly Phe Ala	Ser Met Ala Ala Ala Ala Arg	Leu	Arg Leu
20	25	30	
Leu Ser Arg Arg Ala Ser Ser Ser Ser Leu Ser Ala Leu Leu Arg Arg	40	45	
35	50	55	
Gly Ala Val Pro Glu Gln Ser Leu Val Leu Arg Pro Ala Val Val Ala	60		
65	70	75	
Ala Ala Ser Arg Leu Gly Phe Gln Arg Gly Met Ala Arg Arg Pro Gly	80		
Gly Asp Gly Tyr Val Ser Thr Arg Ser Gly Ala Gly Gly Asp Arg Ala	90	95	
100	105	110	
Xaa Met Ala Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu			
115	120	125	
His Trp Leu Ile Val Met Asp Lys Pro Gly Gly Glu Gly Ala Ser Lys			
130	135	140	
Gln Gln Met Ile Asp Cys Tyr Ile Gln Thr Leu Ala Lys Val Leu Gly			
145	150	155	
Ser Glu Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser Cys Glu Arg			
160	165	170	
Tyr Phe Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Asn Lys Leu			
175	180	185	
Glu Gly Leu Pro Gly Cys Ser Leu Cys Ala Pro Gly Phe Val Cys			
		190	

(2) INFORMATION FOR SEQ ID NO:3843:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1578467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3843:

Met Ala Ala Ala Ala Ala Arg Arg Leu Leu Ser Arg Arg Ala Ser Ser	5	10	15
1	20	25	30
Ser Ser Leu Ser Ala Leu Leu Arg Arg Gly Ala Val Pro Glu Gln Ser			
35	40	45	
Leu Val Leu Arg Pro Ala Val Val Ala Ala Ala Ser Arg Leu Gly Phe			
50	55	60	
Gln Arg Gly Met Ala Arg Arg Pro Gly Gly Asp Gly Tyr Val Ser Thr			
65	70	75	
Arg Ser Gly Ala Gly Gly Asp Arg Ala Xaa Met Ala Thr Glu Met Ala			
80	85	90	
Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp Leu Ile Val Met Asp			
95	100	105	
Lys Pro Gly Gly Glu Gly Ala Ser Lys Gln Gln Met Ile Asp Cys Tyr			
110	115	120	
Ile Gln Thr Leu Ala Lys Val Leu Gly Ser Glu Glu Glu Ala Lys Lys			
125	130	135	
Lys Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe Gly Phe Gly Cys Glu			
140	145	150	
Ile Asp Glu Glu Thr Ser Asn Lys Leu Glu Gly Leu Pro Gly Cys Ser			
155	160		
Leu Cys Ala Pro Gly Phe Val Cys			
165			

(2) INFORMATION FOR SEQ ID NO:3844:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..714
(D) OTHER INFORMATION: / Ceres Seq. ID 1578468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3844:

acatcccgat	ccttctctcg	gcgcccggt	ggtcacgtga	ctcatccccc	tgtgctctcc	60
tctcgtggcc	ttgtttcccg	gcggcgacgg	ctggtcgagc	ggcgccgccc	ttggctaggt	120
cttcgctggg	tccttccccc	gcgacgagcg	tccatctggg	gtcgactgaa	ctgagcaggc	180
agttaggaag	gacactatgt	tgttctcttc	ctacttcCaa	ggagctgggt	gggaaggagg	240
tgacagtggg	gctcaagaat	gaactggcga	tcgcggggac	gctccactcg	gttgaccagt	300
acctcaacat	caagctcgag	aacacccgcg	tagtcgacca	ggacaagtat	ccccacatgc	360
tttcagtgcg	gaactgcttc	atcaggggct	cggtggtgcg	gtacgtgctg	ctccccgaag	420
acggcgtgga	catcgacatc	ctccacgacg	ccaccaggag	ggaggcgcg	ggaggctgat	480
cctgatggcg	accgcctccc	tcacctgctg	gctgctgctt	catccccgat	tgtacgaagc	540
atgcatgtac	gggtgtgtgt	agacagatgc	cccagtttag	ttctttgggt	gttgcctgac	600
atagatatcc	caggttggat	gatgacctga	atcacctgat	atattattgt	catatcatat	660
gcaatggtct	tgcatggggt	tgctatatata	ttaccatata	gtattatcac	atcg	

(2) INFORMATION FOR SEQ ID NO:3845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1578469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3845:

Thr	Ser	Arg	Ser	Phe	Ser	Arg	Arg	Pro	Val	Gly	His	Val	Thr	His	Pro
1			5						10				15		
Pro	Val	Leu	Ser	Ser	Arg	Gly	Leu	Val	Ser	Trp	Arg	Arg	Arg	Leu	Val
			20					25					30		
Glu	Arg	Arg	Arg	Pro	Trp	Leu	Gly	Leu	Arg	Trp	Val	Leu	Pro	Arg	Arg
			35					40					45		
Arg	Ala	Ser	Ile	Trp	Gly	Arg	Leu	Asn							
			50					55							

(2) INFORMATION FOR SEQ ID NO:3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1578470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3846:

Ile	Pro	Ile	Leu	Leu	Ser	Ala	Ala	Arg	Trp	Ser	Arg	Asp	Ser	Ser	Pro
1			5						10				15		
Cys	Ala	Leu	Leu	Ser	Trp	Pro	Cys	Phe	Leu	Ala	Ala	Thr	Ala	Gly	Arg
			20						25				30		
Ala	Ala	Pro	Pro	Leu	Ala	Arg	Ser	Ser	Leu	Gly	Pro	Ser	Pro	Ala	Thr
			35						40				45		
Ser	Val	His	Leu	Gly	Ser	Thr	Glu	Leu	Ser	Arg	Gln				
			50						55				60		

(2) INFORMATION FOR SEQ ID NO:3847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1578471
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3847:
Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr
1 5 10 15
Val Leu Leu Pro Gln Asp Gly Val Asp Ile Asp Ile Leu His Asp Ala
20 25 30
Thr Arg Arg Glu Ala Arg Gly Gly
35 40

(2) INFORMATION FOR SEQ ID NO:3848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 905 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..905
(D) OTHER INFORMATION: / Ceres Seq. ID 1578472
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3848:
aaacagatatac acacacactc gggtaaaagt atctcgagct agctagctgc tghtaascgtt 60
gccatggcca aaatgggtgt gctctgcgtg ctctctctct tctctctgat gcccttgggc 120
tccttagccc tgaagcagga cttctgcgtc gccgacctga cctgcagcga cagcgccggc 180
gggtaccctg gcaagtcacg cgtcaaccgc aacgacttct acttccacgg cctggccggc 240
caggggcaaaa taaacccaat catcaaggcc gccgtgacct cggtctctgt gggccagttc 300
ccggggcgta acgccttggc atctctgcgg ccaggctcga catcgagggt ggcggcgctg 360
tgccgctgca caccaccctg gccggctcag agctctctct cgtgacctga ggcaccgntc 420
gccgcggcgt tcattcagct cggctccaac accgtctaca ccaagacgct gtacgcggcg 480
gacatcatgg tggttcccca gggcctgctc cactaccagt acaacgcggc canccggcgc 540
tgccgtgggc ctctctgctc tcagcagccc caaccccgcc ctgcagatca ccgactttgc 600
gctctttggc aacaacctcc cgtccgcccgt cgtggagaag gtcaccttct tggacgacgc 660
gcaggtgaag aagctcaaga gtgtgctcgg cggcagcggt taacttgttt ttcgagacaa 720
tacagtgcag gctgggtatg catcgctcgc gtcgtcgtct tgggtccgtg tcatcgaaatg 780
gaacgcgtgt gcttgcgtgt cgtacgctgc gtgcacctgt cgtcgcgtgt caaagtactc 840
gtggtctatt tcattctacc cttatttatt catctacttt tcattcaggg atgtattcag 900
ttccc

(2) INFORMATION FOR SEQ ID NO:3849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1578473
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3849:
Met Ala Lys Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met
1 5 10 15
Pro Leu Ala Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu
20 25 30

Thr Cys Ser Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr
35 40 45
Ala Asn Asp Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn
50 55 60
Pro Leu Ile Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro
65 70 75 80
Gly Val Asn Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp
85 90 95
Ala Ala Ser Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser
100 105 110
Ser

(2) INFORMATION FOR SEQ ID NO:3850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3850:

Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met Pro Leu Ala
1 5 10 15
Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu Thr Cys Ser
20 25 30
Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr Ala Asn Asp
35 40 45
Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn Pro Leu Ile
50 55 60
Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro Gly Val Asn
65 70 75 80
Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp Ala Ala Ser
85 90 95
Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:3851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3851:

Met Val Phe Pro Gln Gly Leu Leu His Tyr Gln Tyr Asn Ala Gly Xaa
1 5 10 15
Arg Arg Cys Arg Gly Pro Arg Arg Leu Gln Gln Pro Gln Pro Arg Pro
20 25 30
Ala Asp His Arg Leu Cys Ala Leu Cys Gln Gln Pro Pro Val Arg Arg
35 40 45
Arg Gly Glu Gly His Leu Leu Gly Arg Arg Ala Gly Glu Glu Ala Gln
50 55 60
Glu Cys Ala Arg Arg Gln Arg Leu Thr Cys Phe Ser Arg Gln Tyr Ser
65 70 75 80
Ala Gly Trp Val Cys Ile Val Ala Val Val Leu Val Arg Arg His

85 90 95
Arg Met Glu Arg Val Cys Leu Leu His Ala Cys Val His Leu Ser
100 105 110
Ser Arg Val Lys Val Leu Val Val Tyr Phe Ile Leu Pro Leu Phe Ile
115 120 125
His Leu Leu Phe Ile Gln Gly Cys Ile Gln Phe
130 135

(2) INFORMATION FOR SEQ ID NO:3852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3852:

aaatcgaatc	gagcccatcc	atctccattt	cmrcmgchgc	mgccgcccgag	agaccccaac	60
cccacccatc	caccaccatg	tndmcmgccc	tccacaccct	arcmccegcc	ttgcgcaggg	120
ctaccgccgc	cgccgcgggg	gcccctgcGg	cgccgcgctc	ctctgcagcc	cgccgcggcc	180
cgctctcttc	ggcggtctacg	gcggtggcgg	cgccgcgtac	gggtggcgcg	gcggctacgg	240
tgggtggtgc	ggcggtctacg	gcggtggcaa	ccgtggcgcg	ggctacggca	actccagcgg	300
gaactggagg	aactgagcgg	tggggcccgcc	gcggccaagt	tatccctgttc	gctaccgtgt	360
tgtttaccct	agtcacagagg	gtttatcttc	gttcgtctca	tgtttgtgtg	tgcccatctg	420
tgtttttgat	tgcaaggtcg	ctttgtgtca	gttgtagtg	ctgtgttcac	ctccggtccc	480
agcagaccca	tgcataccac	agcatggact	cgcatcgat	ggatgctgtt	acccccgtca	540
ggctttatcc	taagttaatc	ttcaaggaaa	aaatggtgct	tcttgggtgct		

(2) INFORMATION FOR SEQ ID NO:3853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3853:

Lys	Ser	Asn	Arg	Ala	His	Pro	Ser	Pro	Phe	Xaa	Xaa	Xaa	Xaa	Pro	Pro
1		5							10					15	
Arg	Asp	Pro	Asn	Pro	Thr	His	Pro	Pro	Pro	Cys	Xaa	Xaa	Ala	Ser	Thr
		20							25					30	
Pro	Xaa	Xaa	Pro	Pro	Cys	Ala	Gly	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Pro
		35					40						45		
Leu	Arg	Arg	Pro	Pro	Pro	Leu	Gln	Pro	Ala	Pro	Pro	Arg	Ser	Pro	Arg
		50				55				60					
Arg	Leu	Arg	Arg	Trp	Arg	Arg	Arg	Leu	Arg	Trp	Arg	Arg	Arg	Leu	Arg
		65				70				75				80	
Trp	Trp	Trp	Arg	Arg	Leu	Arg	Arg	Trp	Gln	Pro	Trp	Arg	Arg	Leu	Arg
			85						90					95	
Gln	Leu	Arg	Arg	Glu	Leu	Glu	Leu	Ser	Gly	Gly	Ala	Arg	Ala	Ala	
			100				105						110		
Lys	Leu	Ser	Cys	Ser	Leu	Pro	Cys	Cys	Leu	Pro					
			115				120								

(2) INFORMATION FOR SEQ ID NO:3854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..151
(D) OTHER INFORMATION: / Ceres Seq. ID 1578481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3854:

```
Ile Glu Ser Ser Pro Ser Ile Ser Ile Xaa Xaa Xaa Xaa Ala Ala Glu
1      5      10      15
Arg Pro Gln Pro His Pro Ser Thr Thr Met Xaa Xaa Xaa Leu His Thr
20      25      30
Leu Xaa Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala Pro
35      40      45
Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser Ala
50      55      60
Ala Thr Ala Val Ala Ala Ala Thr Val Ala Ala Ala Thr Val
65      70      75      80
Val Val Ala Ala Ala Thr Ala Val Ala Thr Val Ala Ala Thr Ala
85      90      95
Thr Pro Thr Gly Thr Gly Gly Thr Glu Arg Trp Gly Pro Arg Gly Gln
100      105      110
Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln Arg Val Tyr
115      120      125
Leu Arg Ser Ser His Val Cys Cys Pro Ser Val Phe Leu Ile Ala
130      135      140
Arg Ser Leu Cys Val Ser Cys
145      150
```

(2) INFORMATION FOR SEQ ID NO:3855:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1578482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3855:

```
Met Xaa Xaa Xaa Xaa Leu His Thr Leu Xaa Pro Ala Leu Arg Arg Ala Thr
1      5      10      15
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ser Ala Ala Arg
20      25      30
Ala Ala Pro Leu Ser Ser Ala Ala Thr Ala Val Ala Ala Ala Thr
35      40      45
Val Ala Ala Ala Ala Thr Val Val Ala Ala Thr Ala Val Ala
50      55      60
Thr Val Ala Ala Ala Thr Ala Thr Pro Thr Gly Thr Gly Thr Glu
65      70      75      80
Arg Trp Gly Pro Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe
85      90      95
Thr Leu Val Gln Arg Val Tyr Leu Arg Ser Ser His Val Cys Cys Cys
100      105      110
Pro Ser Val Phe Leu Ile Ala Arg Ser Leu Cys Val Ser Cys
115      120      125
```

(2) INFORMATION FOR SEQ ID NO:3856:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..747
(D) OTHER INFORMATION: / Ceres Seq. ID 1578486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3856:

gacatatcgt	tcatacggtc	cagtcctctc	ccgggatctc	ctccggctat	aaatttcggg	60
cccccaattca	ccaatccag	atgcgcaaac	atcgaatcgt	ctcgctagtg	gctgccctac	120
tcgtgtcgtct	tgccctcgcc	gcggtttcct	ccacgcgcag	cGmacaaaag	gagtcocgcyg	180
ctgacaacgc	cgggatgttg	gcaggcgcca	tcaaggacgt	gcgcgcgaac	gagaacgacc	240
tccagctcca	ggagctcgcg	cgCttcgccg	tcaatgagca	caaccaaaag	gccaatgctc	300
ttctgggggtt	cgagaagcgt	gtgaaggcca	agacacaagt	ggttgtctggc	acgatgtact	360
atctcactat	tgaagtgaag	gattgcgaag	tcaataagct	ctatgaagct	aaggctotggg	420
agaagcccatg	ggagaacttc	aagcagctgc	aggaattcaa	gcctgttgaa	gagggtGcta	480
gcgcctaagg	atctgtcgtc	tcctgtgtca	atttgctgcc	tgaagcgcaa	aactaagttg	540
cagaataaagg	agctgcttcg	gaacatgcca	gagcatgcac	cctcgcgat	tttataaaaa	600
tcagtgtctt	taatgtata	tcttgaaatg	ccgtgccatg	tgtataaagt	aatatcatga	660
ataacagttg	ctattatggg	ttctaaatgt	gtattaacag	ccatccatg	cagagttctc	720
atattacttt	gctgaagctt	ttgttgg				

(2) INFORMATION FOR SEQ ID NO:3857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1578487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3857:

His	Ile	Val	His	Arg	Ile	Gln	Ser	Ser	Pro	Gly	Ile	Ser	Ser	Gly	Tyr	
1			5						10					15		
Lys	Phe	Pro	Ala	Pro	Ile	His	Pro	Ile	Gln	Met	Arg	Lys	His	Arg	Ile	
			20						25					30		
Val	Ser	Leu	Val	Ala	Ala	Leu	Leu	Val	Leu	Leu	Ala	Leu	Ala	Ala	Val	
			35						40					45		
Ser	Ser	Thr	Arg	Ser	Xaa	Gln	Lys	Glu	Ser	Ala	Ala	Asp	Asn	Ala	Gly	
			50				55					60				
Met	Leu	Ala	Gly	Gly	Ile	Lys	Asp	Val	Pro	Ala	Asn	Glu	Asn	Asp	Leu	
			65				70				75			80		
Gln	Leu	Gln	Glu	Leu	Ala	Arg	Phe	Ala	Val	Asn	Glu	His	Asn	Gln	Lys	
			85						90					95		
Ala	Asn	Ala	Leu	Gly	Phe	Glu	Lys	Leu	Val	Lys	Ala	Lys	Thr	Gln		
			100				105						110			
Val	Val	Ala	Gly	Thr	Met	Tyr	Tyr	Leu	Thr	Ile	Glu	Val	Lys	Asp	Gly	
			115				120					125				
Glu	Val	Asn	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Trp	Glu	Lys	Pro	Trp	Glu	
			130				135					140				
Asn	Phe	Lys	Gln	Leu	Gln	Glu	Phe	Lys	Pro	Val	Glu	Glu	Gly	Ala	Ser	
			145			150				155				160		
Ala																

(2) INFORMATION FOR SEQ ID NO:3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3858:

Met Arg Lys His Arg Ile Val Ser Leu Val Ala Ala Leu Leu Val Leu
1 5 10 15
Leu Ala Leu Ala Ala Val Ser Ser Thr Arg Ser Xaa Gln Lys Glu Ser
20 25 30
Ala Ala Asp Asn Ala Gly Met Leu Ala Gly Gly Ile Lys Asp Val Pro
35 40 45
Ala Asn Glu Asn Asp Leu Gln Leu Gln Glu Leu Ala Arg Phe Ala Val
50 55 60
Asn Glu His Asn Gln Lys Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu
65 70 75 80
Val Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr
85 90 95
Ile Glu Val Lys Asp Gly Glu Val Asn Lys Leu Tyr Glu Ala Lys Val
100 105 110
Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln Leu Gln Glu Phe Lys Pro
115 120 125
Val Glu Glu Gly Ala Ser Ala
130 135

(2) INFORMATION FOR SEQ ID NO:3859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3859:

Met Leu Ala Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu
1 5 10 15
Gln Leu Gln Glu Leu Ala Arg Phe Ala Val Asn Glu His Asn Gln Lys
20 25 30
Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln
35 40 45
Val Val Ala Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly
50 55 60
Glu Val Asn Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu
65 70 75 80
Asn Phe Lys Gln Leu Gln Glu Phe Lys Pro Val Glu Glu Gly Ala Ser
85 90 95
Ala

(2) INFORMATION FOR SEQ ID NO:3860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..781
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3860:

```

agacagcctc cccattcctc agattcagat cagatcgtag cagccaagga ttccgcgcctc    60
cgggggtgcc atgaagctga agctcctctc tcctctcctt ctctctcctg ccttctttgc    120
cacccggcgg tacgcggcgt cggcgctcgc gtcgcgcgcg gcggcgctcg tcaggggcgc    180
ggcgcccccg tcgcagtcgg agttggagtc ggaccgggag aaccagtcgc tgtacacggc    240
gtacgtgcgg acgggggtcca tctggaaggc cggcacggac tcgaccatcg gcgtgacgct    300
gotggggcgc cgaaggcgcg ggcacccgga tcggggacct ggccgggtgg ggcggcctca    360
tggggcgccg ccaagactac tacgagcgcg gcaacctgga catcttcagc ggccgggggc    420
cctgcctagg ccaGGGcgcc ctgcGvcctg aacctcactc ccgacggcac cggcgcgcac    480
cacggctggt actgcaacta cctcgaggcc acggtcacgg ggcgccacct cgggtgcgcg    540
cagcagctct tcaccgtcga gcaagtggctc gccacgcagc cgtgcgcccta ccgctgttac    600
gcggtcgtcg acaagtgcga gacgaagsgg caggagncgc gacgctgcgc ggccggcgag    660
gccgaggcca cgtgaccgcg gctctaggta cgaccagtag taaatcatcg acagagcta    720
gctcctgcct ctgctgtgtg taattactgt atgtgagtga ccgatcccat cggattgcgt    780

```

(2) INFORMATION FOR SEQ ID NO:3861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3861:

```

Arg Gln Pro Pro His Ser Ser Asp Ser Asp Gln Ile Val Ala Ala Lys
1      5      10      15
Asp Ser Ala Leu Arg Gly Cys His Glu Ala Glu Ala Pro Leu Ser Leu
      20      25      30
Pro Ser Pro Pro Arg Leu Leu Cys His Arg Gly Val Arg Gly Val Gly
      35      40      45
Val Gly Val Ala Arg Gly Gly Arg Arg Gln Gly Arg Gly Arg Pro Val
      50      55      60
Ala Val Gly Val Gly Val Gly Pro Gly Glu Pro Val Arg Val His Gly
      65      70      75      80
Val Arg Ala Asp Gly Val His Leu Glu Gly Arg His Gly Leu Asp His
      85      90      95
Arg Arg Asp Ala Ala Gly Arg Pro Thr Ala Arg Ala Ser Gly Ser Gly
      100     105     110
Thr Trp Arg Gly Gly Ala Ala Ser Trp Ala Pro Ala Thr Thr Thr Thr
      115     120     125
Ser Ala Ala Thr Trp Thr Ser Ser Ala Ala Gly Ala Pro Ala
      130     135     140

```

(2) INFORMATION FOR SEQ ID NO:3862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3862:

```

Met Lys Leu Lys Leu Leu Ser Pro Cys Leu Leu Leu Leu Ala Phe Phe
1      5      10      15
Ala Thr Ala Ala Tyr Ala Ala Ser Ala Ser Ala Ser Arg Ala Ala Ala
      20      25      30
Val Val Arg Gly Ala Gly Ala Pro Ser Gln Ser Glu Leu Glu Ser Asp

```

35	40	45	
Pro Glu Asn Gln Cys Val Tyr Thr Val Tyr Val Arg Thr Gly Ser Ile			
50	55	60	
Trp Lys Gly Gly Thr Asp Ser Thr Ile Gly Val Thr Leu Leu Gly Ala			
65	70	75	80
Arg Arg His Gly His Pro Asp Pro Gly Pro Gly Gly Val Gly Arg Pro			
85	90	95	
His Gly Arg Arg Pro Arg Leu Leu Arg Ala Arg Gln Pro Gly His Leu			
100	105	110	
Gln Arg Pro Gly Pro Leu His Glu Pro Gly Arg Pro Ala Xaa			
115	120	125	

(2) INFORMATION FOR SEQ ID NO:3863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: -
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3863:

Met Gly Ala Gly His Asp Tyr Tyr Glu Arg Gly Asn Leu Asp Ile Phe	
1	15
Ser Gly Arg Gly Pro Cys Met Ser Gln Gly Ala Leu Xaa His Glu Pro	
20	30
His Leu Arg Arg His Arg Arg Ala Pro Arg Leu Val Leu Gln Leu Pro	
35	45
Arg Gly His Gly His Gly Ala Pro Pro Arg Val Arg Ala Ala Ala Leu	
50	60
His Arg Arg Ala Val Ala Arg His Arg Arg Val Ala Leu Pro Pro Val	
65	80
Arg Gly Arg Arg Gln Val Gln Asp Glu Xaa Ala Gly Xaa Ala Thr Leu	
85	95
Ala Gly Arg Arg Gly Arg Gly His Arg Asp Arg Ala Leu Gly Thr Thr	
100	110
Ser Ser Lys Ser Ser Thr Glu Ala Ser Ser Cys Leu Cys Cys Val	
115	125

(2) INFORMATION FOR SEQ ID NO:3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3864:

atcagctcg attgattcgt cttcccttcc ctcgatctc cattctccag tgtggtcg	60
cagtgattctc ttctcttgcc gagatacag atcgaagatc gcccttgarc ccatcccatg	120
gctgcgctct cctctctccc tccagcaacg ccggcmgccc tccGgcacgg ggcgtgccac	180
gggctGggggc tggcgctacc gaggaNgttt kycGccgtcg cGgGcaaNcg cgatgcgccg	240
cgCtaacggc ggaacgcagc accagtcacg aggcgcgctg gtggacgagg	300
gcattgccgt gctgcggcgg cggatccggg aggcgtggat ggtggagacc aactacgagg	360
cgccgcggca gtggggcgcg tgggagaagc ggtactaccc cgcctaCgtc tccagctgtg	420
ctagcctcgt cggcgcgctg cagctgctgc tcatggggcac caggcccccgc gtcgcatcgt	480
ccgtgcggcg cctggtgctg gccagcgtcc ccgtgtccac cgtgcgccgg ctacacatct	540
ggcgatgggt gccgagggcg tctcgcagtc cgtccatcac atttcttgat ccagtcggac	600

catcttttgg tctctctttt tcttttcatt tgtaaccttg aggcagctcg ccgcgtgaat 660
agtattggag gcttgtagtt gcagctggat tgatctaaag attcttttagc cttg

(2) INFORMATION FOR SEQ ID NO:3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3865:

Gln Pro Arg Leu Ile Arg Leu Pro Phe Pro Ser Ile Ser Ile Leu Gln
1 5 10
Cys Gly Arg Ala Val Phe Ser Phe Leu Pro Glu Ile Arg Tyr Glu Asp
20 25 30
Gln Pro Leu Xaa Arg Ser His Gly Cys Xaa Phe Pro Leu Pro Ser Ser
35 40 45
Asn Ala Gly Xaa Ala Pro Ala Arg Gly Val Pro Arg Ala Gly Ala Gly
50 55 60
Ala Thr Glu Xaa Val Xaa Arg Arg Arg Gln Xaa Arg Cys Ala Ala
65 70 75 80
Leu Arg Arg Asp Ala Ser Gly Gly Arg Asp Gln Tyr Gly Gly Ala Leu
85 90 95
Val Asp Glu Gly Met Pro Val Leu Arg Arg Arg Ile Arg Glu Ala Trp
100 105 110
Met Val Glu Thr Asn Tyr Glu Ala Pro Ala Glu Trp Ala Pro Trp Glu
115 120 125
Lys Arg Tyr Tyr Pro Ala Tyr Val Ser Asp Val Ser Ser Leu Val Gly
130 135 140
Ala Leu Gln Leu Leu Leu Met Gly Thr Arg Pro Gly Val Ala Ile Ala
145 150 155 160
Val Ala Ala Leu Val Leu Ala Ser Val Pro Val Ser Thr Val Ala Ala
165 170 175
Leu His Ile Trp Arg Trp Trp Pro Arg Pro Ser Cys Ser Pro Ser Ile
180 185 190
Thr Phe Leu Asp Pro Val Gly Pro Ser Phe Gly Leu Leu Phe Ser Phe
195 200 205
His Leu
210

(2) INFORMATION FOR SEQ ID NO:3866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3866:

Met Ala Xaa Ala Ser Leu Ser Arg Pro Ala Thr Pro Xaa Ala Leu Arg
1 5 10 15
His Gly Ala Cys His Gly Leu Gly Leu Ala Leu Pro Arg Xaa Phe Xaa
20 25 30
Ala Val Gly Gly Xaa Arg Asp Ala Pro Arg Tyr Ala Gly Thr Arg Ala
35 40 45
Ala Ala Gly Thr Ser Thr Glu Ala Arg Trp Trp Thr Arg Ala Cys Pro

aagcagacc	ggcggggcc	tggcaattca	cgcacctsgc	gtgcacacag	acacaggcag	60
gccacacgc	caatcacgct	cgcgcctcgc	agtcgtactc	acgggtctcg	acacaccgct	120
cccatcctc	tccgggtgtc	ctcatccctc	ccgtgcacgc	ccgcgtccgc	ccgcgcgaac	180
ccgacctgtg	tcaatcgcca	tgactacctc	aaggcgtctt	gctgatagga	agatatcacg	240
ttatcgaga	aatatcacaa	agaggggcgc	tgcttcctga	acgacgaata	agcgaacga	300
ttatctcgtt	ggcctcatca	tctctggggt	ctttgtcttc	atgagttctg	gattcctctc	360

ctttcagatc atcaagacag catcaaacgc tgggtctattc tgaggtgaat cgggtgacac 420
atgcagtttg tcaatagaaa ctatacaagt gtagggcggtg gcttaatgac gccttttttaa 480
tgttgtaccg tggagagttt taagttatat atgtaatgga agtgctaatt taagtcaacct 540
gtctgacacg aagaatgttg gagtagtCca taatacatat cgagtatagt tatagttcgt 600
gttaaattatt tctatgctca aattggtcgc atcattgggc tattgtactc ttcgatttat 660
cgagtaattt ggtaatcttt cgc

(2) INFORMATION FOR SEQ ID NO:3869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3869:

Lys Gln Thr Arg Ala Gly Pro Gly Asn Ser Arg Thr Xaa Arg Ala His
1 5 10 15
Arg His Arg Gln Ala His Ser Ala Ile Thr Val Ser Pro Arg Ser Arg
20 25 30
Thr His Gly Leu Ala His Thr Arg Pro His Pro Leu Pro Val Ser Pro
35 40 45
Ser Pro Pro Ser Thr Ala Ala Ser Gly Arg Gly Asn Pro Thr Cys Val
50 55 60
Asn Arg His Asp Tyr Leu Lys Ala Ser Cys
65 70

(2) INFORMATION FOR SEQ ID NO:3870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1578526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3870:

Ser Arg Pro Gly Arg Ala Leu Ala Ile His Ala Pro Xaa Val His Thr
1 5 10 15
Asp Thr Gly Arg His Thr Ala Gln Ser Pro Ser Arg Leu Ala Val Val
20 25 30
Leu Thr Val Leu His Thr Pro Val Pro Ile Leu Phe Arg Cys Arg His
35 40 45
Pro Leu Arg Arg Pro Pro Arg Pro Ala Ala Ala Thr Arg Pro Val Ser
50 55 60
Ile Ala Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg
65 70 75 80
Phe Glu Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys
85 90 95
Lys Ala Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val
100 105 110
Phe Val Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser
115 120 125
Asn Ala Gly Leu Phe
130

(2) INFORMATION FOR SEQ ID NO:3871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..67
(D) OTHER INFORMATION: / Ceres Seq. ID 1578527
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3871:
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg Phe Glu
1 5 10 15
Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys Lys Ala
20 25 30
Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe Val
35 40 45
Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser Asn Ala
50 55 60
Gly Leu Phe
65

(2) INFORMATION FOR SEQ ID NO:3872:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..707
(D) OTHER INFORMATION: / Ceres Seq. ID 1578540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3872:

atccatatgc actagcagta tcacctcatt taatatgcgg cgggcactgt cgccagagct 60
ctcgataaag ctgcgccagas tctcatctca tacgcggag gtgctccaga gacgagggt 120
gaagagggtgc ggcaagagct gcaggctgag gtacaccaac tatcgcgcg tgatctgggc 180
gacgaactgc gtgcgcgTtt tgcaggtggt cctgatcgc gaaGcagctg ccggggcgga 240
cgggcaacga cgtgaggaac cgttggaaca cgaaaactgag agcaaacgagc tgcggcagcg 300
cgggatcgac cccaccgcgc ccacgcgcgg cctcatgcac atcttcgtcg gcgcctctc 360
cttacgcgca cgacgcgcac ggaacgacga cggcacggga gagatcatcg acgccaccct 420
ggactgRcga caagaagaca cgggtggacc agctcatcgc ctgctgctg gccgaccggg 480
cctactacgc tggctcctcc tccgagatgg gctggatcat gggcttgatg aatgctgatt 540
aattagcggT tatacaatgg atccatgagg ctaaaagcaaa ctgactgaaa tagtcaacttt 600
agaggctaaa gtttcaaaca taaagaacta aaagggaacta aaatgtttta gctcctttag 660
cttgaagga cgagttaaac tgactaaaa cagctggtcc cacaccc

(2) INFORMATION FOR SEQ ID NO:3873:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..178
(D) OTHER INFORMATION: / Ceres Seq. ID 1578541
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3873:

Ser Ile Cys Thr Ser Ser Ile Thr Ser Phe Asn Met Arg Pro Ala Ser
1 5 10 15
Ser Pro Glu Leu Ser Ile Arg Leu Ala Arg Xaa Ser Ser His Thr Pro
20 25 30
Glu Val Leu Gln Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg
35 40 45

Leu Arg Tyr Thr Asn Tyr Arg Ala Leu Ile Trp Ala Thr Asn Cys Val
50 55 60
Arg Val Leu Gln Val Val Pro Asp Arg Glu Ala Ala Gly Ala Asp
65 70 75 80
Gly Gln Arg Arg Glu Pro Leu Glu His Glu Thr Glu Ser Lys Gln
85 90 95
Leu Arg Gln Arg Gly Ile Asp Pro Thr Ala Pro Ile Ala Gly Leu Met
100 105 110
His Ile Phe Val Gly Ala Leu Ser Leu Arg Arg Arg Arg His Gly Asn
115 120 125
Asp Asp Gly Thr Gly Glu Ile Ile Asp Ala Thr Leu Asp Xaa Arg Gln
130 135 140
Glu Asp Thr Gly Gly Pro Ala His Arg Leu Ala Ala Gly Arg Pro Gly
145 150 155 160
Leu Leu Arg Trp Leu Leu Leu Arg Asp Gly Leu Asp His Gly Leu Asp
165 170 175
Glu Cys

(2) INFORMATION FOR SEQ ID NO:3874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3874:

Met Arg Pro Ala Ser Ser Pro Glu Leu Ser Ile Arg Leu Ala Arg Xaa
1 5 10 15
Ser Ser His Thr Pro Glu Val Leu Gln Arg Ala Gly Leu Lys Arg Cys
20 25 30
Gly Lys Ser Cys Arg Leu Arg Tyr Thr Asn Tyr Arg Ala Leu Ile Trp
35 40 45
Ala Thr Asn Cys Val Arg Val Leu Gln Val Val Pro Asp Arg Glu Ala
50 55 60
Ala Ala Gly Ala Asp Gly Gln Arg Arg Glu Glu Pro Leu Glu His Glu
65 70 75 80
Thr Glu Ser Lys Gln Leu Arg Gln Arg Gly Ile Asp Pro Thr Ala Pro
85 90 95
Ile Ala Gly Leu Met His Ile Phe Val Gly Ala Leu Ser Leu Arg Arg
100 105 110
Arg Arg His Gly Asn Asp Asp Gly Thr Gly Glu Ile Ile Asp Ala Thr
115 120 125
Leu Asp Xaa Arg Gln Glu Asp Thr Gly Gly Pro Ala His Arg Leu Ala
130 135 140
Ala Gly Arg Pro Gly Leu Leu Arg Trp Leu Leu Arg Asp Gly Leu
145 150 155 160
Asp His Gly Leu Asp Glu Cys
165

(2) INFORMATION FOR SEQ ID NO:3875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..697

(D) OTHER INFORMATION: / Ceres Seq. ID 1578543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3875:

aaacagctctc	ggcctctctc	cccgctcttc	tcacacggca	ctccagccgc	tagccctcac	60
tcaaccagac	aaccagtaca	ccaccgccc	caagcccggg	cgaataact	ctgccgggca	120
accgcccgc	tccgcccga	aagaacgccc	accagatcca	ccccggcctg	ctatggagtc	180
cgcgggtgaac	ccgaaGgcgt	accgcctggc	tgatgcgcaG	ctgacgatgg	gtatcctcga	240
tatcatccag	caggcccgcca	actacaagca	gctcaagaag	ggagcgaaag	aagcgacgaa	300
aaccctgaat	agggggatat	cggagtctgt	tgtgatggcg	gcggacacgg	agcctctcga	360
gatcctgtct	cacctccctt	tgtagccga	ggataagaac	gtcccatatg	tatttgttcc	420
atcgaaacaa	gctcttggcc	gtgcttggg	tgtagacaag	cccgctattg	cttgctcagt	480
gaccgacaat	gagggtagcc	agctgaaaca	acagatacag	ggctctcaag	actcgattga	540
gaagctcttc	atctgattta	cctaagatct	ttcagtgtag	tgggcctcgg	cgacacattt	600
ttcagaggct	tggagtggg	atgggtgtct	gtttacatta	cgctttccaa	actatatattg	660
aacactgcta	agtcaatcat	atttgaattg	tgcttcg			

(2) INFORMATION FOR SEQ ID NO:3876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1578544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3876:

Asn	Ser	Leu	Gly	Leu	Ser	Ser	Arg	Leu	Pro	His	Thr	Ala	Leu	Gln	Pro	
1			5					10						15		
Leu	Ala	Leu	Thr	Gln	Pro	Asp	Asn	Gln	Tyr	Thr	Thr	Ala	Thr	Lys	Pro	
			20					25					30			
Gly	Pro	Asn	Asn	Ser	Ala	Gly	Gln	Pro	Pro	Phe	Ala	Gly	Lys	Glu		
			35					40				45				
Arg	Pro	Pro	Asp	Pro	Pro	Arg	Pro	Ala	Met	Glu	Ser	Ala	Val	Asn	Pro	
			50				55					60				
Lys	Ala	Tyr	Pro	Leu	Ala	Asp	Ala	Gln	Leu	Thr	Met	Gly	Ile	Leu	Asp	
			65				70					75			80	
Ile	Ile	Gln	Gln	Ala	Ala	Asn	Tyr	Lys	Gln	Leu	Lys	Lys	Gly	Ala	Asn	
			85					90						95		
Glu	Ala	Thr	Lys	Thr	Leu	Asn	Arg	Gly	Ile	Ser	Glu	Phe	Val	Val	Met	
			100					105					110			
Ala	Ala	Asp	Thr	Glu	Pro	Leu	Glu	Ile	Leu	Leu	His	Leu	Pro	Leu	Leu	
			115					120				125				
Ala	Glu	Asp	Lys	Asn	Val	Pro	Tyr	Val	Phe	Val	Pro	Ser	Lys	Gln	Ala	
			130				135					140				
Leu	Gly	Arg	Ala	Cys	Gly	Val	Thr	Arg	Pro	Val	Ile	Ala	Cys	Ser	Val	
			145				150				155				160	
Thr	Ser	Asn	Glu	Gly	Ser	Gln	Leu	Lys	Gln	Gln	Ile	Gln	Gly	Leu	Lys	
			165					170					175			
Asp	Ser	Ile	Glu	Lys	Leu	Leu	Ile									
			180													

(2) INFORMATION FOR SEQ ID NO:3877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3877:

Met	Glu	Ser	Ala	Val	Asn	Pro	Lys	Ala	Tyr	Pro	Leu	Ala	Asp	Ala	Gln
1				5				10					15		
Leu	Thr	Met	Gly	Ile	Leu	Asp	Ile	Ile	Gln	Gln	Ala	Ala	Asn	Tyr	Lys
			20				25					30			
Gln	Leu	Lys	Lys	Gly	Ala	Asn	Glu	Ala	Thr	Lys	Thr	Leu	Asn	Arg	Gly
			35			40					45				
Ile	Ser	Glu	Phe	Val	Val	Met	Ala	Ala	Asp	Thr	Glu	Pro	Leu	Glu	Ile
	50				55				60						
Leu	Leu	His	Leu	Pro	Leu	Leu	Ala	Glu	Asp	Lys	Asn	Val	Pro	Tyr	Val
65				70					75					80	
Phe	Val	Pro	Ser	Lys	Gln	Ala	Leu	Gly	Arg	Ala	Cys	Gly	Val	Thr	Arg
				85				90				95			
Pro	Val	Ile	Ala	Cys	Ser	Val	Thr	Ser	Asn	Glu	Gly	Ser	Gln	Leu	Lys
			100				105					110			
Gln	Gln	Ile	Gln	Gly	Leu	Lys	Asp	Ser	Ile	Glu	Lys	Leu	Leu	Ile	
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1578546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3878:

Met	Gly	Ile	Leu	Asp	Ile	Ile	Gln	Gln	Ala	Ala	Asn	Tyr	Lys	Gln	Leu
1			5					10					15		
Lys	Lys	Gly	Ala	Asn	Glu	Ala	Thr	Lys	Thr	Leu	Asn	Arg	Gly	Ile	Ser
			20					25				30			
Glu	Phe	Val	Val	Met	Ala	Ala	Asp	Thr	Glu	Pro	Leu	Glu	Ile	Leu	Leu
			35				40					45			
His	Leu	Pro	Leu	Leu	Ala	Glu	Asp	Lys	Asn	Val	Pro	Tyr	Val	Phe	Val
	50				55				60						
Pro	Ser	Lys	Gln	Ala	Leu	Gly	Arg	Ala	Cys	Gly	Val	Thr	Arg	Pro	Val
65				70					75					80	
Ile	Ala	Cys	Ser	Val	Thr	Ser	Asn	Glu	Gly	Ser	Gln	Leu	Lys	Gln	Gln
				85				90				95			
Ile	Gln	Gly	Leu	Lys	Asp	Ser	Ile	Glu	Lys	Leu	Leu	Ile			
			100				105								

(2) INFORMATION FOR SEQ ID NO:3879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1578582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3879:

gatcagtttag	tagttcacca	gagttcacac	aaaaatcaca	agcaagcagt	cgcgtgtgta	60
gctcgcaaca	atggcgacga	accocggcct	cttcacggag	tggccgtgga	agaagctcgg	120
caacttcaag	gtagctcccg	gcacccggccc	cgtctcaagta	ccctgcgtgc	gtacgtccat	180
ggcacagagc	gggggagaag	gtgaaggaaa	attagcaact	cgtctcttcg	tcacccggcg	240
cgtgccatgc	catggcaatc	tggggcgcat	ggtatatggc	catgtgcggc	acgCagtgtc	300

ggaacatgca tgcacgcatg gacttgctat acatacatgc atgcaccggc agccgtgaga 360
ccatctgtgc atgagttetta tgctctctgtg catctcatgt tccggccgac ccatgagcat 420
ggaaggaagc caccaaaagt tcattaattt gataggctgc gtgtgcatgg ct

(2) INFORMATION FOR SEQ ID NO:3880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3880:

Asp Gln Leu Val Val His Gln Ser Ser His Lys Asn His Lys Gln Ala
1 5 10 15
Val Ala Cys Val Ala Arg Asn Asn Gly Asp Glu Pro Arg Pro Leu His
20 25 30
Arg Val Ala Val Glu Glu Ala Arg Gln Leu Gln Gly Ser Ser Arg His
35 40 45
Arg Pro Arg Leu Ser Thr Leu Arg Ala Tyr Val His Gly Thr Glu Arg
50 55 60
Gly Arg Arg
65

(2) INFORMATION FOR SEQ ID NO:3881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3881:

Met Ala Thr Asn Pro Gly Leu Phe Thr Glu Trp Pro Trp Lys Lys Leu
1 5 10 15
Gly Asn Phe Lys Val Ala Pro Gly Thr Gly Pro Val Ser Val Pro Cys
20 25 30
Val Arg Thr Ser Met Ala Gln Ser Gly Gly Glu Gly Glu Gly Lys Leu
35 40 45
Ala Thr Arg Leu Leu Leu Thr Gly Gly Val Pro Cys His Gly Asn Leu
50 55 60
Gly Arg Met Val Tyr Gly His Val Arg His Ala Val Ser Glu His Ala
65 70 75 80
Cys Thr His Gly Leu Ala Ile His Thr Cys Met His Arg Gln Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3882:

Met Pro Trp Gln Ser Trp Ala His Gly Ile Trp Pro Cys Ala Ala Arg
1 5 10 15
Ser Val Gly Thr Cys Met His Ala Trp Thr Cys Tyr Thr Tyr Met His
20 25 30
Ala Pro Ala Ala Val Arg Pro Ser Val His Glu Ser Tyr Ala Pro Val
35 40 45
His Leu Met Phe Arg Pro Thr His Glu His Gly Arg Lys Pro Pro Lys
50 55 60
Val His
65

(2) INFORMATION FOR SEQ ID NO:3883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 780 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..780

(D) OTHER INFORMATION: / Ceres Seq. ID 1578586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3883:

aattcacgac	cttattgata	ctccccactg	cacaaagatg	acatatagagaa	acatgtgaag	60
gagctcttgg	cctcgggtat	gactgtcccc	agtaaatgcc	catttgcctc	cccgggtttg	120
tgtcaattac	tggaaagtta	actcactatc	aaaaaccggt	ttccccattcc	gatcatcgat	180
gaaattcttg	acgagttggc	aggcaccaaa	ctttcaccca	agctggacat	gagatcgggt	240
taccatcaag	tccgggatga	ttcagatgat	gagtttaaaa	cgacattcaa	aatacatcat	300
ggacattttc	agtttcatgt	ttgacagact	tcagttcgca	agacctgttg	ccggatcaac	360
ttctggactg	tgccttggtg	aagaaaggca	gtaaggcggt	tccacaagtg	ttagtccaat	420
ggcgcaactc	tctagctgct	tctgctacgt	gggaggactg	gtacgtgttg	aagaatcact	480
ttccacacat	ggctgcttgg	ggacaggcat	caactgaagg	ggaggggagt	gtagcgCccg	540
acgtgtcGgg	tgcgttacag	gagttcgag	aagccgtgcc	caagtgaagg	cgtaatgtgt	600
taggctccgt	catttacttt	gttaagagtc	atttaaggta	ccattgggtg	gctcaatgta	660
atgaccagca	actatgctgt	taaggtcctt	gtggtcggaa	cctgaggaac	attatcatgc	720
aaaaagaata	tacacgaag	tgaactcggg	gttgcttgc	ctcgcaagtt	catcatccct	780

(2) INFORMATION FOR SEQ ID NO:3884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1578587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3884:

Met Ile Val Pro Ser Asn Ser Pro Phe Ala Ser Pro Val Leu Cys Gln	5	10	15
Leu Leu Glu Val Lys Leu Thr Ile Lys Asn Arg Phe Pro Ile Pro Ile	20	25	30
Ile Asp Glu Ile Leu Asp Glu Leu Ala Gly Thr Lys Leu Phe Thr Lys	35	40	45
Leu Asp Met Arg Ser Gly Tyr His Gln Val Gly Met His Ser Asp Asp	50	55	60
Glu Phe Lys Thr Thr Phe Lys Ile His His Gly His Phe Gln Phe His	65	70	75
Cys			80

(2) INFORMATION FOR SEQ ID NO:3885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1578588
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3885:
Met Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser
1 5 10 15
Phe Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr
20 25 30
Ser Gly Leu Ser Leu Gly Glu Glu Arg Gln
35 40
(2) INFORMATION FOR SEQ ID NO:3886:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: / Ceres Seq. ID 1578589
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3886:
Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser Phe
1 5 10 15
Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr Ser
20 25 30
Gly Leu Ser Leu Gly Glu Glu Arg Gln
35 40
(2) INFORMATION FOR SEQ ID NO:3887:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..514
(D) OTHER INFORMATION: / Ceres Seq. ID 1578590
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3887:
atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag cttctgggcag cgtgcgcacg 60
trgggtacct agctcgtctct gctagcctac catggctgat caccaccggg gcgcgacggg 120
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcagCa 180
gcagcagaag caggcgccca tgatgacggc gctcaaggcc gcgacggccg cgacctcctt 240
gaaccactgc cggcgccggcg gcatatggcc cttaaaggcg gtggctgctg ctacgtacgc 300
tgccgtagag tctcgtgcgc cgcgatagCt ctagctatgc gtttatgtgt tgtgctttgt 360
gtgtgcatgc ttgtgtctgg ggccatgcag tgcagtgcag tactatatgc tgtatgcgtc 420
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggcgtgcacg 480
tttatgatga ggaataaaa gcagtgttca ggtg
(2) INFORMATION FOR SEQ ID NO:3888:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..66
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578591
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3888:
Arg Thr Arg Ser Arg Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln
1 5 10 15
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu
 20 25 30
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser
 35 40 45
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg
50 55 60
Ala Pro
65
(2) INFORMATION FOR SEQ ID NO:3889:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578592
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3889:
Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly
1 5 10 15
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln Gln
 20 25 30
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr
 35 40 45
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val
50 55 60
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg
65 70 75
(2) INFORMATION FOR SEQ ID NO:3890:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..55
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578593
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3890:
Met His Gly Glu Ala Gln Gln Gln Gln Lys Gln Gly Ala Met Met Thr
1 5 10 15
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg
 20 25 30
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala
35 40 45
Val Glu Ser Arg Ser Pro Arg
50 55
(2) INFORMATION FOR SEQ ID NO:3891:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1077
(D) OTHER INFORMATION: / Ceres Seq. ID 1578630
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3891:

```

gtaccttgggt tcatgctcag ttgatggaa aattgaagtc tggggattatc ttagtggaaga
gctctaaaaag gatcttcaat atcaagccga tgaaagcttt atgatgcacg aggaacctgt
gctgtgtgtgt gatttttagta gggatltcta aatgctggca tctggatcac aggatggaaa
gattaagggtt tggcgctatac gaactgggtca gtgcttgcaa gccttgagc gtgcacattc
gaaagggtgtt acaagtggtta caatttccac tgatggaacc caaatattga gtacatctct
tgacactacc gcgaggggtac atggcctcaa gtctggaag atgctgaaa aatttcgagg
tcatttctca tatgtaaat atgcatctt cactactgac ggtagccgtg tcattacagc
ttccagtgtat tgtactgtta aggtctggGa tactaaaaca acagattgct tgcatacttt
caagccacca cctcctttga ggggaggaga tgcctctgtt aattctgtcc atttatttcc
aaaaataact gatcacattg ttgtctgcaa taagacttca tcaatattca tcatKgactt
tacaaaggaca ggtttgtgaag agtttctcat caggtaagcg agaaggggga gattttgttg
cagcttccagt ttcacaaaaa ggagaattgga tatattgtgt tgggtgaagc atgaacatgt
attgcttttag ctaccaactc ggtaaaactg agcatctgat gaaggtgcac gagaaggatg
tcattagcact tacgcaccat cctcacagga acttagtagc caccattgtg gaggattgta
tgatgaagat atggaagcct tgactttttt tcttttttaa aaaaacctga accgatgatt
aaataggatg tattttgttt tgtaatttag ataactggta ggcgctacag ctatggactc
gttggtgctt atgtgcccc atgtcttact accattgtat cctgtactag atttagggac
cttcaatggg tgtaaacaca gcttactacg actcctcgct acaagttcat tatggtc

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(2) INFORMATION FOR SEQ ID NO:3892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..211
(D) OTHER INFORMATION: / Ceres Seq. ID 1578631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3892:

```

Tyr Leu Val Ser Cys Ser Val Asp Gly Ile Ile Glu Val Trp Asp Tyr
1 5 10 15
Leu Ser Gly Lys Leu Lys Lys Asp Leu Gln Tyr Gln Ala Asp Glu Ser
20 25 30
Phe Met Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp
35 40 45
Ser Glu Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp
50 55 60
Arg Ile Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser
65 70 75 80
Lys Gly Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu
85 90 95
Ser Thr Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly
100 105 110
Lys Met Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala
115 120 125
Ile Phe Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys
130 135 140
Thr Val Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe
145 150 155 160
Lys Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val

```

(xi) SEQUENCE DESCRIPTION: SUB-TRACTED															
Met	His	Glu	Glu	Pro	Val	Leu	Cys	Val	Asp	Phe	Ser	Arg	Asp	Ser	Glu
1				5				10						15	
Met	Leu	Ala	Ser	Gly	Ser	Gln	Asp	Gly	Lys	Ile	Lys	Val	Trp	Arg	Ile
			20					25					30		
Arg	Thr	Gly	Gln	Cys	Leu	Gln	Arg	Leu	Glu	Arg	Ala	His	Ser	Lys	Gly
		35					40					45			

Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu Ser Thr
50 55 60
Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly Lys Met
65 70 75 80
Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala Ile Phe
85 90 95
Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys Thr Val
100 105 110
Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe Lys Pro
115 120 125
Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val His Leu
130 135 140
Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr Ser Ser
145 150 155 160
Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe Leu Ile
165 170 175
Arg

(2) INFORMATION FOR SEQ ID NO:3895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..906
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3895:

aatgatattc	agcttagtat	tcgtatgccc	agtggaaata	gactggagat	caaactaaca	60
aaacaagatg	ttttaaggaa	agtgaagaat	ttcgtggatg	aaaaccaagg	caatgggctt	120
ggctcatatg	acotttctct	ggtttatcct	aaaagagttt	tctctgaaca	agatatggaa	180
gcaacactat	ccgagctggg	tattcaaaac	cgctatgcaa	tgattgttgt	tccacatcgg	240
cagtcctggc	aggtatcaag	gggtcactcc	tcggcatctt	atgatattgg	tgtaattcca	300
ggtgccgatg	atgttgggtg	caattcaggt	gcggggggat	actttggtta	cctgagaacc	360
gtcctgtctt	atgtgaatcc	actctcttac	ctgaggggaa	ataccaactc	atcaaataca	420
gagctacagt	caaatgaagG	Cctgcggcag	cttagacatg	gatctgtgtc	atggagttag	480
ccacggcttc	ttggcaatag	gggccatgaa	gtgactgatg	cagactctgc	aaacacgtcg	540
cgaagcgccg	ctagaccatt	tggtgccaat	atccacactc	tggggagcga	ggatcatggt	600
ccgtctgatg	aaagaaatgt	tttctggaac	gggaactcga	cagagttttg	aggcgacgac	660
agaaaaatag	ttgtggcgtg	gctggcaggg	cctgggacga	cactatcaga	cagaatcaaa	720
gttggggaata	gacagctgaa	acaaaatgcc	cgacaggctt	attgaggaat	aagtatttag	780
attatagtgc	tgaataatc	gctgaattgt	gatgtttaca	tttgtggaaa	catacggtcg	840
ctggatccgt	atactcgttg	tatagtacat	agccacagat	atattaaatc	cgaactgctt	900
ggttcc						

(2) INFORMATION FOR SEQ ID NO:3896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3896:

Asn Asp Ile Gln Leu Ser Ile Arg Met Pro Ser Gly Asn Arg Leu Glu						
1	5	10	15			
Ile Lys Leu Thr Lys Gln Asp Val Leu Arg Lys Val Lys Asn Phe Val						

20	25	30
Asp Glu Asn Gln Gly	Asn Gly Leu Gly Ser Tyr Asp	Leu Ser Leu Val
35	40	45
Tyr Pro Lys Arg Val Phe	Ser Glu Gln Asp Met Glu Ala Thr	Leu Ser
50	55	60
Glu Leu Gly Ile Gln Asn Arg His Ala Met	Ile Val Val Pro His Arg	
65	70	75
Gln Ser Gly Gln Val Ser Arg Arg His Ser Ser Ala Ser Tyr Asp Met		80
	85	90
Gly Val Asn Ser Gly Ala Asp Asp Val Gly Gly Asn Ser Gly Ala Gly		95
	100	105
Gly Tyr Phe Gly Tyr Leu Arg Thr Val Leu Ser Tyr Val Asn Pro Leu		110
	115	120
Ser Tyr Leu Arg Gly Asn Thr Asn Ser Ser Asn Thr Glu Leu Gln Ser		125
	130	135
Asn Glu Gly Leu Arg Gln Leu Arg His Gly Ser Gly Pro Trp Ser Glu		140
145	150	155
Pro Arg Pro Leu Gly Asn Arg Gly His Glu Val Thr Asp Ala Asp Ser		160
	165	170
Ala Asn Thr Leu Arg Arg Arg Pro Arg Pro Phe Gly Ala Asn Ile His		175
	180	185
Thr Leu Gly Ser Glu Asp His Gly Pro Ser Asp Glu Arg Asn Val Phe		190
	195	200
Trp Asn Gly Asn Ser Thr Glu Phe Gly Gly Asp Asp Arg Lys		205
	210	215
		220

(2) INFORMATION FOR SEQ ID NO:3897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1578676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3897:

Met Pro Ser Gly Asn Arg Leu Glu Ile Lys Leu Thr Lys Gln Asp Val	
1	5
Leu Arg Lys Val Lys Asn Phe Val Asp Glu Asn Gln Gly Asn Gly Leu	10
	15
	20
Gly Ser Tyr Asp Leu Ser Leu Val Tyr Pro Lys Arg Val Phe Ser Glu	25
	30
	35
Gln Asp Met Glu Ala Thr Leu Ser Glu Leu Gly Ile Gln Asn Arg His	40
	45
	50
Ala Met Ile Val Val Pro His Arg Gln Ser Gly Gln Val Ser Arg Arg	55
	60
	65
His Ser Ser Ala Ser Tyr Asp Met Gly Val Asn Ser Gly Ala Asp Asp	70
	75
	80
	85
Val Gly Gly Asn Ser Gly Ala Gly Gly Tyr Phe Gly Tyr Leu Arg Thr	90
	95
	100
Val Leu Ser Tyr Val Asn Pro Leu Ser Tyr Leu Arg Gly Asn Thr Asn	105
	110
	115
Ser Ser Asn Thr Glu Leu Gln Ser Asn Glu Gly Leu Arg Gln Leu Arg	120
	125
	130
His Gly Ser Gly Pro Trp Ser Glu Pro Arg Pro Leu Gly Asn Arg Gly	135
	140
	145
His Glu Val Thr Asp Ala Asp Ser Ala Asn Thr Leu Arg Arg Arg	150
	155
	160
	165
Arg Pro Phe Gly Ala Asn Ile His Thr Leu Gly Ser Glu Asp His Gly	170
	175
	180
	185
	190

Pro Ser Asp Glu Arg Asn Val Phe Trp Asn Gly Asn Ser Thr Glu Phe
195 200 205
Gly Gly Asp Asp Arg Lys
210

(2) INFORMATION FOR SEQ ID NO:3898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1578677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3898:

Met	Glu	Ala	Thr	Leu	Ser	Glu	Leu	Gly	Ile	Gln	Asn	Arg	His	Ala	Met
1				5					10					15	
Ile	Val	Val	Pro	His	Arg	Gln	Ser	Gly	Gln	Val	Ser	Arg	Arg	His	Ser
			20					25					30		
Ser	Ala	Ser	Tyr	Asp	Met	Gly	Val	Asn	Ser	Gly	Ala	Asp	Asp	Val	Gly
			35				40					45			
Gly	Asn	Ser	Gly	Ala	Gly	Gly	Tyr	Phe	Gly	Tyr	Leu	Arg	Thr	Val	Leu
			50			55					60				
Ser	Tyr	Val	Asn	Pro	Leu	Ser	Tyr	Leu	Arg	Gly	Asn	Thr	Asn	Ser	Ser
			65		70				75					80	
Asn	Thr	Glu	Leu	Gln	Ser	Asn	Glu	Gly	Leu	Arg	Gln	Leu	Arg	His	Gly
			85					90						95	
Ser	Gly	Pro	Trp	Ser	Glu	Pro	Arg	Pro	Leu	Gly	Asn	Arg	Gly	His	Glu
			100				105						110		
Val	Thr	Asp	Ala	Asp	Ser	Ala	Asn	Thr	Leu	Arg	Arg	Arg	Pro	Arg	Pro
			115				120					125			
Phe	Gly	Ala	Asn	Ile	His	Thr	Leu	Gly	Ser	Glu	Asp	His	Gly	Pro	Ser
			130			135					140				
Asp	Glu	Arg	Asn	Val	Phe	Trp	Asn	Gly	Asn	Ser	Thr	Glu	Phe	Gly	Gly
			145		150				155					160	
Asp	Asp	Arg	Lys												

(2) INFORMATION FOR SEQ ID NO:3899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..745

(D) OTHER INFORMATION: / Ceres Seq. ID 1578682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3899:

cagacaataa	tatacaaatgc	tgtgtttaag	gctcataatg	ctgttatatc	agacatgcgg	60
ctgggagtta	attggatgga	tatgcacaaa	ttagcagaac	gggcaatact	tgaatctctc	120
agggaaggaa	aaattgtaca	aggggatggt	gatgatatga	tggctcaaa	gttagggggt	180
gtttttcagc	ctcatgtgtct	tggccactta	cttggtattg	acaccatga	tccaggagcc	240
taccctgagc	gattggagag	gcccaaggat	ccaggactga	actccttgcg	gaccacaaga	300
gaactgaaag	aagggaatggt	tatcacagt	gagccaggct	gctatttcat	tgatgctttg	360
ctaactaaaa	caagggatga	tccaatttcc	tcaaagtctc	tcaactggca	agaggttgaa	420
aagtataaaa	gctttgtgtg	cgttcgcatt	gaaagtgat	tgtatgtgac	ggctcaagga	480
tgccggaacc	tcacaaactg	cccagagag	acctggggaga	tcgaggctgt	aatGgctggc	540
gcaccatggc	ctctgccggc	ttcaaGttct	atggtggtag	cagcagagAa	tagcaatgac	600
atatctaaag	cgtcgtaatt	ttctctatgc	tcaatccata	tcccgagttg	aaacaaattc	660

gacctggatt cttatatattca ataaatagtg agcgctgaggc gcaaaacatt gttggattga 720
tggtggaaaa acatttcata cgccc

(2) INFORMATION FOR SEQ ID NO:3900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3900:

Gln Thr Ile Ile Tyr Asn Ala Val Phe Lys Ala His Asn Ala Val Ile
1 5 10 15
Ser Asp Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala
20 25 30
Glu Arg Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly
35 40 45
Asp Val Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro
50 55 60
His Gly Leu Gly His Leu Gly Ile Asp Thr His Asp Pro Gly Gly
65 70 75 80
Tyr Pro Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu
85 90 95
Arg Thr Thr Arg Glu Leu Lys Glu Gly Met Val Ile Thr Val Glu Pro
100 105 110
Gly Cys Tyr Phe Ile Asp Ala Leu Leu Thr Lys Thr Arg Asp Asp Pro
115 120 125
Ile Ser Ser Lys Phe Phe Asn Trp Gln Glu Val Glu Lys Tyr Lys Ser
130 135 140
Phe Gly Gly Val Arg Ile Glu Ser Asp Val Tyr Val Thr Ala Gln Gly
145 150 155 160
Cys Arg Asn Leu Thr Asn Cys Pro Arg Glu Thr Trp Glu Ile Glu Ala
165 170 175
Val Met Ala Gly Ala Pro Trp Pro Leu Pro Ala Ser Ser Ser Met Val
180 185 190
Val Ala Ala Glu Asn Ser Asn Asp Ile Ser Lys Ala Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:3901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3901:

Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala Glu Arg
1 5 10 15
Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly Asp Val
20 25 30
Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro His Gly
35 40 45
Leu Gly His Leu Leu Gly Ile Asp Thr His Asp Pro Gly Gly Tyr Pro
50 55 60
Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu Arg Thr

65				70					75					80
Thr	Arg	Glu	Leu	Lys	Glu	Gly	Met	Val	Ile	Thr	Val	Glu	Pro	Gly
				85					90					95
Tyr	Phe	Ile	Asp	Ala	Leu	Leu	Thr	Lys	Thr	Arg	Asp	Asp	Pro	Ile
			100					105					110	Ser
Ser	Lys	Phe	Phe	Asn	Trp	Gln	Glu	Val	Glu	Lys	Tyr	Lys	Ser	Phe
			115				120					125		Gly
Gly	Val	Arg	Ile	Glu	Ser	Asp	Val	Tyr	Val	Thr	Ala	Gln	Gly	Cys
			130			135					140			Arg
Asn	Leu	Thr	Asn	Cys	Pro	Arg	Glu	Thr	Trp	Glu	Ile	Glu	Ala	Val
				145		150				155				160
Ala	Gly	Ala	Pro	Trp	Pro	Leu	Pro	Ala	Ser	Ser	Met	Val	Val	Ala
				165				170					175	
Ala	Glu	Asn	Ser	Asn	Asp	Ile	Ser	Lys	Ala	Ser				
			180					185						

(2) INFORMATION FOR SEQ ID NO:3902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1578685
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3902:

Met	Asp	Met	His	Lys	Leu	Ala	Glu	Arg	Ala	Ile	Leu	Glu	Ser	Leu	Arg
				5								10		15	
Lys	Glu	Gln	Ile	Val	Gln	Gly	Asp	Val	Asp	Asp	Met	Met	Ala	Gln	Arg
			20				25					30			
Leu	Gly	Ala	Val	Phe	Met	Pro	His	Gly	Leu	Gly	His	Leu	Leu	Gly	Ile
			35				40				45				
Asp	Thr	His	Asp	Pro	Gly	Gly	Tyr	Pro	Glu	Gly	Leu	Glu	Arg	Pro	Lys
			50			55					60				
Asp	Pro	Gly	Leu	Asn	Ser	Leu	Arg	Thr	Thr	Arg	Glu	Leu	Lys	Glu	Gly
			65		70				75					80	
Met	Val	Ile	Thr	Val	Glu	Pro	Gly	Cys	Tyr	Phe	Ile	Asp	Ala	Leu	Leu
			85					90						95	
Thr	Lys	Thr	Arg	Asp	Asp	Pro	Ile	Ser	Ser	Lys	Phe	Phe	Asn	Trp	Gln
			100				105						110		
Glu	Val	Glu	Lys	Tyr	Lys	Ser	Phe	Gly	Gly	Val	Arg	Ile	Glu	Ser	Asp
			115				120					125			
Val	Tyr	Val	Thr	Ala	Gln	Gly	Cys	Arg	Asn	Leu	Thr	Asn	Cys	Pro	Arg
			130			135					140				
Glu	Thr	Trp	Glu	Ile	Glu	Ala	Val	Met	Ala	Gly	Ala	Pro	Trp	Pro	Leu
			145		150				155					160	
Pro	Ala	Ser	Ser	Ser	Met	Val	Val	Ala	Ala	Glu	Asn	Ser	Asn	Asp	Ile
				165				170						175	
Ser	Lys	Ala	Ser												
			180												

(2) INFORMATION FOR SEQ ID NO:3903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..789

(D) OTHER INFORMATION: / Ceres Seq. ID 1578692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3903:

aagagccaac	agagcaacgc	ccagggcacac	acgacacgaa	ccargcagcc	agccgcggag	60
ggagggaacc	tagcggaaca	ggtgacggcg	gcgcgctacc	ggtgacgggg	gatacggcgg	120
catcgctccc	tctccatccc	ccggcgcgccg	ggcgacgacg	ccggcctgca	ggctgtttga	180
agagctcgcc	atttaattcc	aattggaagcc	aagtttttcc	gtttcctgaa	gctcgttggt	240
gtcgggttca	aagcgaggtc	agagagccaa	ggcgcgtgag	tgcttcttaa	actgggcttc	300
agccatgagg	tgcaagttcac	cgctcctcca	gctgtccgtg	tctttcgctt	aaaacccaac	360
ataatctgct	gcaccggcat	cgataaggac	agggtgcacc	agttcgccgg	cgccatccgg	420
agctctaaag	ctccagaggt	gtacaagggg	aaggggatcc	tgtacattga	cgaggttacc	480
aagctgaagc	ccggaaagaa	gcgaaaaaat	aagtgaacat	ccgaaGgcgt	tacaactttt	540
tctgtctttt	Aaocccattc	ttcgacattg	tagtgatctg	gatctggggt	ctgctgtgtt	600
gtgtgtgtga	cttgctgtgt	gctaacacaga	tcaccattat	cttaccttta	cctcagctgc	660
atgtaggacc	atgagtgagg	ataagttacc	agtttggtga	tatgagctgg	aacgtttgct	720
tgcaatttgg	attgattacc	cgagtgggat	gttttggttc	aaacttgaag	tctttcaata	780
gattgttgc						

(2) INFORMATION FOR SEQ ID NO:3904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3904:

Glu	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Thr	His	Asp	Thr	Asn	Xaa	Ala	Ala	
1			5					10					15			
Ser	Arg	Gly	Gly	Arg	Asn	Pro	Ser	Gly	Thr	Gly	Asp	Gly	Gly	Ala	Leu	
			20					25					30			
Pro	Val	Thr	Gly	Asp	Thr	Ala	Ala	Ser	Ser	Pro	Pro	Pro	Ser	Pro	Ala	
			35					40					45			
Arg	Arg	Arg	Ser	Ser	Arg	Pro	Ala	Gly	Cys	Leu	Lys	Ser	Ser	Pro	Phe	
			50					55					60			
Asn	Leu	Asn	Gly	Ser	Gln	Val	Phe	Pro	Phe	Pro	Glu	Ala	Arg	Trp	Gly	
			65					70					75		80	
Arg	Leu	Gln	Ser	Glu	Val	Arg	Glu	Pro	Arg	Pro						
			85					90								

(2) INFORMATION FOR SEQ ID NO:3905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3905:

Met	Glu	Ala	Lys	Phe	Phe	Arg	Phe	Leu	Lys	Leu	Val	Gly	Val	Gly	Phe	
1			5					10					15			
Lys	Ala	Arg	Ser	Glu	Ser	Gln	Gly	Arg	Glu	Leu	Phe	Leu	Lys	Leu	Gly	
			20					25					30			
Phe	Ser	His	Glu	Val	Gln	Phe	Thr	Ala	Pro	Pro	Ala	Val	Arg	Val	Phe	
			35					40					45			
Cys	Phe	Lys	Pro	Asn	Ile	Ile	Cys	Cys	Thr	Gly	Ile	Asp	Lys	Asp	Arg	
			50					55					60			
Val	His	Gln	Phe	Ala	Gly	Ala	Ile	Arg	Ser	Ser	Lys	Ala	Pro	Glu	Val	

(2) INFORMATION FOR SEQ ID NO:3906:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..625

(D) OTHER INFORMATION: / Ceres Seq. ID 1578695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3906:

TAX2_SUG2						
gacatcgagctg	cctcgggtcga	tttctaatttc	tctctgcagag	cccaaacctct	aaacctaaac	60
ccttcgaacagg	cngcgcgcgcg	cgccgcgcgtc	cgccgcacaga	cctccgtatgc	gcccgacgcgc	120
cgtaggaacggg	gagggagagcca	gcaccagagcca	ccatgggtctg	cgctgcgcacc	aagacgcgtga	180
agaaagacctc	caggcagggtg	ataggaagaat	actactcccg	catgaccttc	gaotctccaca	240
ccacaacagaa	gtgtcgtggaa	gagtgcttcca	tctctcccttc	gaagcgcctc	cgcgaacaagg	300
ttgcgcgctct	caccacccacg	ctgatgcgcgc	gcattccaaag	ggggcccccgt	cctctttctcc	360
ggcgcgtcggtg	cagccacccag	gtgtgtggcgc	ctacggcgctc	ggggggcgctc	gtctgaaggag	420
ctgatctgtgc	ggcccatcct	ggctctggcgc	gaatttatctt	ttctatctatc	agtatcgtgt	480
taccgttgctg	ttctgttcacc	gtgttagtgtt	cggttctacc	tttgatttag	gtgtgtgttac	540
cctctgttgtt	cccttgtggtt	gtctccgccta	tgaaacagaga	cgagagaaga	atgagcaagg	600
tttttgtttgt	cagctatgtt	tgctc				

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3907:

1	Ser	Gly	Cys	Leu	Gly	Arg	Phe	Leu	Ile	Leu	Leu	Ala	Ser	Pro	Asn	Pro
5										10					15	
1	Lys	Pro	Lys	Pro	Phe	Thr	Arg	Xaa	Arg	Arg	Arg	Arg	Arg	Arg	Arg	His
20									25					30		
1	His	Ile	Arg	Ser	Ala	Gln	Pro	Pro	Glu	Lys	Arg	Arg	Glu	Pro	Ala	Pro
35								40					45			
1	Ala	Thr	Met	Gly	Arg	Val	Arg	Thr	Lys	Thr	Val	Lys	Lys	Thr	Ser	Arg
50							55					60				
1	Gln	Val	Ile	Glu	Lys	Tyr	Tyr	Ser	Arg	Met	Thr	Leu	Asp	Phe	His	Thr
65						70					75				80	
1	Asn	Lys	Lys	Val	Leu	Glu	Glu	Val	Ser	Ile	Leu	Pro	Ser	Lys	Arg	Leu
85										90					95	
1	Arg	Asn	Lys	Val	Ala	Gly	Phe	Thr	Thr	His	Leu	Met	Arg	Arg	Ile	Gln
100									105						110	
1	Arg	Gly	Pro	Arg	Pro	Leu	Leu	Arg	Arg	Leu	Gly	Ala	Thr	Glu	Val	Val
115								120					125			
1	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Xaa	Ala	Gly	Gly	Thr	Asp	Val	Trp	Ala
130							135					140				
1	His	Pro	Gly	Phe	Gly	Arg	Val	Ile	Leu	Ser	Ile	Tyr	Ser	Ile	Val	Leu
145						150					155				160	
1	Pro	Phe	Ala	Ser	Val	Thr	Val	Leu	Val	Ser	Val	Leu	Pro	Leu	Asp	

165 170 175

(2) INFORMATION FOR SEQ ID NO:3908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1578697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3908:

Met	Gly	Arg	Val	Arg	Thr	Lys	Thr	Val	Lys	Lys	Thr	Ser	Arg	Gln	Val
1						5			10					15	
Ile	Glu	Lys	Thr	Tyr	Ser	Arg	Met	Thr	Leu	Asp	Phe	His	Thr	Asn	Lys
			20					25					30		
Lys	Val	Leu	Glu	Glu	Val	Ser	Ile	Leu	Pro	Ser	Lys	Arg	Leu	Arg	Asn
		35					40					45			
Lys	Val	Ala	Gly	Phe	Thr	Thr	His	Leu	Met	Arg	Arg	Ile	Gln	Arg	Gly
		50					55				60				
Pro	Arg	Pro	Leu	Leu	Arg	Arg	Leu	Gly	Ala	Thr	Glu	Val	Val	Ala	Ala
65					70					75					80
Thr	Ala	Ala	Ala	Ala	Xaa	Ala	Gly	Gly	Thr	Asp	Val	Trp	Ala	His	Pro
				85					90					95	
Gly	Phe	Gly	Arg	Val	Ile	Leu	Ser	Ile	Tyr	Ser	Ile	Val	Leu	Pro	Phe
			100					105					110		
Ala	Ser	Val	Thr	Val	Leu	Val	Ser	Val	Leu	Pro	Leu	Asp			
		115				120					125				

(2) INFORMATION FOR SEQ ID NO:3909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1578698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3909:

Met	Thr	Leu	Asp	Phe	His	Thr	Asn	Lys	Lys	Val	Leu	Glu	Glu	Val	Ser
1								5		10				15	
Ile	Leu	Pro	Ser	Lys	Arg	Leu	Arg	Asn	Lys	Val	Ala	Gly	Phe	Thr	Thr
				20					25					30	
His	Leu	Met	Arg	Arg	Ile	Gln	Arg	Gly	Pro	Arg	Pro	Leu	Leu	Arg	Arg
		35					40					45			
Leu	Gly	Ala	Thr	Glu	Val	Val	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Xaa	Ala
		50					55				60				
Gly	Gly	Thr	Asp	Val	Trp	Ala	His	Pro	Gly	Phe	Gly	Arg	Val	Ile	Leu
65					70					75					80
Ser	Ile	Tyr	Ser	Ile	Val	Leu	Pro	Phe	Ala	Ser	Val	Thr	Val	Leu	Val
			85					90						95	
Ser	Val	Leu	Pro	Leu	Asp										
		100													

(2) INFORMATION FOR SEQ ID NO:3910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 592 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..592

(D) OTHER INFORMATION: / Ceres Seq. ID 1578699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3910:

acacacacca	tcgtcctctc	ctttgccagc	gcgcgcgaac	cgcgccaccg	cctctcccca	60
tcctcgaagc	acggaaggct	ccagaagga	gctctcacct	cgcagccatc	tcctggcacgt	120
ccgtccttct	tctcctcggg	tcctccccc	tctccacagc	tatcggattg	gcgttggagat	180
ggagatcgac	ccgggctcgg	aattcccttc	gttggttaag	aaccttaatt	tggtcagatg	240
ggatttccaa	cttcgcacaa	gccgcgcagg	tcgatcgatc	tcagttgacg	cgaggggattg	300
gaaaaactaag	ttgcgggtgt	agttaatttt	ctaggaagat	tggggtttca	gctcaaaactc	360
ccatgctcga	cgtcgaggac	gaccctggcg	ggagatgacg	aggatctctg	tcgacgcgcg	420
gaccgcgcgc	tcctcgtcca	gtcccgccg	ctcgacacgc	cagccagtcg	agccggcagc	480
agctgcccg	gaggaggagt	tgccgctgca	acctcaacca	cagctgcgcg	agctattggc	540
catagatgat	acaactgata	atttaaatga	gggcagcgag	aatatcagca	at	

(2) INFORMATION FOR SEQ ID NO:3911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3911:

Thr	His	Thr	Ile	Val	Leu	Ser	Phe	Ala	Ser	Ala	Ala	Glu	Pro	Ala	Thr
1		5						10				15			
Ser	Leu	Leu	Pro	Ser	Ser	Lys	His	Gly	Arg	Leu	Pro	Glu	Gly	Ala	Leu
		20					25					30			
Thr	Ser	Gln	Pro	Ser	Leu	Ala	Arg	Pro	Ser	Phe	Phe	Ser	Leu	Gly	Pro
		35				40					45				
Ser	Pro	Ser	Pro	Gln	Leu	Ser	Asp	Trp	Arg	Trp	Ser	Gly	Asp	Arg	Pro
		50				55					60				
Gly	Leu	Gly	Ile	Pro	Phe	Val	Gly	Lys	Glu	Pro					
		70							75						

(2) INFORMATION FOR SEQ ID NO:3912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1578701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3912:

His	Thr	Pro	Ser	Ser	Ser	Pro	Leu	Pro	Ala	Pro	Pro	Asn	Pro	Pro	Pro
1		5					10					15			
Ala	Phe	Ser	His	Pro	Arg	Ser	Thr	Glu	Gly	Ser	Gln	Lys	Glu	Leu	Ser
		20					25					30			
Pro	Arg	Ser	His	Leu	Trp	His	Val	Arg	Pro	Ser	Ser	Pro	Ser	Val	Pro
		35				40					45				
Pro	Leu	Leu	His	Ser	Tyr	Arg	Ile	Gly	Val	Gly	Val	Glu	Ile	Asp	Pro
		50				55					60				
Gly	Ser	Glu	Phe	Pro	Ser	Leu	Val	Arg	Asn	Pro	Asn	Leu	Val	Arg	Trp
		70							75					80	
Asp	Phe	Gln	Leu	Arg	Gln	Ser	Pro	Arg	Gly	Arg	Ser	Ile	Ser	Val	Asp

85 90 95
Ala Arg Asp Trp Lys Thr Lys Leu Arg Val
100 105
(2) INFORMATION FOR SEQ ID NO:3913:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1578702
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3913:
Thr His His Arg Pro Leu Leu Cys Gln Arg Arg Thr Arg His Gln
1 5 10 15
Pro Ser Pro Ile Leu Glu Ala Arg Lys Ala Pro Arg Arg Ser Ser His
20 25 30
Leu Ala Ala Ile Ser Gly Thr Ser Val Leu Leu Leu Pro Arg Ser Leu
35 40 45
Pro Phe Ser Thr Ala Ile Gly Leu Ala Leu Glu Trp Arg Ser Thr Arg
50 55 60
Ala Arg Asn Ser Leu Arg Trp
65 70

(2) INFORMATION FOR SEQ ID NO:3914:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1051
(D) OTHER INFORMATION: / Ceres Seq. ID 1578703
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3914:
gagccaccac gagatccacg aatataccca tccattcccc cacaaggctc cgtcccttcg 60
gcggcgccga tgtctctccc cctrgcccg gcggacagtg gcgccggcac cggagacgac 120
tggtctctcg actgrrgcac cctcgacgac ctgcccgcgc cggcctgcgc ggccctcccg 180
tgggacgcgt ccccgctcgc ttccaacccc agtgtggaag tgggcagcta tgtaaacgcc 240
aatgatgcac tcaaggagcc caatgatgtc ttcaaggagc ctggcagcac taaacgttta 300
cggctcagat ccagtgatat gccaacatct aaagcttgca gggaaagaat gaggaggaac 360
aagctgaatg acagggtttc tgaactgggg tctgcattag aacctgggaa gccagtgaac 420
gctgacaaag ctgcccattc taagcgatgc tactcgcatg gttattcaag tccgttcaga 480
atcacagcaa ctgaaggaga ctaatggcac cctcgaagaa aagattaaag aactaaaggc 540
cgagaaggac gagttcgaga cgagaagcac aaactgaaac tggagaagga gactctagag 600
caccagatga agctgatggc atcggctcca gcctacatgc cccatcgac cctgatgccg 660
gcgcctttcg cccaggcgcc cctaactcca ttccatgccc agggccaagc tgcaggggag 720
aagctgatga tgccttctgt cggctaccaca gggtaaccac tgtggcagtt catgcgcct 780
tcagaggtcg acacctcgaa ggacagcgag gcgtgccctc ctgtcgcatg atcaccttga 840
tggggctggt cctgctcaca ccatgtggat tagccgcaac tagttgtgtg tgcgatcca 900
ttgatgggtg ataactgatg ttcttaggct atctccagca gcctctctat cctattctct 960
atcttactcc cttattttaa ttttactctg taaacagtac agtctatagt gtaagacaat 1020
gttttgcagt tttatatcca cgccttgctg g

(2) INFORMATION FOR SEQ ID NO:3915:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3915:

```
Glu Pro Pro Arg Asp Pro Arg Ile Tyr Pro Ser His Ser Pro Gln Gly
1      5      10      15
Ser Val Pro Ser Ala Ala Ala Met Ser Leu Pro Pro Xaa Pro Ala Asp
      20      25      30
Ser Gly Ala Gly Thr Gly Asp Asp Trp Phe Leu Asp Cys Xaa Ile Leu
      35      40      45
Asp Asp Leu Pro Ala Ala Ala Cys Gly Ala Phe Pro Trp Asp Ala Ser
      50      55      60
Pro Ser Ser Ser Asn Pro Ser Val Glu Val Gly Ser Tyr Val Asn Ala
      65      70      75
Asn Asp Ala Phe Lys Glu Pro Asn Asp Val Phe Lys Glu Pro Gly Ser
      85      90      95
Ser Lys Arg Leu Arg Ser Gly Ser Ser Asp Met Pro Thr Ser Lys Ala
      100     105     110
Cys Arg Glu Arg Met Arg Arg Asn Lys Leu Asn Asp Arg Phe Leu Glu
      115     120     125
Leu Gly Ser Ala Leu Glu Pro Gly Lys Pro Val Lys Ala Asp Lys Ala
      130     135     140
Ala Ile Pro Lys Arg Cys Tyr Ser His Gly Tyr Ser Ala Pro Phe Arg
      145     150     155
Ile Thr Ala Thr Glu Gly Asp
      165
```

(2) INFORMATION FOR SEQ ID NO:3916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1578705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3916:

```
Met Ser Leu Pro Pro Xaa Pro Ala Asp Ser Gly Ala Gly Thr Gly Asp
1      5      10      15
Asp Trp Phe Leu Asp Cys Xaa Ile Leu Asp Asp Leu Pro Ala Ala Ala
      20      25      30
Cys Gly Ala Phe Pro Trp Asp Ala Ser Pro Ser Ser Asn Pro Ser
      35      40      45
Val Glu Val Gly Ser Tyr Val Asn Ala Asn Asp Ala Phe Lys Glu Pro
      50      55      60
Asn Asp Val Phe Lys Glu Pro Gly Ser Ser Lys Arg Leu Arg Ser Gly
      65      70      75
Ser Ser Asp Met Pro Thr Ser Lys Ala Cys Arg Glu Arg Met Arg Arg
      85      90      95
Asn Lys Leu Asn Asp Arg Phe Leu Glu Leu Gly Ser Ala Leu Glu Pro
      100     105     110
Gly Lys Pro Val Lys Ala Asp Lys Ala Ala Ile Pro Lys Arg Cys Tyr
      115     120     125
Ser His Gly Tyr Ser Ala Pro Phe Arg Ile Thr Ala Thr Glu Gly Asp
      130     135     140
```

(2) INFORMATION FOR SEQ ID NO:3917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..991
(D) OTHER INFORMATION: / Ceres Seq. ID 1578737
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3917:

```

aaaaatcgaa  tcgagcccat  ccattcccat  ttccgccgcc  gccgccgccg  agagacccca      60
accccaccca  tccaccacca  tgtggcgccg  cctccacacc  ctagcccccg  cettgcgcag      120
ggctacccgc  gccgcgccgc  gggccctctc  ccgctttccg  ccgcaccagc  ccgtctctct  caggggacaa      180
ccgcctctcc  tcggcgccgc  ccgctttccg  ccgcaccagc  ccgtctctct  caggggacaa      240
ggccgagctc  aaggggaaga  agcggtttga  catggatccc  ctggtcggcc  ccttcggtac      300
caaggaggaa  ccattctgtg  ttgagtccta  ctataacaag  cggtatagtc  gctgccccgt      420
tggtgaggga  gaggatgaac  acgatgttgt  atggttcttg  ttgaaaaaag  atgagccgca      480
tgagtgtcca  gtctgtctgc  aatactttgt  gcttaaggtc  attggtgatG  ggtggtgatc      540
cagatgttca  tgacgatgaa  gatgatggac  atcactaagg  atgcctttgt  gttctgaaaa      600
taagaatttg  gtgaggcaga  tgaatccaat  acactttttt  ttctagaacc  agactgtctc      660
acggcatcct  tgtttatgaa  aagacagttg  gccatcaagc  aggtggtagt  ttccacctag      720
gtattttgtc  caaacaanaa  ctgtttgaga  ttgacccttt  gcgtttcttt  aagagcatcg      780
tcgaataaaa  gatgactgca  gtcagattgc  ttctctttta  tacctaatat  tggcccatcg      840
gggtgtgtag  acatgtaata  ttccagtaag  gaacagcccc  atttctatgc  tttagcgtgt      900
gggaattttg  acaaggcctc  cctatatcat  tgacgagttt  taagccagag  ttgatgatc      960
caacatgttt  atgaccattg  ttttaatagc  c

```

(2) INFORMATION FOR SEQ ID NO:3918:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1578738
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3918:

```

Lys Asn Arg Ile Glu Pro Ile His Leu His Phe Arg Arg Arg Arg Arg
1      5      10      15
Arg Glu Thr Pro Thr Pro Pro Ile His His Val Ala Pro Pro Pro
20      25      30
His Pro Ser Pro Arg Leu Ala Gln Gly Tyr Arg Arg Arg Arg Gly
35      40      45
Pro Cys Gly Val Arg Leu Leu Cys Ser Pro Arg Arg Pro Ala Leu Leu
50      55      60
Gly Gly Arg Arg Phe Pro Pro His Gln Pro Ala Pro Leu Arg Gly Gln
65      70      75      80
Ala Gly Glu Cys Gly Gly Arg His Ala His Arg His Gly Ala Arg Ala
85      90      95
Gly Gly Ala Gly Gly Arg Ala Gln Gly Glu Glu Ala Val
100      105

```

(2) INFORMATION FOR SEQ ID NO:3919:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1578739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3919:

Lys Ile Glu Ser Ser Pro Ser Ile Ser Ile Ser Ala Ala Ala Ala Ala
1 5 10 15
Glu Arg Pro Gln Pro His Pro Ser Thr Thr Met Trp Arg Arg Leu His
20 25 30
Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala
35 40 45
Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser
50 55 60
Ala Ala Ala Ala Phe Arg Arg Thr Ser Pro Leu Ser Gly Asp Lys
65 70 75 80
Pro Ala Ser Val Glu Asp Val Met Pro Ile Ala Thr Gly Leu Glu Arg
85 90 95
Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys Lys Arg Phe Asp Met Asp
100 105 110
Pro Leu Val Gly Pro Phe Gly Thr Lys Glu Glu Pro Ser Val Val Glu
115 120 125
Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys Pro Gly Gly Glu Gly Glu
130 135 140
Asp Glu His Asp Val Val Trp Phe Trp Leu Lys Lys Asp Glu Pro His
145 150 155 160
Glu Cys Pro Val Cys Ser Gln Tyr Phe Val Leu Lys Val Ile Gly Asp
165 170 175
Gly Trp

(2) INFORMATION FOR SEQ ID NO:3920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1578740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3920:

Met Trp Arg Arg Leu His Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr
1 5 10 15
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg
20 25 30
Ala Ala Pro Leu Ser Ser Ala Ala Ala Ala Phe Arg Arg Thr Ser Pro
35 40 45
Leu Leu Ser Gly Asp Lys Pro Ala Ser Val Glu Asp Val Met Pro Ile
50 55 60
Ala Thr Gly Leu Glu Arg Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys
65 70 75 80
Lys Arg Phe Asp Met Asp Pro Leu Val Gly Pro Phe Gly Thr Lys Glu
85 90 95
Glu Pro Ser Val Val Glu Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys
100 105 110
Pro Gly Gly Glu Gly Glu Asp Glu His Asp Val Val Trp Phe Trp Leu
115 120 125
Lys Lys Asp Glu Pro His Glu Cys Pro Val Cys Ser Gln Tyr Phe Val
130 135 140
Leu Lys Val Ile Gly Asp Gly Trp
145 150

(2) INFORMATION FOR SEQ ID NO:3921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..865
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3921:

gttggacatc	gcggcctcac	gcgttgcagc	tgccgcgcgtg	cggtactcgt	cgctgcgggg	60
ccgcggcgct	tgttgatcga	cactgtagta	tatagaacga	gccatccacg	cacataaagc	120
tacagcatct	gtcgcgtcgt	ctagcttggg	cggtggaccg	agagaccacg	cagctagatg	180
gcgcgcaggg	cggtcggcgt	tctactggcc	gtggccgcgc	tcttcggcgc	ggcgacggcg	240
agggcgggcg	acgacgacga	caagacgcag	ccctggcagt	gcttcaagtc	atgctccaga	300
rgctgccacc	accaccacga	ccacgaccac	gacaaacggc	ctgctgcctg	ggcggaattc	360
ctctccgggg	ccgcgcgcaa	ggtctccgcc	gccgtcaccc	gcgagtgcaa	gaacaacagc	420
tgccatgaca	acgcgtgctt	caaggacctg	ccggccatca	cctaccgcga	gtgcgccatc	480
gccacctgcc	Ctcagccatc	cgccaccatg	cagaaagaaa	acggcgctgt	tgaaggactg	540
ctgcgagaag	tgcttcatca	atggccacc	tgccgctggc	ccacctgcgc	ctggcccgcc	600
tgctgcctgg	ccacctgcgc	ctggcccgcc	tgctcctggt	cccagccoga	cgccaccatc	660
tccgcgcaat	taagcccatg	ttgcatggat	gctcttggtg	cacatgcatg	aagtagtaga	720
gagcaacggt	caacttactc	cttatattcc	cataataata	aaatacttag	gagtagctac	780
ttcaaaaaaa	gaaggatctc	atgactgtaa	ccgaagtgc	attttctctt	gagttggggt	840
gtaacataaa	cccagcacca	aagcc				

(2) INFORMATION FOR SEQ ID NO:3922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3922:

Met	Ala	Arg	Arg	Ala	Val	Gly	Val	Leu	Leu	Ala	Val	Ala	Ala	Leu	Leu
1			5					10					15		
Ala	Ala	Ala	Thr	Ala	Arg	Ala	Ala	Asp	Asp	Asp	Asp	Lys	Thr	Gln	Pro
			20					25					30		
Trp	Gln	Cys	Phe	Lys	Ser	Cys	Ser	Arg	Xaa	Cys	His	His	His	His	Asp
		35						40			45				
His	Asp	His	Asp	Asn	Gly	Ala	Ala	Ala	Val	Ala	Asp	Phe	Leu	Ser	Gly
		50			55						60				
Ala	Ala	Ala	Lys	Val	Ser	Ala	Ala	Val	Thr	Arg	Glu	Cys	Lys	Asn	Asn
		65			70				75				80		
Ser	Cys	His	Asp	Asn	Ala	Cys	Phe	Lys	Asp	Leu	Pro	Ala	Ile	Thr	Tyr
		85						90				95			
Pro	Gln	Cys	Ala	Ile	Ala	Thr	Cys	Pro	Gln	Pro	Ser	Ala	Pro		
		100						105				110			

(2) INFORMATION FOR SEQ ID NO:3923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1578746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3923:

Met	Thr	Thr	Arg	Ala	Ser	Arg	Thr	Cys	Arg	Pro	Ser	Pro	Thr	Arg	Ser
1				5				10						15	
Ala	Pro	Ser	Pro	Pro	Ala	Leu	Ser	His	Pro	His	His	Ser	Arg	Lys	Lys
				20				25					30		
Thr	Ala	Cys	Leu	Lys	Asp	Cys	Cys	Glu	Lys	Cys	Phe	Ile	Asn	Gly	Pro
				35				40					45		
Pro	Ala	Pro	Gly	Pro	Pro	Ala	Pro	Gly	Pro	Pro	Val	Pro	Gly	Pro	Pro
				50				55				60			
Ala	Pro	Gly	Pro	Pro	Ala	Pro	Gly	Pro	Ser	Pro	Thr	Pro	Pro	Ser	Pro
					70					75				80	
65															
Pro	Asn														

(2) INFORMATION FOR SEQ ID NO:3924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..857
(D) OTHER INFORMATION: / Ceres Seq. ID 1578754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3924:

acagccgcac	agccgcgcgc	gtccatccca	ctctccaca	ccatctgacg	ctgcttccac	60
cgagggtctcc	aaggctcaact	cctcaccagc	ttctgctctc	tcctctctca	ttctgtctct	120
gctctgaccc	gttaactctc	cagctcccc	tcgtctcggt	ccctccgcgc	caaatcacgc	180
ggaccaccac	cgctctcttc	aagatcgccg	ggcgggcacc	ggcgggcgat	gacatccacc	240
gtcaccacaa	ccgttgggtg	cggggggctc	ccgtccgcgc	cggttgcgac	agcgaccaga	300
ggagcggccac	gcagatgcGg	ccgtccgagc	ccaggccgcg	ggagcgratg	cctccaatga	360
taagtccagt	gaggtccatg	gcaagtcttc	cgagcagtag	gcccgcgcgc	ccaacacttt	420
cttctgcgcc	gacaagacag	tcactgcgct	cgatcatcaag	ggacttgctg	atcacaggga	480
tactcttgga	gctcctctat	gcccttgtag	gcattatgat	gacaaagctg	cggaggtagc	540
acaaggattt	tggaattgcc	catgtgtccc	catgcgtgag	aggaaggaat	gccactgtat	600
gctttttctt	actcccgata	atgactttgc	tggaagagat	caggttatct	ccctcgaggga	660
gatcaaaag	gcgacatcga	agtctcaagc	ccttgatttt	gtcacggagt	gtttacttga	720
cagctaattt	tttatatgta	tatgtactta	agtagcatct	ataagatatg	ccatcaggaa	780
aattttcata	aaatgtgcag	taaacagcac	ttcgcaaggc	tgccgatcat	ataagncncg	840
ttcggccttt	ttattgc					

(2) INFORMATION FOR SEQ ID NO:3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..178
(D) OTHER INFORMATION: / Ceres Seq. ID 1578755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3925:

Ser	Arg	Thr	Ala	Ala	Ala	Pro	Ser	Thr	Ser	Pro	His	His	Leu	Thr
1				5				10					15	
Leu	Leu	Pro	Pro	Arg	Ser	Pro	Arg	Leu	Thr	Pro	His	Gln	Leu	Leu
				20				25				30		
Ser	Pro	Ser	Ser	Ser	Leu	Leu	Cys	Ser	Gly	Pro	Leu	Thr	Leu	Gln
					35			40				45		

Pro Leu Ala Pro Phe Pro Ser Ala Gln Ile Thr Gly Thr Thr Thr Ala
50 55 60
Phe Phe Lys Ile Gly Gly Arg Ala Pro Ala Gly Asp Asp Ile His Arg
65 70 75 80
His His Asn Arg Trp Val Arg Gly Ala Pro Arg Pro Pro Val Val Asp
85 90 95
Ser Asp Gln Arg Thr Pro Thr Gln Met Pro Pro Ser Glu Pro Arg Pro
100 105 110
Arg Glu Xaa Met Pro Pro Met Ile Ser Gln Trp Arg Ser Cys Ala Ser
115 120 125
Ser Pro Ser Ser Thr Pro Ala Ala Pro Thr Leu Ser Ser Ala Pro Thr
130 135 140
Arg Gln Ser Leu Pro Ser Ser Ser Arg Asp Leu Leu Ile Thr Gly Ile
145 150 155 160
Leu Leu Glu Leu Leu Tyr Ala Leu Val Gly Ile Met Met Thr Lys Leu
165 170 175
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1578756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3926:

Met Arg Lys Phe Ser Glu Gln Tyr Ala Arg Arg Ser Asn Thr Phe Phe
1 5 10 15
Cys Ala Asp Lys Thr Val Thr Ala Val Val Ile Lys Gly Leu Ala Asp
20 25 30
His Arg Asp Thr Leu Gly Ala Pro Leu Cys Pro Cys Arg His Tyr Asp
35 40 45
Asp Lys Ala Ala Glu Val Ala Gln Gly Phe Trp Asn Cys Pro Cys Val
50 55 60
Pro Met Arg Glu Arg Lys Glu Cys His Cys Met Leu Phe Leu Thr Pro
65 70 75 80
Asp Asn Asp Phe Ala Gly Lys Asp Gln Val Ile Ser Phe Glu Glu Ile
85 90 95
Lys Glu Ala Thr Ser Lys Phe
100

(2) INFORMATION FOR SEQ ID NO:3927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1578759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3927:

acactatata	accttctctc	ttcgccgtgc	tccgatttga	cacacctccc	aaaccttaca	60
ctcccgcg	cgcgccgcgc	ggcgcasagc	ggcagcagca	tccgaagatg	gtgaagtccc	120
tcaagcccg	caagcccggt	atcctcctcc	agggccgCtt	cgccggcagg	aaggcagtta	180
tcgtgcgcgt	gttcgagagag	ggcaccgcgc	accgcccccta	tggccactgc	ctcgtcgcag	240
gcctcgccaa	gtaccctaaa	aaggtgatcc	gcaaggactc	cgccaagaag	actgcgaaga	300

agtcgcgcgt caagtgtctt atcaagctcg tcaacttcac tcaacttcac cccaccgcgt 360
acaccctcga cgtcgatttc aaggatgtcg ccaacgggtg gcccgacgca ctctctacc 420
acgacaagaa ggtgcgccgc tcaagacgg ccaagcgcg ccttgaggag aggttcaaga 480
cggacaagaa cagggtgttc ttaccacgC tccgtctcta gatgtcggc ctcccgaaata 540
gtcgtgtttt agctgtcgat ttgtgttata ggacacact catctctgtt ttgctattac 600
catgaatatt tctgtTttta gtccgtgggc tctcagagat aaatttgcta agatatgccg 660
ttgtgtgttt acatgttttc gtgataggtc tggttaaaat tttgtctgtt ttc

(2) INFORMATION FOR SEQ ID NO:3928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1578760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3928:

Met	Val	Lys	Phe	Leu	Lys	Pro	Gly	Lys	Ala	Val	Ile	Leu	Leu	Gln	Gly
1		5						10					15		
Arg	Phe	Ala	Gly	Arg	Lys	Ala	Val	Ile	Val	Arg	Val	Phe	Glu	Glu	Gly
		20						25					30		
Thr	Arg	Asp	Arg	Pro	Tyr	Gly	His	Cys	Leu	Val	Ala	Gly	Leu	Ala	Lys
		35					40					45			
Tyr	Pro	Lys	Lys	Val	Ile	Arg	Lys	Asp	Ser	Ala	Lys	Lys	Thr	Ala	Lys
		50				55					60				
Lys	Ser	Arg	Val	Lys	Cys	Phe	Ile	Lys	Leu	Val	Asn	Phe	Thr	His	Leu
		65			70					75				80	
Met	Pro	Thr	Arg	Tyr	Thr	Leu	Asp	Val	Asp	Phe	Lys	Asp	Val	Ala	Thr
			85				90						95		
Gly	Gly	Pro	Asp	Ala	Leu	Ser	Thr	His	Asp	Lys	Lys	Val	Ala	Ala	Cys
		100					105						110		
Lys	Thr	Ala	Lys	Ala	Arg	Leu	Glu	Glu	Arg	Phe	Lys	Thr	Gly	Lys	Asn
		115				120						125			
Arg	Trp	Phe	Phe	Thr	Lys	Lys	Arg	Phe							
		130				135									

(2) INFORMATION FOR SEQ ID NO:3929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..889

(D) OTHER INFORMATION: / Ceres Seq. ID 1578777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3929:

catgaggatg	gaaactttta	ccctggaact	ggagctgctc	atgagggtggg	agttcttgat	60
gggtcaaggat	tctcagttta	tataccttgg	agccgtgtgtg	gtgttgaggag	tgatgactac	120
atcttctggt	tctcagactgt	ggtgtctoca	atagcttcag	agtttgcgcg	agacatcact	180
ataaatctcg	caggattcga	tgcagctaga	ggtgaccctc	tgggtttgtt	tgcgtcact	240
ccaactggat	actcttggat	gacatccctg	ctagctgggt	ccctcaaatgg	aagattgttg	300
gtgatacctg	aggaggagata	caatctcccg	tcatatcct	catcagctac	tgaagttgtt	360
aaggtccctac	tgggggaggg	tcccaatcgt	gcttcatttg	tagtttcacc	atcaaaagag	420
gccttgcgta	ctgttttctca	agtcctgaag	attcaacaac	aattttggcc	agttttaggt	480
ccaacatacg	catcaactaca	ggcgcaGcag	gggtcggttt	cttccaactca	tagcaatgag	540
ctgaagaaaa	ggaagcgcttc	aggaggagga	ccagggccct	tctggtggaa	gatgggaagc	600
aaaagggttc	tatacgaagc	gcttatttag	cctcgacgac	gtccgaggaa	actcaagggg	660
tcaactgggt	cagcagcgcc	ttagatgtgg	gcagtttgct	ggccgttgat	cttctagaca	720

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tgaacagggt agctcgctga ccgcgtttcc tcaagcagag taggctgcgt ttacgtagaa 780
aacctacttt tggctggtta cttgcatgat ggtcgacogt ttcagatgga gtttgacagc 840
aaaccggttg tggtaaccat gcgtggcgta tcagccgatg tttcatgcc

(2) INFORMATION FOR SEQ ID NO:3930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3930:

His	Glu	Asp	Gly	Asn	Phe	Tyr	Pro	Gly	Thr	Gly	Ala	Ala	His	Glu	Val
1			5					10					15		
Gly	Val	Leu	Asp	Gly	Gln	Gly	Phe	Ser	Val	Asn	Ile	Pro	Trp	Ser	Arg
			20				25				30				
Gly	Gly	Val	Gly	Asp	Asp	Asp	Tyr	Ile	Phe	Ala	Phe	Gln	Thr	Val	Val
			35				40					45			
Leu	Pro	Ile	Ala	Ser	Glu	Phe	Ala	Ala	Asp	Ile	Thr	Ile	Ile	Ser	Ala
			50				55			60					
Gly	Phe	Asp	Ala	Ala	Arg	Gly	Asp	Pro	Leu	Gly	Cys	Cys	Asp	Val	Thr
65			70				75						80		
Pro	Thr	Gly	Tyr	Ser	Trp	Met	Thr	Ser	Leu	Leu	Ala	Gly	Ser	Ser	Asn
			85				90						95		
Gly	Arg	Leu	Leu	Val	Ile	Leu	Glu	Gly	Gly	Tyr	Asn	Leu	Arg	Ser	Ile
			100				105						110		
Ser	Ser	Ser	Ala	Thr	Glu	Val	Val	Lys	Val	Leu	Leu	Gly	Glu	Gly	Pro
			115				120					125			
Asn	Arg	Ala	Ser	Phe	Val	Val	Ser	Pro	Ser	Lys	Glu	Ala	Leu	Arg	Thr
			130				135				140				
Val	Ser	Gln	Val	Leu	Lys	Ile	Gln	Gln	Gln	Phe	Trp	Pro	Val	Leu	Gly
145			150							155				160	
Pro	Thr	Tyr	Ala	Ser	Leu	Gln	Ala	Gln	Gln	Gly	Ser	Val	Ser	Ser	Asn
			165				170						175		
His	Ser	Asn	Glu	Leu	Lys	Lys	Arg	Lys	Arg	Ser	Gly	Gly	Gly	Pro	Gly
			180				185						190		
Pro	Phe	Trp	Trp	Lys	Met	Gly	Ser	Lys	Arg	Leu	Leu	Tyr	Glu	Ala	Leu
			195				200					205			
Ile	Glu	Pro	Arg	Ser	Arg	Pro	Arg	Lys	Leu	Lys	Gly	Ser	Thr	Gly	Ser
			210				215				220				
Ala	Ala	Pro													
225															

(2) INFORMATION FOR SEQ ID NO:3931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3931:

Met	Thr	Ser	Leu	Leu	Ala	Gly	Ser	Ser	Asn	Gly	Arg	Leu	Leu	Val	Ile
1			5							10			15		
Leu	Glu	Gly	Gly	Tyr	Asn	Leu	Arg	Ser	Ile	Ser	Ser	Ser	Ala	Thr	Glu
			20				25						30		

Val Val Lys Val Leu Leu Gly Glu Gly Pro Asn Arg Ala Ser Phe Val
35 40 45
Val Ser Pro Ser Lys Glu Ala Leu Arg Thr Val Ser Gln Val Leu Lys
50 55 60
Ile Gln Gln Gln Phe Trp Pro Val Leu Gly Pro Thr Tyr Ala Ser Leu
65 70 75 80
Gln Ala Gln Gln Gly Ser Val Ser Ser Asn His Ser Asn Glu Leu Lys
85 90 95
Lys Arg Lys Arg Ser Gly Gly Gly Pro Gly Pro Phe Trp Trp Lys Met
100 105 110
Gly Ser Lys Arg Leu Leu Tyr Glu Ala Leu Ile Glu Pro Arg Ser Arg
115 120 125
Pro Arg Lys Leu Lys Gly Ser Thr Gly Ser Ala Ala Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..810

(D) OTHER INFORMATION: / Ceres Seq. ID 1578782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3932:

gatgatatt tgcagattag tctacacgag tcacgatagg aggaagactg gaagaggagg 60
cgagcacggt tgcggtgcc accctcacgc tccactccaa aaccccaaat ccagttccgt 120
tccaatcgcc gagaaggcca gcaaaaggga gaaaaaaag gaaaacgatr gmgcgccg 180
gcggcgagaa cagcgcgcg gngcgaggcg gagggcgagt ttacctcgcg ctactacgtg 240
ggtccaaagg gcaagttcgg gcacgagttc ctcgagttcg agttccgccc cgacggcaag 300
ctccgCtaacg ccaacaactc caactacaag aacgacacca tgatccgcaa ggaggtcttc 360
gtctcgccct ccgtccctcg cgaggccagg aggatcatcc aggagtcoga catcatgaag 420
gaggacgaca gcaactggcc cgagcccgac cgcatcgcc gccaggagct cgagatcgtc 480
atgggcaacg agcacatttc attcaccact tccaagatcg gctccctcgt cgatgtccag 540
tccagcaagg acccgaggagg cctccggatc ttctactacc ttgtccagga tetgaagtgt 600
ttcgtgttct cgctcatcaa ccttcacttc aagatcaagc caatccagtc ttgagctcca 660
tcccaagcct tcatgtagct ggtttgtgag actgcgagtg ttttgagaga gaacctttta 720
accatgtaag atgatgttga tattgtggac gatgcgcgag atcgacctg tegtgtgcac 780
ttagtgaag tggaaacccc ctttgcattt

(2) INFORMATION FOR SEQ ID NO:3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1578783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3933:

Met Asp Ile Cys Arg Leu Val Tyr Thr Ser His Asp Arg Arg Lys Thr
1 5 10 15
Gly Arg Gly Gly Glu His Val Cys Gly Ala His Pro His Arg Pro Leu
20 25 30
Gln Asn Pro Lys Ser Ser Ser Val Pro Ile Ala Glu Lys Gly Ser Lys
35 40 45
Gly Glu Lys Lys Lys Glu Asn Asp Xaa Xaa Xaa Arg Arg Arg Glu Gln
50 55 60
Arg Arg Xaa Ala Arg Ala Arg Ala Ser Phe Thr Cys Ala Thr Thr Trp

65				70						75					80
Val	Thr	Arg	Ala	Ser	Ser	Gly	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ala
				85						90					95
Pro	Thr	Ala	Ser	Ser	Ala	Thr	Pro	Thr	Thr	Pro	Thr	Thr	Arg	Thr	Thr
			100					105					110		
Pro															

(2) INFORMATION FOR SEQ ID NO:3934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3934:

Met	Ile	Arg	Lys	Glu	Val	Phe	Val	Ser	Pro	Ser	Val	Leu	Arg	Glu	Ala
1			5						10					15	
Arg	Arg	Ile	Ile	Gln	Glu	Ser	Asp	Ile	Met	Lys	Glu	Asp	Asp	Ser	Asn
			20					25				30			
Trp	Pro	Glu	Pro	Asp	Arg	Ile	Gly	Arg	Gln	Glu	Leu	Glu	Ile	Val	Met
			35				40					45			
Gly	Asn	Glu	His	Ile	Ser	Phe	Thr	Thr	Ser	Lys	Ile	Gly	Ser	Leu	Val
			50			55					60				
Asp	Val	Gln	Ser	Ser	Lys	Asp	Pro	Glu	Gly	Leu	Arg	Ile	Phe	Tyr	Tyr
65					70				75					80	
Leu	Val	Gln	Asp	Leu	Lys	Cys	Phe	Val	Phe	Ser	Leu	Ile	Asn	Leu	His
			85					90					95		
Phe	Lys	Ile	Lys	Pro	Ile	Gln	Ser								
			100												

(2) INFORMATION FOR SEQ ID NO:3935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..653
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3935:

aagactggcg	aaacgcggtg	ttttctctct	ttccccaagg	caaccaaacc	atctcgattc	60
tcgactcgtcg	gggaagtctt	gctctcrccg	cgctcgacgg	cctaggggtc	gaggaacgtc	120
cgctcgtccg	tcgggggaag	gagcggttag	gagggcgaga	tgatcgaggt	ggtgctcaac	180
gaccgcctcg	ggaagaaggt	gcgggtcaag	tgcaacgagg	acgacaccat	cggcgacctc	240
aagaagctcg	tgccggcgca	gacgggggac	cgccccgaga	agatcgcat	ccagaagtgg	300
tacaacatct	acaaggacca	catcacccct	aaggactacg	aggtccacga	cggcgatggg	360
ctcgagctct	actacaactg	agccgcgcgc	cctctctccc	tctcgtcagg	ttggctctgaa	420
ttctgaagtc	atgggtgcga	ttCkcttcgc	ggtgatctct	taagctcatc	acatatataa	480
aagcaacctc	atgtggctct	gtaagacatg	gcgtgccaaa	ctatcagtga	ccactgacag	540
ctttgcaata	cggtgtgtga	tggtcaacct	gcaaaccttg	tgtaactgcta	ctcgtactact	600
aaataacata	gggttttaac	cttggttgtg	tataagtgca	tctttttctca	ttc	

(2) INFORMATION FOR SEQ ID NO:3936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578787
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3936:
Arg Leu Ala Lys Arg Val Val Phe Leu Phe Ser Pro Arg Gln Pro Asn
1 5 10 15
His Leu Asp Ser Arg Leu Val Gly Lys Phe Arg Ser Xaa Arg Arg Arg
 20 25 30
Arg Pro Arg Val Arg Gly Thr Ser Val Arg Pro Ser Gly Glu Gly Ala
 35 40 45
Val Gly Arg Arg Arg
50

(2) INFORMATION FOR SEQ ID NO:3937:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578788
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3937:
Asp Trp Arg Asn Ala Leu Phe Ser Ser Phe Pro Gln Gly Asn Gln Thr
1 5 10 15
Ile Ser Ile Leu Asp Ser Trp Gly Ser Phe Ala Leu Xaa Gly Val Asp
 20 25 30
Gly Leu Gly Phe Glu Glu Arg Pro Ser Val Arg Pro Gly Lys Glu Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3938:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..73
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578789
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3938:
Met Ile Glu Val Val Leu Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15
Lys Cys Asn Glu Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Val Ala
 20 25 30
Ala Gln Thr Gly Thr Arg Pro Glu Lys Ile Arg Ile Gln Lys Trp Tyr
 35 40 45
Asn Ile Tyr Lys Asp His Ile Thr Leu Lys Asp Tyr Glu Val His Asp
50 55 60
Gly Met Gly Leu Glu Leu Tyr Tyr Asn
65 70

(2) INFORMATION FOR SEQ ID NO:3939:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..713
(D) OTHER INFORMATION: / Ceres Seq. ID 1578793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3939:

gctagcggtc	cgacaccaact	caccggtg	ctccaaactc	atttctcccg	agcgccgcg	60
cgagcctctg	tccagcttc	gttcattggt	tcctcaccg	gatccgctct	ctcctttg	120
agcccgctca	agcaatcag	cattaatgt	gtctcttCc	tctggtctaa	ggaagataa	180
tgtagcctc	cgcttcgac	cagtgccaca	aagattcgct	gtctgctgtc	ctgctaaaaa	240
ggagactgtg	gategggttt	gtgatattgt	caagaagcag	cttgacattc	ctgagggcac	300
tgaagctctg	ggctcctcta	agtttcaaga	cctcggtgct	gattcgttgg	acactgttta	360
gattgttatg	ggccttgagg	aggctttcaa	gatcactgta	gaggagtcga	gcgcgcagtc	420
aatcgcaact	gtggaagatg	ctgctaattc	catcgacgaa	cttggttcag	gagcagcaaa	480
ctatgctttaa	actcgtggtc	gtattgcgtt	gggtgctgta	ccagggcattc	actgtttgtt	540
ctatgcccc	ttccctacta	gattttcttt	tctaccctgg	gcttgagag	atgtttctgt	600
catgactgtc	attgtggatc	tcgggatatt	gttatattga	agctttttgt	ctgttcaag	660
aaaagaaaat	gttggtgcga	tatatattgt	attatatgta	attttttttt	gtc	

(2) INFORMATION FOR SEQ ID NO:3940:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1578794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3940:

Leu	Ala	Val	Arg	Thr	His	Ser	Pro	Val	Ala	Ser	Lys	Leu	Ile	Ser	Pro
1			5						10					15	
Glu	Arg	Arg	Arg	Glu	Pro	Leu	Phe	Gln	Leu	Arg	Ser	Trp	Leu	Pro	Ser
			20					25					30		
Pro	Asp	Pro	Leu	Ser	Pro	Leu	Arg	Gly	Pro	Ser	Arg	Gln	Ser	Ala	Leu
			35					40					45		
Ser	Leu	Ser	Leu	Ser	Ser	Gly	Leu	Arg	Lys	Asp	Asn	Val	Ala	Phe	Arg
			50				55				60				
Leu	Gln	Pro	Val	Pro	Gln	Arg	Phe	Ala	Val	Cys	Cys	Pro	Ala	Lys	Lys
			65			70			75				80		
Glu	Thr	Val	Asp	Arg	Val	Cys	Asp	Ile	Val	Lys	Lys	Gln	Leu	Ala	Leu
			85				90						95		
Pro	Glu	Gly	Thr	Glu	Val	Cys	Gly	Ser	Lys	Phe	Gln	Asp	Leu	Gly	
			100				105					110			
Ala	Asp	Ser	Leu	Asp	Thr	Val	Glu	Ile	Val	Met	Gly	Leu	Glu	Glu	Ala
			115				120					125			
Phe	Lys	Ile	Thr	Val	Glu	Glu	Ser	Ser	Ala	Gln	Ser	Ile	Ala	Thr	Val
			130				135					140			
Glu	Asp	Ala	Ala	Asn	Leu	Ile	Asp	Glu	Leu	Val	Ala	Gly	Ala	Ala	Lys
			145			150				155					160
Ser	Cys														

- (2) INFORMATION FOR SEQ ID NO:3941:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..674
(D) OTHER INFORMATION: / Ceres Seq. ID 1578799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3941:

attatgcagc	agattgtgaa	gaaacagctg	tctccaaagc	gagaagacga	agaaggggga	60
aatcgagaga	tgaagctacca	gagagtcacct	cccgagggaac	cctaccctcc	tccaggacat	120
cctcgatctc	agggcgacccc	ttaccacaccg	ccaccagatg	tgtacccgcc	teccccctcg	180
ggccatggac	atccaccacc	accccatggc	gtgtaccocg	cgccgcgcga	gggtccttac	240
ccccaccac	agcagctcc	accgggttac	cagggctact	tcaacgacca	gcagcgtcct	300
tactaacggc	cgccgatgg	agagcatcaa	cacaaccacc	accagggaaa	ccagggtagc	360
tcctctgggt	tcctcaagg	atgtttggct	gctctctctg	ctgctgcgtg	ctggaggaaat	420
gctgcggctg	ctctgagac	gtgagatgtc	cggaatccg	atcgcaagtt	atcgctgcta	480
gcattcgagg	gcacccacgt	tattatcata	taatagtaac	tggtgcttga	aataatctgg	540
agcagcagtg	ttcatgagct	ccagcccccg	catattatatt	ctcataattt	gtagtacgtt	600
ctatgattta	tccgaaaata	aaggactcta	tatatgggat	tctaataaag	gtatttgcat	660
atttcaggg	atcc					

(2) INFORMATION FOR SEQ ID NO:3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1578800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3942:

Ile	Ser	Gln	Gln	Ile	Val	Lys	Lys	Gln	Leu	Ser	Pro	Lys	Arg	Glu	Asp	
1				5				10						15		
Glu	Glu	Arg	Gly	Asn	Arg	Glu	Met	Ser	Tyr	Gln	Arg	Val	Pro	Pro	Glu	
			20					25					30			
Glu	Pro	Tyr	Pro	Pro	Pro	Gly	His	Pro	Arg	Ser	Gln	Ala	His	Pro	Tyr	
			35				40					45				
Pro	Pro	Pro	Pro	Asp	Val	Tyr	Pro	Pro	Pro	Pro	Arg	Gly	His	Gly	His	
			50			55						60				
Pro	Pro	Pro	Pro	His	Gly	Val	Tyr	Pro	Pro	Pro	Pro	Gln	Gly	Pro	Tyr	
65				70				75						80		
Pro	Pro	Pro	Gln	Gln	Pro	Pro	Pro	Gly	Tyr	Gln	Gly	Tyr	Phe	Asn	Asp	
			85					90						95		
Gln	Gln	Arg	Pro	Tyr	Tyr	Pro	Pro	Pro	His	Gly	Glu	His	Gln	His	Asn	
			100					105					110			
His	His	Gln	Gly	Asn	Gln	Gly	Ser	Ser	Ser	Gly	Phe	Leu	Lys	Gly	Cys	
			115				120					125				
Leu	Ala	Ala	Leu	Ser	Ala	Ala	Ala	Cys	Trp	Arg	Asn	Ala	Ala	Ala	Ala	
130					135						140					
Ser	Glu	Thr														
145																

(2) INFORMATION FOR SEQ ID NO:3943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..124
(D) OTHER INFORMATION: / Ceres Seq. ID 1578801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3943:

Met Ser Tyr Gln Arg Val Pro Pro Glu Glu Pro Tyr Pro Pro Pro Gly
1 5 10 15
His Pro Arg Ser Gln Ala His Pro Tyr Pro Pro Pro Asp Val Tyr
20 25 30
Pro Pro Pro Pro Arg Gly His Gly His Pro Pro Pro His Gly Val
35 40 45
Tyr Pro Pro Pro Pro Gln Gly Pro Tyr Pro Pro Gln Gln Pro Pro
50 55 60
Pro Gly Tyr Gln Gly Tyr Phe Asn Asp Gln Gln Arg Pro Tyr Tyr Pro
65 70 75 80
Pro Pro His Gly Glu His Gln His Asn His Gln Gly Asn Gln Gly
85 90 95
Ser Ser Ser Gly Phe Leu Lys Gly Cys Leu Ala Ala Leu Ser Ala Ala
100 105 110
Ala Cys Trp Arg Asn Ala Ala Ala Ala Ser Glu Thr
115 120

(2) INFORMATION FOR SEQ ID NO:3944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3944:

Met Cys Thr Arg Leu Pro Leu Gly Ala Met Asp Ile His His His Pro
1 5 10 15
Met Ala Cys Thr Arg Arg Arg Arg Arg Val Leu Thr Pro His His Ser
20 25 30
Ser Leu His Arg Gly Thr Arg Ala Thr Ser Thr Thr Ser Ser Val Leu
35 40 45
Thr Thr Arg Arg Arg Met Glu Ser Ile Asn Thr Thr Thr Thr Arg Glu
50 55 60
Thr Arg Val Ala Pro Leu Gly Ser Ser Lys Asp Val Trp Leu Leu Ser
65 70 75 80
Leu Leu Leu Arg Ala Gly Gly Met Leu Arg Leu Leu Arg Arg Glu
85 90 95
Met Ser Gly Asn Pro Ile Ala Ser Tyr Arg Arg
100 105

(2) INFORMATION FOR SEQ ID NO:3945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3945:

agaagctcct	ccggtctcc	cttctctccg	tagaaacatt	tcccgacggg	tgtttccac	60
gccggaatgg	accagccggc	accataagcc	caagattcgt	ttgatgagtt	tgtacgatac	120
tggctctaca	gttaggagaa	cacatttaac	ctaccttcac	tagcatcag	taatgccttt	180
gcctaataca	gaactggggg	cataactctt	tagtagagaa	ccaagaagat	gcaggcatct	240
agggcaaggc	ttttcaagga	gtacaaggag	gtacagcgag	agaagtcagc	tgacctgat	300
atccaattaa	tatgtgatga	ttctaacata	ttcaagtgga	ctgctcttat	caaGggccct	360
tctgaaacac	cttatgaag	tggtgtgttt	caacttgcat	tcgcaattcc	agagcagtat	420

ccctctgctgc ctcctcaagt tcgatttttg accaaaaactt tccacccaaa tgtgcatttc 480
aagacagggtg agattttgctt ggatatatgtg Aaagaatgca tggagCccta tatggaccct 540
tcagtcctggt tgtagagcca taattgctct gatggccac cctgaaccag acagccact 600
taactgtgat tcaaggcaatc tctgcggtcc ggtgatatca gaggctatca atcaatggcc 660
cgcatgtata caaggctggc ggcctatgcca aagaaaggtt agccgtaaaa catgtgccag 720
gccaaagacc tattgtccat gcatggctac atgtgtgtag gtctgccttg tgctgtctgt 780
atgaactttg tggttcttga ttcattgaaat actaaccgtt cgtgtgttgc gtgtgtgtct 840
ggggtaatga gaggacactc gggttctcga tgggtgtggt ctgtgatga tttagtaata 900
agaaaaataaa aaatgatttc tcg

(2) INFORMATION FOR SEQ ID NO:3946:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1578818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3946:

Met Gln Ala Ser Arg Ala Arg Leu Phe Lys Glu Tyr Lys Glu Val Gln
1 5 10 15
Arg Glu Lys Ser Ala Asp Pro Asp Ile Gln Leu Ile Cys Asp Asp Ser
20 25 30
Asn Ile Phe Lys Trp Thr Ala Leu Ile Lys Gly Pro Ser Glu Thr Pro
35 40 45
Tyr Glu Gly Gly Val Phe Gln Leu Ala Phe Ala Ile Pro Glu Gln Tyr
50 55 60
Pro Leu Leu Pro Pro Gln Val Arg Phe Leu Thr Lys Thr Phe His Pro
65 70 75 80
Asn Val His Phe Lys Thr Gly Glu Ile Cys Leu Asp Ile Leu Lys Glu
85 90 95
Cys Met Glu Pro Tyr Met Asp Pro Ser Val Cys Leu
100 105

(2) INFORMATION FOR SEQ ID NO:3947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1578819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3947:

Met Ala His Pro Glu Pro Asp Ser Pro Leu Asn Cys Asp Ser Gly Asn
1 5 10 15
Leu Cys Gly Pro Val Ile Ser Glu Ala Ile Asn Gln Trp Pro Ala Cys
20 25 30
Ile Gln Gly Trp Arg Pro Cys Gln Arg Lys Val Ser Arg Lys Thr Cys
35 40 45
Ala Arg Pro Arg Ala Tyr Cys Pro Cys Met Ala Thr Cys Cys Gln Val
50 55 60
Cys Leu Val Leu Ser Val
65 70

(2) INFORMATION FOR SEQ ID NO:3948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..626
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578834
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3948:
gatgcaacca gaaccatag ctgacgacac caccgtgtgg tcgacaaaat aaaaaggaga 60
gagagagaga tggctctgtc gtctcgccgt atggccgccg caccattctt cgtcgtcgtc 120
cttctcgtcc tcgtggcggc agagaggacg atggcgaggg tgggtggtga agagagcgtc 180
tgcttgctgc agagccatgc ctccaaaggc gtgtgcotca gcaacaccaa ctgcgacaac 240
gtatgcaaga cggagaagtt cacaggcgcc gagtgcaaga tggacggcgt catgcgcaag 300
tgctactgca agaaggtctg ctaggcgcatg accggcgagca agNCCCCag ccgtacgggt 360
gggtgtgaccc ggttgacac cgtttgggca cgcggtcatt ttccgggttc tcggctttat 420
ttattttctt tttgttataa taaatagact ctgttagtca ggtgcgtttt agtcgggttc 480
gtacgtttatt aattctctag tgtattgtat ttRcgcaacCG cgcgtgttac ttaacgtagc 540
caggcatgta ttccggttgc gtggtcgaga ggccaacgat ttattcttgat tgtacaaaaa 600
aattatataa atttgtgatg gtggtc
(2) INFORMATION FOR SEQ ID NO:3949:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578835
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3949:
Met Ala Leu Ser Ser Arg Arg Met Ala Ala Ala Pro Phe Phe Val Val
1 5 10 15
Val Leu Leu Val Leu Val Ala Ala Glu Arg Thr Met Gly Arg Val Val
20 25 30
Val Glu Glu Thr Leu Cys Leu Ser Gln Ser His Ala Phe Lys Gly Val
35 40 45
Cys Leu Ser Asn Thr Asn Cys Asp Asn Val Cys Lys Thr Glu Lys Phe
50 55 60
Thr Gly Gly Glu Cys Lys Met Asp Gly Val Met Arg Lys Cys Tyr Cys
65 70 75 80
Lys Lys Val Cys
(2) INFORMATION FOR SEQ ID NO:3950:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1578836
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3950:
Met Ala Ala Ala Pro Phe Phe Val Val Val Leu Leu Val Ala
1 5 10 15
Ala Glu Arg Thr Met Gly Arg Val Val Glu Glu Thr Leu Cys Leu
20 25 30
Ser Gln Ser His Ala Phe Lys Gly Val Cys Leu Ser Asn Thr Asn Cys
35 40 45

Asp Asn Val Cys Lys Thr Glu Lys Phe Thr Gly Gly Glu Cys Lys Met
50 55 60
Asp Gly Val Met Arg Lys Cys Tyr Cys Lys Lys Val Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3951:

Met	Gln	Asp	Gly	Glu	Val	His	Arg	Arg	Val	Gln	Asp	Gly	Arg	Arg
1		5						10					15	
His	Ala	Gln	Val	Leu	Leu	Gln	Glu	Gly	Leu	Leu	Gly	His	Asp	Arg
		20						25				30		
Gln	Xaa	Pro	Gln	Pro	Tyr	Gly	Trp	Cys	Asp	Pro	Val	Ala	His	Arg
		35					40					45		
Gly	Thr	Arg	Ser	Cys	Ser	Gly	Phe	Ser	Ala	Leu	Phe	Ile	Ser	Ser
		50				55					60			
Leu														
65														

(2) INFORMATION FOR SEQ ID NO:3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..950
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3952:

gtcaggccacc	caagcacc	acgcgacgsg	cacttcac	aggtggatag	cgaaccac	60
gcacgtctcc	atctctgggt	tgaccgccgc	cgccgccgc	ctacgcggct	acgcacggcg	120
ccgaggccctt	cgctcgccatt	tctctcgcca	agcactcacc	aggtattcag	ccatgggtttt	180
ctcttgaggca	gagatgtcat	ggaatgtgtt	gatctcacct	agccagctgg	accgcaaggn	240
ccctctgctc	cgcaaggcta	tcattgtgcg	tcttctggag	gatgtcacaa	acaggagggc	300
ttcgaaagag	catggctact	acattgtcgt	taatcagctg	aaggcaatat	ctgaaggagg	360
atgctggtga	ctaactggag	atgttctgtt	cccagtttca	tttacttgca	ttacacagaa	420
gcctatgaag	ggagagggtca	tgggtgggca	cgtggacagg	atcctcaagc	atggcgtgtt	480
ccctaaatcc	ggaccctgtg	agagcatctt	cctgtcgtga	aagtcgatga	gtaattacaa	540
gtacataggt	ggggagaatg	cgatgttcac	gaacgaccac	tcgaagctgg	agaaggacac	600
cgccgtgcgc	ttcaaggctc	tagggttccg	ctggatggag	gctgaccgcc	aattccagct	660
ccttctacag	atcgctgggt	acttccttgg	gccgctgtga	actgcttcca	caggtcaaac	720
aggtttctaat	gtacattgct	cgtagatagg	tggatggatg	gttgatctcg	atgtgtagaa	780
ttaaactttg	ctaccagttg	tttggctctg	tagaacctga	gacatggtag	gtttctctaga	840
tgctgttgcc	agtgataatt	agctotggtt	tgaacgtatc	agtgtaacctg	tatgatgaac	900
aagcgtttgtc	atggagtgac	ctttctctatg	cttgcttga	agttaacggt		

(2) INFORMATION FOR SEQ ID NO:3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1578846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3953:

```
Ser Gly Thr Gln Ala Pro His Ala Thr Xaa Thr Ser Thr Arg Trp Ile
1      5      10      15
Ala Asn Pro Gln His Val Ser Ile Ser Gly Leu Thr Ala Ala Ala Ala
20      25      30
Ala Leu Arg Gly Tyr Ala Arg Arg Arg Gly Leu Arg Arg His Phe Arg
35      40      45
Arg Gln Ala Leu Thr Arg Tyr Ser Ala Met Val Phe Leu Glu Ala Glu
50      55      60
Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa
65      70      75      80
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr
85      90      95
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln
100     105     110
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val
115     120     125
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly
130     135     140
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe
145     150     155     160
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met
165     170     175
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp
180     185     190
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly
195     200     205
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile
210     215     220
Ala Gly Asp Phe Leu Gly Pro Leu
225     230
```

(2) INFORMATION FOR SEQ ID NO:3954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3954:

```
Met Val Phe Leu Glu Ala Glu Met Ser Trp Asn Val Leu Ile Ser Pro
1      5      10      15
Ser Gln Leu Asp Arg Lys Xaa Leu Leu Leu Arg Lys Ala Ile Ile Val
20      25      30
Arg Leu Leu Glu Asp Val Thr Asn Arg Arg Ala Ser Lys Glu His Gly
35      40      45
Tyr Tyr Ile Ala Val Asn Gln Leu Lys Ala Ile Ser Glu Gly Lys Val
50      55      60
Arg Glu Leu Thr Gly Asp Val Leu Phe Pro Val Ser Phe Thr Cys Ile
65      70      75      80
Thr Gln Lys Pro Met Lys Gly Glu Val Met Val Gly His Val Asp Arg
85      90      95
Ile Leu Lys His Gly Val Phe Leu Lys Ser Gly Pro Val Glu Ser Ile
100     105     110
```

Phe Leu Ala Glu Lys Ser Met Ser Asn Tyr Lys Tyr Ile Gly Gly Glu
115 120 125
Asn Ala Met Phe Met Asn Asp His Ser Lys Leu Glu Lys Asp Thr Ala
130 135 140
Val Arg Phe Lys Val Leu Gly Phe Arg Trp Met Glu Ala Asp Arg Gln
145 150 155 160
Phe Gln Leu Leu Ala Thr Ile Ala Gly Asp Phe Leu Gly Pro Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1578848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3955:

Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa
1 5 10 15
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr
20 25 30
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln
35 40 45
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val
50 55 60
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly
65 70 75 80
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe
85 90 95
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met
100 105 110
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp
115 120 125
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly
130 135 140
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile
145 150 155 160
Ala Gly Asp Phe Leu Gly Pro Leu
165

(2) INFORMATION FOR SEQ ID NO:3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..686

(D) OTHER INFORMATION: / Ceres Seq. ID 1578852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3956:

gtctcggcct gtacgcgtga cggtgacggc gtcaggctca gctcgetcgc cccccccacg 60
aaaaacctaa tggcgctccc cctccttcac ctccgcgcgc tcattactcc tccccccacc 120
gtccccgcgc cttccttctc caccgcgcgc agcgcgacc csgcgctctc cgcgctcgtc 180
gacgagatct cggggctcac cctcctcgag gctcttctcc tggccgatgc cctgcgcggc 240
cgctcgcgcg tcgaccagtt gcgcgcacta gctatcctca cggggcgggc cgcaccgcctc 300
gtcggcggcg gactaggtcc cggcgcggcc ggcgaggagg cgaaggccaa ggaggagaa 360
atggcgcttc acgtgaagct ggaggggttc gacgcgcgcg cgaaGctcaa gatcatcaag 420

gagctgaggg cggttcacgaa tctgggtctg aaggaggcca aggatctcgt ggagaaggcg 480
cccgccgtgc tgaaggctgg agttcccaag gaggaggcgg agagtatcgc cgagaagatg 540
cgggcgtcgg cgccaagatt gttctcgagt gaacgacgag agctgtgtat gccctcgttt 600
cttgatttgt ttctgttttc ttgtatgaaa aaaagagaga attttggaac aaggagataa 660
taattagtaa attgactag agatcc

(2) INFORMATION FOR SEQ ID NO:3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3957:

Ala Pro Ala Cys Ser Arg Asp Gly Asp Gly Val Arg Leu Ser Ser Leu
1 5 10 15
Ala Pro Pro Thr Lys Thr Leu Met Ala Ser Arg Leu Leu His Leu Arg
20 25 30
Arg Leu Ile Thr Pro Pro Pro Thr Val Pro Ala Ala Ser Phe Ser Thr
35 40 45
Ala Val Ser Ala Thr Pro Xaa Val Ser Ala Leu Val Asp Glu Ile Cys
50 55 60
Gly Leu Thr Leu Leu Glu Ala Ser Ser Leu Ala Asp Ala Leu Arg Gly
65 70 75 80
Arg Leu Gly Val Asp Gln Leu Pro Pro Leu Ala Ile Leu Thr Gly Gly
85 90 95
Gly Ala Pro Leu Val Gly Gly Gly Val Gly Pro Gly Ala Ala Gly Glu
100 105 110
Glu Ala Lys Ala Lys Glu Glu Lys Met Ala Phe Asp Val Lys Leu Glu
115 120 125
Gly Phe Asp Ala Ala Lys Lys Leu Lys Ile Ile Lys Glu Leu Arg Ala
130 135 140
Phe Thr Asn Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Lys Ala
145 150 155 160
Pro Ala Val Leu Lys Ala Gly Val Pro Lys Glu Glu Ala Glu Ser Ile
165 170 175
Ala Glu Lys Met Arg Arg Ser Ala Pro Arg Leu Phe Ser Ser Glu Arg
180 185 190
Arg Glu Leu Cys Met Pro Ser Phe Leu Asp Leu Phe Arg Val Ser Cys
195 200 205
Met Lys Lys Arg Glu Asn Phe Gly Thr Arg Arg
210 215

(2) INFORMATION FOR SEQ ID NO:3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3958:

Met Ala Ser Arg Leu Leu His Leu Arg Arg Leu Ile Thr Pro Pro Pro
1 5 10 15
Thr Val Pro Ala Ala Ser Phe Ser Thr Ala Val Ser Ala Thr Pro Xaa
20 25 30

Val Ser Ala Leu Val Asp Glu Ile Cys Gly Leu Thr Leu Leu Glu Ala
35 40 45
Ser Ser Leu Ala Asp Ala Leu Arg Gly Arg Leu Gly Val Asp Gln Leu
50 55 60
Pro Pro Leu Ala Ile Leu Thr Gly Gly Gly Ala Pro Leu Val Gly Gly
65 70 75 80
Gly Val Gly Pro Gly Ala Ala Gly Glu Glu Ala Lys Ala Lys Glu Glu
85 90 95
Lys Met Ala Phe Asp Val Lys Leu Glu Gly Phe Asp Ala Ala Lys
100 105 110
Leu Lys Ile Ile Lys Glu Leu Arg Ala Phe Thr Asn Leu Gly Leu Lys
115 120 125
Glu Ala Lys Asp Leu Val Glu Lys Ala Pro Ala Val Leu Lys Ala Gly
130 135 140
Val Pro Lys Glu Glu Ala Glu Ser Ile Ala Glu Lys Met Arg Arg Ser
145 150 155 160
Ala Pro Arg Leu Phe Ser Ser Glu Arg Arg Glu Leu Cys Met Pro Ser
165 170 175
Phe Leu Asp Leu Phe Arg Val Ser Cys Met Lys Lys Arg Glu Asn Phe
180 185 190
Gly Thr Arg Arg
195

(2) INFORMATION FOR SEQ ID NO:3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3959:

aatcaaaccc	tcacagcgaa	ggacacaaaa	acacaggtag	ggttaggcga	cgccgcccgc	60
agagcgcgag	agtaggagga	ggcgctggcc	atgacgggga	agcgcaacrn	angaagcaca	120
cggcgaagga	gatcgccgcg	aagatcgacg	cgccgacgac	gaaccgnrcg	ggcggcaagg	180
tcgggcaggc	ggatcgggcta	gggcaggaca	aggrcgggca	cgcgaaactg	cgtgcccgct	240
ctgccgcacc	ccggcgcccg	acatcaagtc	catgcagatc	caccacgagg	cgccgcaccc	300
caagctccct	ttcgagccgg	agaagctcgt	caacctgcac	tcctccaccc	ccgcgcgcgc	360
cgaggccacc	acctccaagc	ccaagccggc	ggtccgcccgc	agcctcaaga	agtagctggc	420
tggcttgctc	gcctgactgc	ctggggtaat	tcctctgat	ttcaatccca	tcaccgacc	480
cgatctacaa	tcaatcaaa	taccgcccgc	cctccggcgt	cggtgtactg	ttagcttgct	540
gctgctctct	attgttggtt	tattgctgat	acatgtctcg	cgtgatagat	gtgcaactat	600
atatacgtct	cgctgcgcgc	aacactggca	tgcttaaac	tggtgcgctg	ctgctccgtg	660
atgccggcga	ckgctgctat	tagcgttaat	gttagtgtcg	atcggtctc	cttgaacaat	720
ggcaggaatc	tgttgcttgt	ttactctct	ctaattggca	gtaaggtccc	ct	

(2) INFORMATION FOR SEQ ID NO:3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3960:

Ser	Asn	Pro	His	Ser	Glu	Gly	His	Lys	Asn	Thr	Gly	Arg	Val	Arg	Arg
1				5				10					15		

Arg Gly Gly Glu Ser Xaa Arg Val Gly Gly Gly Val Gly His Asp Gly
20 25 30
Glu Gly Glu Xaa Xaa Lys His Thr Ala Lys Glu Ile Ala Ala Lys Ile
35 40 45
Asp Ala Ala Thr Thr Asn Xaa Xaa Gly Gly Lys Val Gly Gln Ala Asp
50 55 60
Arg Leu Gly Gln Asp Lys Xaa Gly His Ala Asn Trp Arg Ala Arg Ser
65 70 75 80
Ala Ala Pro Arg Arg Pro Thr Ser Ser Pro Cys Arg Ser Thr Thr Arg
85 90 95
Arg Ala Ile Pro Ser Ser Leu Ser Ser Arg Arg Ser Ser Ser Thr Cys
100 105 110
Thr Pro Pro Pro Pro Pro Pro Arg Pro Pro Pro Pro Ser Pro Ser
115 120 125
Pro Gly Ser Ala Ala Ala Ser Arg Ser Ser Trp Leu Ala Cys Leu Pro
130 135 140
Asp Cys Leu Gly
145

(2) INFORMATION FOR SEQ ID NO:3961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..825

(D) OTHER INFORMATION: / Ceres Seq. ID 1578909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3961:

actcccaagc	ccaataacac	agcacacgag	catcaacaca	acctcagagg	agcactactg	60
cgagtcaatc	agcgaccagc	acagcaaccg	aactcaaaa	caagacccca	agatcccgagc	120
ggtagggagaa	tccggacatg	gcggcgccag	cgaggcgctc	gtggatgggt	gcgatgagcg	180
tccggcgcggt	ggaggcgctc	aaggaccagg	caggcctctg	ccgtgggaac	tacgccggcg	240
tggtcgggtg	aggagtggag	gtggaacasa	acagctcctg	cgccaagagc	gctgccaggga	300
ggagcatgga	gagcgtcgct	ggcgccggcg	ccgctggggc	ggctcgtcgt	gtcgtccagg	360
tatatgttgg	agctgggtga	gacgaggagc	gaggcgtaga	tgatggcggt	ctcgtgggtc	420
ggcaGcgcct	caggcgggat	ggagccgtcg	gcgcgggaac	gcatacggcg	gtaggcgagc	480
atctgggtgg	ccagcccgtga	ctcccgccgg	ccagcatggc	gatgggctcg	agggcagcga	540
ccccgtggcg	ccgggaacca	tgctgccggc	gcgaggacga	cgacgcgcga	cgatgaggagc	600
gacggggtcg	ggcgagggga	gaccaagagc	ctcatgtggt	tgaagaggtg	ccataggccg	660
agggcctgaga	gcatacgcgc	tgccagggtg	tggtgatgta	ttttatccgc	ggcgccggcg	720
ggcagcatcg	ctatgcggat	cagtgtaagt	cgctctaaact	gttgatgctg	gcttgctgat	780
ttctttgttt	gcaatgcctg	ctcgtatcgg	aaggatttat	ttctct		

(2) INFORMATION FOR SEQ ID NO:3962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1578910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3962:

Met	Ala	Ala	Ala	Arg	Ala	Ser	Trp	Met	Val	Ala	Met	Ser	Val	Gly
1		5					10				15			
Ala	Val	Glu	Ala	Leu	Lys	Asp	Gln	Ala	Gly	Leu	Cys	Arg	Trp	Asn
		20						25				30		
Ala	Gly	Val	Val	Gly	Gly	Gly	Val	Asp	Val	Glu	Xaa	Asn	Ser	Cys

(x1) SEQUENCE DESCRIPTION: SEQ ID: 10

Met	Ser	Val	Gly	Ala	Val	Glu	Ala	Leu	Lys	Asp	Gln	Ala	Gly	Leu	Cys
1			5						10					15	
Arg	Trp	Asn	Tyr	Ala	Gly	Val	Val	Gly	Gly	Gly	Val	Asp	Val	Glu	Xaa
			20					25					30		

```

Asn Ser Ser Cys Ala Lys Ser Ala Ala Arg Arg Ser Met Glu Ser Val
      35              40              45
Val Gly Ala Gly Ala Ala Trp Ala Val Val Val Val Val Gln Val Tyr
      50              55              60
Val Gly Ala Gly Val Asp Glu Glu Arg Gly Val Asp Asp Gly Val Leu
      65              70              75              80
Val Val Arg Gln Pro Leu Arg Arg Asp Gly Ala Val Gly Ala Glu Arg
      85              90              95
His Arg Arg Val Gly Glu His Leu Gly Gly Gln Pro Val Xaa Pro Ala
      100             105             110
Ala Ser Met Ala Met Gly Ser Arg Arg Thr Pro Trp Arg Arg Glu
      115             120             125
Pro Cys Cys Arg Arg Glu Asp Asp Ala Arg Arg
      130             135             140

```

(2) INFORMATION FOR SEQ ID NO:3965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3965:

```

ctagcattta cgcggnvga ctcgagccgc cggcgctcgac gggcgggcgt ggcgacgacc      60
acaacctgga cctgtcgtcg gggagctcgg cggggaacaa aaggggcagc cttgacgacg      120
cgtccccac tcagaaaacc cagccgcgcg cgcctcggcc tccaggttaa cgagtgcgtc      180
ccaccccaag cgccgccatg aagcgcaacc cccgcgtcac gagctccgcg cggaagtgc      240
gcaagggaan cttcacggcc cgttcctcgc tccgcgcgtg gtcctgtcc gcggcgctat      300
cgacggagCt ccgccacaag tacaatgtgc gttccatccc gatccgcaag gacgacgagg      360
tgcaggctcg tgcgggcacc tacaaggccc gtgagggcaa agtggtgca ggtgaccgcc      420
gtcgctgggt catccacgtt gacggatca ccccgagaaa ggtgaacggc tccaccgtga      480
acgtgggcat ccacccttcc aaggtcatgg ttacaaagct gaagctgac aaggaccgca      540
aggcgctcct cgaccgcaag gcccggggcc gcgcccgcga caaggctaag ggcaagttaa      600
ctgccgacga cgtcgccgcc gctgctgggt gcgcgcgcgc cactggcgcg tctctccagg      660
agatcgacta ggcttcgcgg ggatctgatg gtggtcctac cgctattac tctttatcgc      720
tctagttttt gctatcaatg attatgtgct aggagtttta tgttacttat aaactgcttt      780
gagcctcgat gggagttgaa cttaatgtgg agtgatctg agatatgaag aactcattat      840
atggctaata tctcttgttg tttctctgt

```

(2) INFORMATION FOR SEQ ID NO:3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3966:

```

Met Lys Arg Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Lys
  1              5              10              15
Gly Xaa Phe Thr Ala Pro Ser Ser Val Arg Arg Val Leu Met Ser Ala
      20              25              30
Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg Ser Ile Pro
      35              40              45
Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr Tyr Lys Gly
      50              55              60

```

Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp Val Ile His
65 70 75 80
Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr Val Asn Val
85 90 95
Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys Leu Asp Lys
100 105 110
Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg Ala Ala Asp
115 120 125
Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala Ala Ala Gly
130 135 140
Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1578947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3967:

Met Ser Ala Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg
1 5 10 15
Ser Ile Pro Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr
20 25 30
Tyr Lys Gly Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp
35 40 45
Val Ile His Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr
50 55 60
Val Asn Val Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys
65 70 75 80
Leu Asp Lys Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg
85 90 95
Ala Ala Asp Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala
100 105 110
Ala Ala Gly Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp
115 120 125

(2) INFORMATION FOR SEQ ID NO:3968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..557

(D) OTHER INFORMATION: / Ceres Seq. ID 1578951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3968:

agtctaata	ctattgcagt	cggcttctct	aatactgggc	cactgggttc	gctccgcact	60
tccgcgccta	tggcgcgcgc	aacctttccc	gccgcgcggc	gccggtctct	ctccaccgcc	120
gcggcaggca	ngnagaaaac	cgagctcccc	gtccctatcg	cccgatttgc	ccagctcgcc	180
cgcgctggcc	gcctcgacga	catcgacgcg	actctcgcg	ccctgtttcc	ttccaccccc	240
gtcgcgcgcg	ttctgggcct	ctccacgggt	ggcctccccg	ancCgcgcct	ccgcgctgct	300
cggcaccatg	acgtcgccca	ataccgcgca	cctgaacgcg	gtctctcggt	cactctcgct	360
ccgcgcgcgc	ctgAgccggg	ctcgtgccct	caatctctcg	cgcgcgatgc	tctgtcccg	420

gggacgacgt caccgacagc atcctccgcca agtcgctctg cctcacctcg ggcgcgact 480
ccgcgctcca cctcctccgg aagcctctgt cgggagcgcc gccgnygctc cagctcttca 540
caaccatcat cgactcc

(2) INFORMATION FOR SEQ ID NO:3969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3969:

Ser	Leu	Ile	Thr	Ile	Ala	Val	Gly	Phe	Ser	Asn	Thr	Gly	Pro	Leu	Val	
1			5					10					15			
Ser	Leu	Arg	Thr	Ser	Ala	Ala	Met	Ala	Ala	Ala	Thr	Phe	Ser	Ala	Ala	
			20				25					30				
Gly	Arg	Arg	Leu	Leu	Ser	Thr	Ala	Ala	Ala	Gly	Xaa	Xaa	Lys	Thr	Glu	
			35			40					45					
Leu	Pro	Val	Pro	Ile	Ala	Arg	Xaa	Arg	Gln	Leu	Ala	Arg	Ala	Gly	Arg	
			50			55				60						
Leu	Asp	Asp	Ile	Asp	Ala	Thr	Leu	Ala	Pro	Leu	Phe	Pro	Ser	His	Pro	
			65			70				75				80		
Val	Ala	Ala	Leu	Ser	Ala	Leu	Ser	Thr	Val	Gly	Leu	Pro	Xaa	Pro	Arg	
					85				90					95		
Leu	Arg	Ala	Ala	Arg	His	His	Asp	Val	Ala	Gln	Tyr	Arg	Ala	Pro	Glu	
					100			105					110			
Arg	Gly	Pro	Arg	Ser	Thr	Pro	Pro	Pro	Pro	Pro	Glu	Pro	Gly	Ser		
					115		120				125					
Cys	Pro	Gln	Ser	Ser	Pro	Arg	Met	Pro	Leu	Ser	Arg	Gly	Thr	Pro	Ser	
					130		135				140					
Arg	Thr	Ala	Ser	Ser	Pro	Ser	Arg	Ser	Ala	Ser	Pro	Arg	Ala	Pro	Thr	
					145		150			155				160		
Pro	Arg	Ser	Thr	Ser	Ser	Gly	Ser	Leu	Arg	Arg	Glu	Arg	Arg	Xaa	Xaa	
					165			170						175		
Ser	Ser	Ser	Ser	Gln	Pro	Ser	Ser	Thr								
					180			185								

(2) INFORMATION FOR SEQ ID NO:3970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3970:

Met	Ala	Ala	Ala	Thr	Phe	Ser	Ala	Ala	Gly	Arg	Arg	Leu	Leu	Ser	Thr	
1				5					10				15			
Ala	Ala	Ala	Gly	Xaa	Xaa	Lys	Thr	Glu	Leu	Pro	Val	Pro	Ile	Ala	Arg	
				20				25					30			
Xaa	Arg	Gln	Leu	Ala	Arg	Ala	Gly	Arg	Leu	Asp	Asp	Ile	Asp	Ala	Thr	
				35			40					45				
Leu	Ala	Pro	Leu	Phe	Pro	Ser	His	Pro	Val	Ala	Ala	Leu	Ser	Ala	Leu	
				50			55					60				
Ser	Thr	Val	Gly	Leu	Pro	Xaa	Pro	Arg	Leu	Arg	Ala	Ala	Arg	His	His	
				65			70			75				80		

(2) INFORMATION FOR SEQ ID NO:3971:

(2) INFORMATION FOR SEQ ID NO:3972:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3972:

Leu	Gly	Phe	Cys	Pro	Pro	Arg	Ser	Phe	Glu	Leu	Pro	Arg	Ile	Pro
1			5					10					15	
Thr	Thr	Pro	Gly	Ser	Arg	Asp	Leu	Thr	Pro	Leu	Leu	Thr	Ser	Pro
			20					25				30		
Ser	Gly	Asp	His	Gln	Ser	Pro	Ser	Ser	Gly	Val	Ser	Ser	Asp	Pro
			35				40					45		Gln
Lys	Pro	Thr	Pro	Pro	His	Phe	Cys	Arg	Leu	Gly	Arg	Ile	Gly	Arg
			50			55				60				Leu
Leu	Xaa	Met	Ala	Thr	Pro	Leu	Ile	Ala	Gly	Leu	Ala	Val	Ala	Thr
65				70					75				80	
Ala	Leu	Ala	Gly	Arg	Tyr	Gly	Val	Gln	Ala	Trp	Gln	Ala	Tyr	Lys
			85						90				95	Ala

Arg Pro Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln
100 105 110
Pro Thr Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu
115 120 125
Thr Ala Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val
130 135 140
Ala Asn His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile
145 150 155 160
Asn Glu Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser
165 170 175
Ala Phe

(2) INFORMATION FOR SEQ ID NO:3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3973:

Met Ala Thr Pro Leu Ile Ala Gly Leu Ala Val Ala Ala Thr Ala Leu
1 5 10 15
Ala Gly Arg Tyr Gly Val Gln Ala Trp Gln Ala Tyr Lys Ala Arg Pro
20 25 30
Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln Pro Thr
35 40 45
Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu Thr Ala
50 55 60
Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val Ala Asn
65 70 75 80
His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile Asn Glu
85 90 95
Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser Ala Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..848
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3974:

aaaaagataa	agttaggctc	ggcaccgggg	gctcatccgc	aagcctgtgg	acgcgagtg	60
gtgaacaccca	gcggtattgt	cccgaccccg	accgatccctc	gcctgctgca	gccatggcga	120
cctcccgccg	gctctctacc	gcgcgcaatc	ccaccagctc	ctgcgggtcc	cgcgcttcgc	180
tgggcaagcc	ggtgaagggg	cttggcctga	gcattgggccc	cgagcgcgcc	cagcgagcga	240
ttgtgtgcc	ggcgccgagc	agcatctccg	ccgaccgcgt	ccccgacatg	gagaagcgga	300
agctgtgaa	cctctctctc	ctcgccgcga	tctcgttgcc	cacgcgcggc	atggctcgcc	360
cctacggcg	cttcttcgct	ctgcgcggct	ccgggaacgc	cgggcgggg	acctacgcga	420
aggacaagct	gggcaacgac	atcacgggtg	aggcgtggct	caacacgcac	ggtcccaacg	480
accgcacgct	cgcgcgaggg	ctcaagggtg	acccacgcta	cctgtgggtg	gagcaggaca	540

agacgctggc caccctacggg atcaacgcgg tgtgcactca cctcggtctgc gtcgtgccgt 600
ggaacggcgc cgagaacaag ttcatctgcc catgccacgg atcccgatc aacaaccagg 660
gcaaggttgt cgcaggtcca ttccagtgcca tgaaggtgaa gcctgggaga tccaagcgag 720
tctggaaaaga ttgtcgatgt tagtaggctg tcctattttt gtttagagac ttgtggctat 780
gtgatttgta gcgaacaacg gctgtgatgt gtttaacttg cettataata ttttgggtga 840
acgtgctc

(2) INFORMATION FOR SEQ ID NO:3975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1579005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3975:

Lys Asp Lys Val Arg Leu Gly Thr Gly Gly Ser Ser Ala Ser Leu Trp
1 5 10 15
Thr Arg Val Ser Glu His Gln Pro Tyr Cys Pro Asp Pro Asp Arg Ser
20 25 30
Ser Pro Ala Ala Met Ala Thr Ser Ala Ala Leu Ser Thr Ala Ala
35 40 45
Asn Pro Thr Gln Leu Cys Arg Ser Arg Ala Ser Leu Gly Lys Pro Val
50 55 60
Lys Gly Leu Gly Leu Ser Met Gly Arg Glu Arg Ala Gln Arg Ser Ile
65 70 75 80
Val Cys Gln Ala Ala Ser Ser Ile Ser Ala Asp Arg Val Pro Asp Met
85 90 95
Glu Lys Arg Lys Leu Met Asn Leu Leu Leu Gly Ala Ile Ser Leu
100 105 110
Pro Thr Val Gly Met Val Val Pro Tyr Gly Ala Phe Phe Val Pro Ala
115 120 125
Gly Ser Gly Asn Ala Gly Gly Gly Thr Tyr Ala Lys Asp Lys Leu Gly
130 135 140
Asn Asp Ile Thr Val Glu Ala Trp Leu Asn Thr His Gly Pro Asn Asp
145 150 155 160
Arg Thr Leu Ala Gln Gly Leu Lys Gly Asp Pro Thr Tyr Leu Val Val
165 170 175
Glu Gln Asp Lys Thr Leu Ala Thr Tyr Gly Ile Asn Ala Val Cys Thr
180 185 190
His Leu Gly Cys Val Val Pro Trp Asn Gly Ala Glu Asn Lys Phe Ile
195 200 205
Cys Pro Cys His Gly Ser Gln Tyr Asn Asn Gln Gly Lys Val Val Ala
210 215 220
Gly Pro Phe Glu Ser Met Lys Val Lys His Gly Arg Ser Lys Arg Val
225 230 235 240
Trp Lys Asp Cys Arg Cys
245

(2) INFORMATION FOR SEQ ID NO:3976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1579006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3976:

Met	Ala	Thr	Ser	Ala	Ala	Leu	Ser	Thr	Ala	Ala	Asn	Pro	Thr	Gln	Leu
1			5					10						15	
Cys	Arg	Ser	Arg	Ala	Ser	Leu	Gly	Lys	Pro	Val	Lys	Gly	Leu	Gly	Leu
		20						25					30		
Ser	Met	Gly	Arg	Glu	Arg	Ala	Gln	Arg	Ser	Ile	Val	Cys	Gln	Ala	Ala
		35					40					45			
Ser	Ser	Ile	Ser	Ala	Asp	Arg	Val	Pro	Asp	Met	Glu	Lys	Arg	Lys	Leu
	50				55					60					
Met	Asn	Leu	Leu	Leu	Leu	Gly	Ala	Ile	Ser	Leu	Pro	Thr	Val	Gly	Met
	65				70				75					80	
Val	Val	Pro	Tyr	Gly	Ala	Phe	Phe	Val	Pro	Ala	Gly	Ser	Gly	Asn	Ala
			85					90						95	
Gly	Gly	Gly	Thr	Tyr	Ala	Lys	Asp	Lys	Leu	Gly	Asn	Asp	Ile	Thr	Val
		100					105						110		
Glu	Ala	Trp	Leu	Asn	Thr	His	Gly	Pro	Asn	Asp	Arg	Thr	Leu	Ala	Gln
		115					120					125			
Gly	Leu	Lys	Gly	Asp	Pro	Thr	Tyr	Leu	Val	Val	Glu	Gln	Asp	Lys	Thr
	130					135					140				
Leu	Ala	Thr	Tyr	Gly	Ile	Asn	Ala	Val	Cys	Thr	His	Leu	Gly	Cys	Val
	145				150				155					160	
Val	Pro	Trp	Asn	Gly	Ala	Glu	Asn	Lys	Phe	Ile	Cys	Pro	Cys	His	Gly
			165					170						175	
Ser	Gln	Tyr	Asn	Asn	Gln	Gly	Lys	Val	Val	Ala	Gly	Pro	Phe	Glu	Ser
			180					185					190		
Met	Lys	Val	Lys	His	Gly	Arg	Ser	Lys	Arg	Val	Trp	Lys	Asp	Cys	Arg
		195				200						205			
Cys															

(2) INFORMATION FOR SEQ ID NO:3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3977:

Met	Gly	Arg	Glu	Arg	Ala	Gln	Arg	Ser	Ile	Val	Cys	Gln	Ala	Ala	Ser
1			5					10					15		
Ser	Ile	Ser	Ala	Asp	Arg	Val	Pro	Asp	Met	Glu	Lys	Arg	Lys	Leu	Met
		20						25					30		
Asn	Leu	Leu	Leu	Leu	Gly	Ala	Ile	Ser	Leu	Pro	Thr	Val	Gly	Met	Val
		35					40					45			
Val	Pro	Tyr	Gly	Ala	Phe	Phe	Val	Pro	Ala	Gly	Ser	Gly	Asn	Ala	Gly
		50				55				60					
Gly	Gly	Thr	Tyr	Ala	Lys	Asp	Lys	Leu	Gly	Asn	Asp	Ile	Thr	Val	Glu
		65			70				75				80		
Ala	Trp	Leu	Asn	Thr	His	Gly	Pro	Asn	Asp	Arg	Thr	Leu	Ala	Gln	Gly
			85					90					95		
Leu	Lys	Gly	Asp	Pro	Thr	Tyr	Leu	Val	Val	Glu	Gln	Asp	Lys	Thr	Leu
		100					105						110		
Ala	Thr	Tyr	Gly	Ile	Asn	Ala	Val	Cys	Thr	His	Leu	Gly	Cys	Val	Val
		115					120					125			
Pro	Trp	Asn	Gly	Ala	Glu	Asn	Lys	Phe	Ile	Cys	Pro	Cys	His	Gly	Ser
		130				135					140				
Gln	Tyr	Asn	Asn	Gln	Gly	Lys	Val	Val	Ala	Gly	Pro	Phe	Glu	Ser	Met
			145			150				155				160	

Lys Val Lys His Gly Arg Ser Lys Arg Val Trp Lys Asp Cys Arg Cys
165 170 175

(2) INFORMATION FOR SEQ ID NO:3978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3978:

catttgctcc	aagtcccaaa	tactagcarg	cggcaggcgg	ccaagaccgg	tgctccctcga	60
cgaacctgcc	agtgcccgagg	caagcaagac	gcgaggaggc	tgtaagctgc	catcagcagc	120
ggcgatggcg	ggcgccgagg	tgggagaaga	caagtaccgc	tccttcaccc	acggcgagggg	180
cgagagggac	accgtgtgga	ggtacggcgc	ccgcaccaac	tacgacgtgg	tcaacaagct	240
cttcgaggag	gagaggactc	aggtgtggcc	cgagggtctg	ctggaggaga	aggtgcacgc	300
gttgctcaag	agctggggaga	tggagctggt	gcacaargtg	cggcccgagg	accagaagac	360
cgctcaactcg	gagaataact	ctgccagcac	caacgggatg	arcgctctra	cccgggccga	420
gggatgtggcc	atcggcggtc	acaacaactt	cctgcgcacc	aagctgcccc	cggagcaccg	480
catctacagc	ccggacagcg	agaccgtgga	gtcCgcatg	gccaccttca	ccacggcctt	540
cccgccggGC	ttcgcCatcg	aggtgtctga	cgctcacagc	ggcccgccca	ggatcgccctt	600
caagtctccg	cactggggct	acatggaggg	cccttcaagg	gccacccgcc	gcacggccag	660
cggtgtccag	tcttcggcgt	ctgcactctc	catgttgacg	aagacatgaa	gggtggacaa	720
tcagagtact	tctacagcgc	cggaacactc	ctgcggcgct	tcttgagtcg	ccctgccccct	780
gatggctcag	cggtttgcc	cgtagtcgac	gggaactgaa	tgggcctgca	atgggacatt	840
ggaagactag	gcattggaac	attgggatta	ttagcattag	cgatccccgaa	tcgcctttta	900
ttacgggttta	ataattccat	catgtaacat	gacacttgca	tttgtgtttg	aataaacatg	960
tcgtgtcttc	gacatattag	cg				

(2) INFORMATION FOR SEQ ID NO:3979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3979:

Ile	Cys	Ser	Lys	Ser	Gln	Ile	Leu	Ala	Xaa	Gly	Arg	Arg	Pro	Arg	Pro	
1				5					10						15	
Val	Ser	Leu	Asp	Asp	Leu	Pro	Ser	Ala	Glu	Ala	Ser	Lys	Thr	Arg	Gly	
			20					25					30			
Gly	Cys	Lys	Leu	Pro	Ser	Ala	Ala	Ala	Met	Ala	Gly	Ala	Glu	Val	Gly	
			35			40						45				
Glu	Asp	Lys	Tyr	Arg	Ser	Phe	Ile	His	Gly	Glu	Gly	Glu	Arg	Asp	Thr	
			50			55					60					
Val	Trp	Arg	Tyr	Gly	Ala	Pro	Pro	Asn	Tyr	Asp	Val	Val	Asn	Lys	Leu	
			65			70				75				80		
Phe	Glu	Glu	Glu	Arg	Thr	Gln	Val	Trp	Pro	Glu	Gly	Ser	Leu	Glu	Glu	
			85					90					95			
Lys	Val	Gln	Arg	Leu	Leu	Lys	Ser	Trp	Glu	Met	Glu	Leu	Val	His	Xaa	
			100					105				110				
Val	Arg	Pro	Glu	Asp	Gln	Lys	Thr	Val	Asn	Ser	Glu	Lys	Tyr	Ser	Ala	
			115					120				125				

Ser Thr Asn Gly Met Xaa Ala Xaa Thr Arg Ala Glu Val Met Ala Ile
130 135 140
Gly Gly Tyr Asn Asn Phe Leu Arg Thr Lys Leu Pro Glu His Arg
145 150 155 160
Ile Tyr Asp Pro Asp Ser Glu Thr Val Glu Ser Ala Met Ala Thr Phe
165 170 175
Thr Thr Ala Phe Pro Arg Gly Phe Ala Ile Glu Val Leu Asp Val Tyr
180 185 190
Ser Gly Pro Pro Arg Ile Ala Phe Lys Phe Arg His Trp Gly Tyr Met
195 200 205
Glu Gly Pro Ser Arg Ala Thr Arg Arg Thr Ala Ser Gly Ser Ser Ser
210 215 220
Ser Ala Ser Ala Ser Ser Met Leu Thr Lys Thr
225 230 235

(2) INFORMATION FOR SEQ ID NO:3980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3980:

Met Ala Gly Ala Glu Val Gly Glu Asp Lys Tyr Arg Ser Phe Ile His
1 5 10 15
Gly Glu Gly Glu Arg Asp Thr Val Trp Arg Tyr Gly Ala Pro Asn
20 25 30
Tyr Asp Val Val Asn Lys Leu Phe Glu Glu Glu Arg Thr Gln Val Trp
35 40 45
Pro Glu Gly Ser Leu Glu Glu Lys Val Gln Arg Leu Leu Lys Ser Trp
50 55 60
Glu Met Glu Leu Val His Xaa Val Arg Pro Glu Asp Gln Lys Thr Val
65 70 75 80
Asn Ser Glu Lys Tyr Ser Ala Ser Thr Asn Gly Met Xaa Ala Xaa Thr
85 90 95
Arg Ala Glu Val Met Ala Ile Gly Gly Tyr Asn Asn Phe Leu Arg Thr
100 105 110
Lys Leu Pro Pro Glu His Arg Ile Tyr Asp Pro Asp Ser Glu Thr Val
115 120 125
Glu Ser Ala Met Ala Thr Phe Thr Thr Ala Phe Pro Arg Gly Phe Ala
130 135 140
Ile Glu Val Leu Asp Val Tyr Ser Gly Pro Pro Arg Ile Ala Phe Lys
145 150 155 160
Phe Arg His Trp Gly Tyr Met Glu Gly Pro Ser Arg Ala Thr Arg Arg
165 170 175
Thr Ala Ser Gly Ser Ser Ser Ser Ala Ser Ala Ser Ser Met Leu Thr
180 185 190
Lys Thr

(2) INFORMATION FOR SEQ ID NO:3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1579015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3981:

Met	Glu	Leu	Val	His	Xaa	Val	Arg	Pro	Glu	Asp	Gln	Lys	Thr	Val	Asn	
1			5						10					15		
Ser	Glu	Lys	Tyr	Ser	Ala	Ser	Thr	Asn	Gly	Met	Xaa	Ala	Xaa	Thr	Arg	
			20					25						30		
Ala	Glu	Val	Met	Ala	Ile	Gly	Gly	Tyr	Asn	Asn	Phe	Leu	Arg	Thr	Lys	
			35				40					45				
Leu	Pro	Pro	Glu	His	Arg	Ile	Tyr	Asp	Pro	Asp	Ser	Glu	Thr	Val	Glu	
			50				55				60					
Ser	Ala	Met	Ala	Thr	Phe	Thr	Thr	Ala	Phe	Pro	Arg	Gly	Phe	Ala	Ile	
					70					75				80		
Glu	Val	Leu	Asp	Val	Tyr	Ser	Gly	Pro	Pro	Arg	Ile	Ala	Phe	Lys	Phe	
					85				90					95		
Arg	His	Trp	Gly	Tyr	Met	Glu	Gly	Pro	Ser	Arg	Ala	Thr	Arg	Arg	Thr	
					100			105						110		
Ala	Ser	Gly	Ser	Ser	Ser	Ser	Ala	Ser	Ala	Ser	Ser	Met	Leu	Thr	Lys	
			115				120					125				

Thr

(2) INFORMATION FOR SEQ ID NO:3982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1205

(D) OTHER INFORMATION: / Ceres Seq. ID 1579027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3982:

ctctctgtcg	cattcccggt	cctgtccttc	cctaccocgg	cggcttaaac	cctagtcttc	60
actcccatcg	cgcgttcacg	tcgcgcgcag	cagatggagt	tctgggggtct	cgagggtcaag	120
cctgggtcca	ctgttaagt	tgagcctgga	tatggctttg	tgctgcacct	tcccaggct	180
gctcttgggg	aatcgaagaa	gagtgataat	gccttgatgt	atgtcaaaat	tgatgatcag	240
aaacttgcca	ttggaacctt	ctctgtttac	aagaaccocac	acatacaatt	tgatctgggt	300
ttcgataaag	agtttgagct	gtcgcacaca	tcaaaaaacta	ccagcgctctt	cttcaactggc	360
tacaagggtg	agcagccatt	cgaggaagat	gagcctctct	ccacaatgga	tcttgattct	420
gaagatgaag	acgagggagc	ggagtgtcca	gtagtcaagg	aaaaatggcaa	agctgatggg	480
aagaacacga	aaagtcaaga	aaagggcagt	gtctgcacct	caaaatcaag	tccggattcc	540
aagaagagca	asgaTgacTg	atgattctga	tgaggaygag	ackgaygatt	ctgatgaggg	600
tttatcttct	gaagaagggc	atgatgattc	aagtgatgaa	gatgatacca	gtgacgatga	660
ggaggaagac	actcccaact	ctaagaagcc	tgaggtaggc	aagaagagag	ctgctgaaag	720
tcccgctgct	aaaactctct	tatctgataa	gaagacaaag	gttgccacac	cgtcatctca	780
gaagacaggt	ggcaagaagg	gcgcgcgcgt	ccatgtggca	actccacaac	cagcaaaagg	840
caagaccatt	gtaaaccaatg	acaaatcggt	caagtctcca	aaatctgcgc	caaaatctgg	900
gtgcctctgc	aaatcgtgca	gcaagtcatt	catcagtcag	acggcaacttc	agggctcactc	960
gaaggcggaag	catgggggca	agtgagtcgc	aggtccaata	gagtcacaac	caaatgcgaa	1020
acatggggaga	ggaggggtta	cgagagttct	gaagagagtg	cggtgggaag	agggctcaac	1080
ttattttggt	tagagacggg	ctatgcgttc	gatgtagcaa	acaacggctg	ctggtttgtgt	1140
acttcaatat	ttgggtgtgt	tgtttcgaat	ttttttttga	acgtgtctcg	gattgtgtgtg	1200

gtgcc

(2) INFORMATION FOR SEQ ID NO:3983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1579028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3983:

```
Met Glu Phe Trp Gly Leu Glu Val Lys Pro Gly Ser Thr Val Lys Cys
1      5      10      15
Glu Pro Gly Tyr Gly Phe Val Leu His Leu Ser Gln Ala Ala Leu Gly
      20      25      30
Glu Ser Lys Lys Ser Asp Asn Ala Leu Met Tyr Val Lys Ile Asp Asp
      35      40      45
Gln Lys Leu Ala Ile Gly Thr Leu Ser Val Asp Lys Asn Pro His Ile
      50      55      60
Gln Phe Asp Leu Val Phe Asp Lys Glu Phe Glu Leu Ser His Thr Ser
      65      70      75      80
Lys Thr Thr Ser Val Phe Phe Thr Gly Tyr Lys Val Glu Gln Pro Phe
      85      90      95
Glu Glu Asp Glu Pro Ser Ser Thr Met Asp Leu Asp Ser Glu Asp Glu
      100      105      110
Asp Glu Glu Arg Asp Val Pro Val Val Lys Glu Asn Gly Lys Ala Asp
      115      120      125
Gly Lys Lys Gln Lys Ser Gln Glu Lys Ala Val Ala Ala Pro Ser Lys
      130      135      140
Ser Ser Pro Asp Ser Lys Lys Ser Xaa Asp Asp
      145      150      155
```

(2) INFORMATION FOR SEQ ID NO:3984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1579029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3984:

```
Met Ala Lys Leu Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu
1      5      10      15
Leu His Leu Gln Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr
      20      25      30
Asp Asp Ser Asp Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser
      35      40      45
Ser Glu Glu Gly Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp
      50      55      60
Asp Glu Glu Glu Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys
      65      70      75      80
Lys Arg Ala Ala Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys
      85      90      95
Lys Ala Lys Val Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys
      100      105      110
Gly Ala Ala Val His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr
      115      120      125
Ile Val Asn Asn Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys
      130      135      140
Ser Gly Val Pro Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr
      145      150      155      160
Ala Leu Gln Ala His Ser Lys Ala Lys His Gly Gly Lys
      165      170
```

(2) INFORMATION FOR SEQ ID NO:3985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1579030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3985:
Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu Leu His Leu Gln
1 5 10 15
Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr Asp Asp Ser Asp
20 25 30
Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser Ser Glu Glu Gly
35 40 45
Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp Asp Glu Glu Glu
50 55 60
Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys Lys Arg Ala Ala
65 70 75 80
Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys Lys Ala Lys Val
85 90 95
Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys Gly Ala Ala Val
100 105 110
His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr Ile Val Asn Asn
115 120 125
Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys Ser Gly Val Pro
130 135 140
Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr Ala Leu Gln Ala
145 150 155 160
His Ser Lys Ala Lys His Gly Gly Lys
165

(2) INFORMATION FOR SEQ ID NO:3986:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..835

(D) OTHER INFORMATION: / Ceres Seq. ID 1579042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3986:

attgtwcccg cgtgtttccc caattcgcgc ccagscaggg taaaaaaaaa aaagagggaag 60
aaaaactcct gcaattccca ttccatcgat ccagctcccg tccaagccaa agcttttctc 120
gcoccaaacc ttgttcaact ccaatgtcgg actttcttct cgggagcccg ttcgccgcgc 180
ttttccacgc gcgcoccttc catgccgtcg actggtctct cgccgcggcg gcggccatcg 240
actgggttga gaccocgtcc tcccaactgc tgcgcgtcaa cgtgccggga ctgcggcaagg 300
acgacgtcaa ggtccaggtc gaagagggca aagtgtctac catcaagggg gccccgcgcc 360
cgcccaagga gaagggaagg gaggacgagg agggggggac ggtgtggcac gtgcgcgaGc 420
gcggcaagcc ggagttcgcg cgggcctgtg cgctgccgga gaacgtgcgc gtggacggga 480
tcagggcggc cttggagaac ggggttttca cgtcgttgt gcccaaggaa gtgcgcccg 540
cccgcccaa gcacaggtcc atcgcgtct ccagcaagct ctgatgagt tgaggcgatg 600
agtggcacag tgtaacgtgc agtgttaaac catgcccaa atggcgggta cgtctgaatt 660
ctggtcgtgt ggtgtccgt gtcacctaga aaacgcgcac ccgtgttaaa ttgcgatac 720
atttcacga agtaatccga ttgagtgaaa atggctgcta gccaaaaacg gtgcattctg 780
aatatgcagt ttgcaataaa ctaaaataaa aggaaaaggc atgtttgaat atgtg

(2) INFORMATION FOR SEQ ID NO:3987:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..218
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579043
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3987:

Ile	Xaa	Pro	Ala	Val	Phe	Pro	Asn	Ser	Pro	Pro	Xaa	Arg	Val	Lys	Lys
1				5				10						15	
Lys	Lys	Arg	Lys	Lys	Thr	Ser	Cys	Asn	Ser	His	Ser	Ile	Asp	Pro	Ala
			20					25					30		
Pro	Val	Gln	Ala	Lys	Ala	Phe	Phe	Ala	Pro	Asn	Leu	Val	Gln	Leu	Gln
			35					40					45		
Cys	Arg	Thr	Ser	Ser	Ser	Gly	Ala	Arg	Ser	Ala	Ala	Ser	Ser	Thr	Arg
			50				55				60				
Ala	Pro	Ser	Met	Pro	Ser	Thr	Gly	Pro	Pro	Pro	Arg	Arg	Arg	Pro	Trp
65					70					75				80	
Thr	Gly	Trp	Arg	Pro	Arg	Pro	Pro	Thr	Cys	Cys	Ala	Ser	Thr	Cys	Arg
				85					90					95	
Asp	Ser	Ala	Arg	Thr	Thr	Ser	Arg	Ser	Arg	Ser	Thr	Arg	Ala	Lys	Cys
			100						105				110		
Ser	Pro	Ser	Gly	Ala	Pro	Arg	Pro	Arg	Pro	Arg	Arg	Arg	Gly	Arg	Arg
			115						120				125		
Thr	Arg	Arg	Arg	Gly	Arg	Cys	Gly	Thr	Trp	Arg	Ser	Ala	Ala	Ser	Arg
			130				135					140			
Ser	Ser	Arg	Gly	Pro	Trp	Arg	Cys	Arg	Arg	Thr	Cys	Ala	Trp	Thr	Gly
			145				150				155			160	
Ser	Gly	Pro	Ala	Trp	Arg	Thr	Gly	Phe	Ser	Pro	Ser	Leu	Cys	Pro	Arg
			165					170					175		
Lys	Ser	Pro	Arg	Pro	Gly	Pro	Ser	Pro	Gly	Pro	Ser	Pro	Ser	Pro	Ala
			180					185					190		
Ser	Ser	Asp	Glu	Ser	Glu	Ala	Met	Ser	Gly	Arg	Val	Tyr	Gly	Ala	Val
			195				200					205			
Leu	Asn	His	Ala	Ala	Asn	Gly	Gly	Tyr	Val						
			210				215								

(2) INFORMATION FOR SEQ ID NO:3988:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..193
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579044
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3988:

Cys	Xaa	Arg	Arg	Leu	Pro	Gln	Phe	Ala	Ala	Xaa	Gln	Gly	Lys	Lys	Lys
1				5						10				15	
Lys	Glu	Glu	Glu	Asn	Leu	Leu	Gln	Phe	Pro	Phe	His	Arg	Ser	Ser	Ser
			20					25					30		
Gly	Pro	Ser	Gln	Ser	Phe	Leu	Arg	Pro	Lys	Pro	Cys	Ser	Thr	Pro	Met
			35				40					45			
Ser	Asp	Phe	Phe	Phe	Gly	Ser	Pro	Phe	Arg	Leu	Phe	His	Ala	Arg	
			50				55				60				
Pro	Phe	His	Ala	Val	Asp	Trp	Ser	Ser	Ala	Ala	Ala	Ala	Ala	Met	Asp
65					70					75				80	
Trp	Val	Glu	Thr	Pro	Ser	Ser	His	Val	Leu	Arg	Val	Asn	Val	Pro	Gly
				85					90					95	

Leu Gly Lys Asp Asp Val Lys Val Gln Val Asp Glu Gly Lys Val Leu
100 105 110
Thr Ile Arg Gly Ala Pro Pro Ala Ala Lys Glu Lys Gly Lys Glu Asp
115 120 125
Glu Glu Glu Gly Thr Val Trp His Val Ala Glu Arg Gly Lys Pro Glu
130 135 140
Phe Ala Arg Ala Val Ala Leu Pro Glu Asn Val Arg Val Asp Gly Ile
145 150 155 160
Arg Ala Gly Leu Glu Asn Gly Val Leu Thr Val Val Val Pro Lys Glu
165 170 175
Val Ala Pro Ala Arg Pro Lys Pro Arg Ser Ile Ala Val Ser Ser Lys
180 185 190
Leu

(2) INFORMATION FOR SEQ ID NO:3989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3989:

Met Pro Ser Thr Gly Pro Pro Pro Arg Arg Pro Trp Thr Gly Trp
1 5 10 15
Arg Pro Arg Pro Pro Thr Cys Cys Ala Ser Thr Cys Arg Asp Ser Ala
20 25 30
Arg Thr Thr Ser Arg Ser Arg Ser Thr Arg Ala Lys Cys Ser Pro Ser
35 40 45
Gly Ala Pro Arg Pro Arg Pro Arg Arg Gly Arg Arg Thr Arg Arg
50 55 60
Arg Gly Arg Cys Gly Thr Trp Arg Ser Ala Ala Ser Arg Ser Ser Arg
65 70 75 80
Gly Pro Trp Arg Cys Arg Arg Thr Cys Ala Trp Thr Gly Ser Gly Pro
85 90 95
Ala Trp Arg Thr Gly Phe Ser Pro Ser Leu Cys Pro Arg Lys Ser Pro
100 105 110
Arg Pro Gly Pro Ser Pro Gly Pro Ser Pro Ser Pro Ala Ser Ser Asp
115 120 125
Glu Ser Glu Ala Met Ser Gly Arg Val Tyr Gly Ala Val Leu Asn His
130 135 140
Ala Ala Asn Gly Gly Tyr Val
145 150

(2) INFORMATION FOR SEQ ID NO:3990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..827
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3990:

gtcgccccc	cgctagtcgc	ccaaactacg	caaccgatat	attccccagc	acccccgttc	60
cagccgtcca	accgagacac	cgctgctgaa	ccaagcagac	cccagcagaa	gaagcgaagt	120
cgtcgccgga	gcaggaggaa	gagcgagcag	caagatgtcg	tggcaggcgt	acgtcgatga	180

```

ccacctgctg  tgcgacatcg  aaggccagca  cctcagcgcc  gcgcgccatg  tcggccacga      240
Cggcagcgctc  tgggacacagt  ccgagaacct  ccccgagtta  aagcctgagg  aggttgctgg      300
gatgataaag  gactttgatg  aacctggaa  ccttgaccca  actggtcttt  ttgttgagg      360
tacgAagtac  atggtgatcc  aaggtgaacc  tggagtgtgc  atccgaggaa  agaagggcac      420
tggaggcatt  actatcaaga  aaactggcat  gtccttgatt  atcggtatct  atgatgagcc      480
aatgactcca  gggcaatgca  atatggtggt  ggagaggctc  ggcgattacc  tgatcgaaaca     540
Ggggtctcta  agtttgcata  aatgctattt  tggcatttgg  gcaacttaagt  ttgcacctca     600
tttggtctct  taatatgtgg  gcttgtgcat  gtgctggcg  tattgcacgc  agtgaataat     660
ttatcttcgc  gttgggttgg  tgacaatggt  gggaacggat  ttgaattggg  gtttatgctt     720
gccatctcct  catatctcga  actcagctgc  tgtttcactg  agtaatgtac  atttccctgg     780
taatggtaact  tgtgcactcg  gctgctttat  gaaaagagat  gcatcttt

```

(2) INFORMATION FOR SEQ ID NO:3991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3991:

```

Arg Pro His Ala Ser Arg Pro Asn Tyr Ala Thr Asp Ile Phe Pro Ser
1      5      10      15
Thr Pro Val Pro Ala Val Gln Pro Arg His Arg Val Arg Thr Lys Gln
20      25      30
Thr Pro Ala Glu Glu Ala Lys Ser Ser Pro Glu Gln Glu Glu Arg
35      40      45
Ala Ala Arg Cys Arg Gly Arg Arg Thr Ser Met Thr Thr Cys Cys Ala
50      55      60
Thr Ser Lys Ala Ser Thr Ser Ala Pro Pro Pro Ser Ser Ala Thr Thr
65      70      75      80
Ala Ala Ser Gly His Ser Pro Arg Thr Ser Pro Ser
85      90

```

(2) INFORMATION FOR SEQ ID NO:3992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3992:

```

Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Asp Ile Glu
1      5      10      15
Gly Gln His Leu Ser Ala Ala Ala Ile Val Gly His Asp Gly Ser Val
20      25      30
Trp Ala Gln Ser Glu Asn Phe Pro Glu Leu Lys Pro Glu Glu Val Ala
35      40      45
Gly Met Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly
50      55      60
Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65      70      75      80
Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly Ile Thr Ile Lys Lys
85      90      95
Thr Gly Met Ser Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
100      105      110

```


Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu
115 120 125
Gln Gly Leu Leu Ser Leu Ser
130 135

(2) INFORMATION FOR SEQ ID NO:3993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1579081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3993:

Met Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly Leu
1 5 10 15
Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly Val
20 25 30
Val Ile Arg Gly Lys Lys Gly Thr Gly Ile Thr Ile Lys Lys Thr
35 40 45
Gly Met Ser Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro Gly
50 55 60
Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu Gln
65 70 75 80
Gly Leu Leu Ser Leu Ser
85

(2) INFORMATION FOR SEQ ID NO:3994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..833

(D) OTHER INFORMATION: / Ceres Seq. ID 1579082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3994:

atcctagaag gaaacaggaa caggcagctc tgaagactg aaactcacgg ccatggccat 60
ctcgggccc ctcaggctcg cgccgtctcc acccgccctc gccggcgctg cgccaccggc 120
tacgtcgccg tctgcggctg tacgtctctc cgtgcacttc cactcgccca atgccggcgc 180
cgccgcgctc ngctcgccgc tgcctctctc ccgcgcgacc cgccgtggct ttcattggag 240
gaggaccgta cgggaagcag gtgacgcggg ggcaggacct caccggcaag gacttcaagg 300
gccagacct catcaagcag gacttcaaga cgtctatctt gaggcaggcg aacttcaaaag 360
gcgcgaaact gctcggcgcg agctctctct atgcagacct cacaagcgct gatctctctg 420
acgtgatct tagagcgctt gatttgcgc tggcggaatt aacgaaggca aacttatcaa 480
atgccaaact agaaggggca cttgccactg ggaacacttc ttccaaagggt gccagacataa 540
ctggggcgaga ttttaccgat gtgcgcgtcg gagatgatca acgggagtac cctctgcaaaa 600
tcgctgacgg agtaaaattca accactggaa acccaacaaa ggagactctg ttcctgcagct 660
gatcgacgga aggacactggg acttgtgact tattcaacgt cttgataaac ttgcattctgc 720
tgctgtaagc acgtgaggaa tgtaaatgta gttatagagg gttcctagaa ataataactg 780
gtaattacgt gtaaaataac caacaataaa agtgtgtgct gccctttgaa tgt

(2) INFORMATION FOR SEQ ID NO:3995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3995:

Met Ala Ile Leu Gly Ala Leu Arg Leu Ala Pro Ser Pro Pro Ala Leu
1 5 10 15
Ala Gly Ala Ala Pro Pro Ala Thr Ser Pro Ser Ala Ala Val Arg Ser
20 25 30
Ser Val His Phe His Leu Ala Asn Ala Gly Ala Ala Leu Xaa Arg
35 40 45
Arg Leu Ala Pro Arg Arg Arg Pro Arg Arg Gly Phe His Trp Arg Arg
50 55 60
Thr Val Arg Glu Ala Gly Asp Ala Gly Ala Gly Pro His Arg Gln Gly
65 70 75 80
Leu Gln Arg Pro Asp Thr His Gln Ala Gly Leu Gln Asp Val Tyr Thr
85 90 95
Glu Ala Gly Glu Leu Gln Arg Arg Glu Pro Ala Arg Arg Glu Leu Leu
100 105 110
Arg Cys Arg Pro His Lys Arg
115

(2) INFORMATION FOR SEQ ID NO:3996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3996:

Met Pro Ala Pro Pro Arg Xaa Val Ala Ala Ser Leu Leu Ala Ala Asp
1 5 10 15
Pro Ala Val Ala Phe Ile Gly Gly Gly Pro Tyr Gly Lys Gln Val Thr
20 25 30
Arg Gly Gln Asp Leu Thr Gly Lys Asp Phe Ser Gly Gln Thr Leu Ile
35 40 45
Lys Gln Asp Phe Lys Thr Ser Ile Leu Arg Gln Ala Asn Phe Lys Gly
50 55 60
Ala Asn Leu Leu Gly Ala Ser Phe Phe Asp Ala Asp Leu Thr Ser Ala
65 70 75 80
Asp Leu Ser Asp Ala Asp Leu Arg Gly Ala Asp Leu Ser Leu Ala Asn
85 90 95
Leu Thr Lys Ala Asn Leu Ser Asn Ala Asn Leu Glu Gly Ala Leu Ala
100 105 110
Thr Gly Asn Thr Ser Phe Lys Gly Ala Asp Ile Thr Gly Ala Asp Phe
115 120 125
Thr Asp Val Pro Leu Arg Asp Asp Gln Arg Glu Tyr Leu Cys Lys Ile
130 135 140
Ala Asp Gly Val Asn Ser Thr Thr Gly Asn Pro Thr Lys Glu Thr Leu
145 150 155 160
Phe Cys Ser

(2) INFORMATION FOR SEQ ID NO:3997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..871

(D) OTHER INFORMATION: / Ceres Seq. ID 1579106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3997:

atcgatcgag	cttgggttgc	cggcagcagc	tagcaatggc	cgccaaggga	ggtgatgagc	60
tgaagctgct	ggcggtgtgg	aacagcccg	acgtcaacag	ggtccagatc	gtgctcaacc	120
tcaagggcct	cagctacgag	tacgtggagg	aggacctcct	cagcaagagc	gagctccctc	180
tcaagtccaa	cccggtgcac	aagaaaagtc	ccgtgctcat	ccaacggcgc	aagcgggtgc	240
ccgagtcgca	ggccatcatt	cagtacctcg	acgaggcttt	ccccggcgcc	acgttccctg	300
cggctctcca	agcgcacccc	tacgcacgtg	caactgccgc	cttctgggcc	gcttctgctg	360
acgacaaggt	cggtgtctcca	tggcacacgg	tcctgttctg	cgaggaccac	gggaagaagg	420
cggcagcggc	gtcgcgggat	gtcgcggcgc	tggagacgct	ggaggcgccg	ttcaaggact	480
gctccggcgg	gaggggactac	ttcggcgccg	gcgCoatcgg	cttcgtggac	gtggctcctc	540
gcgagctact	gggtgtgttc	aaggtgttgc	agaagatggt	cggcgtcagg	gtcctggagc	600
tggcgaggac	gcccgtctct	ccgcgtgggg	ggagcgtgtt	cgcccgccgc	gaagcgccca	660
aggacgtcct	gccggatgac	gttgacaagg	tgctcgagtt	ccctcagaag	ttcctggact	720
agggtcgccg	cagcgccacc	atgtgctcgc	gtgtccaaat	cccaatgttt	gtttgtcttg	780
gtcattttcg	gtgcgctgtt	aatggccctc	agatgtttgc	cagttgattt	tatagaatta	840
agagctaatt	tggtaatcac	atttttttc	g			

(2) INFORMATION FOR SEQ ID NO:3998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1579107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3998:

Arg	Ser	Ser	Leu	Val	Ala	Arg	Gln	Gln	Leu	Ala	Met	Ala	Lys	Gly
1				5				10					15	
Gly	Asp	Glu	Leu	Lys	Leu	Leu	Gly	Val	Trp	Asn	Ser	Pro	Tyr	Val
			20				25						30	
Arg	Val	Gln	Ile	Val	Leu	Asn	Leu	Lys	Gly	Leu	Ser	Tyr	Glu	Tyr
			35				40					45		
Glu	Glu	Asp	Leu	Leu	Ser	Lys	Ser	Glu	Leu	Leu	Leu	Lys	Ser	Asn
			50			55						60		
Val	His	Lys	Lys	Val	Pro	Val	Leu	Ile	His	Ala	Gly	Lys	Pro	Val
65				70				75					80	
Glu	Ser	Gln	Ala	Ile	Ile	Gln	Tyr	Leu	Asp	Glu	Ala	Phe	Pro	Gly
			85					90					95	
Thr	Phe	Pro	Ser	Val	Leu	Pro	Ala	Asp	Pro	Tyr	Ala	Arg	Ala	Thr
			100					105					110	
Arg	Phe	Trp	Ala	Ala	Phe	Val	Asp	Asp	Lys	Val	Gly	Ser	Pro	Trp
			115			120					125			
Thr	Val	Leu	Phe	Ala	Arg	Asp	His	Gly	Lys	Lys	Ala	Asp	Ala	Ser
			130			135					140			
Arg	Ile	Val	Ala	Ala	Leu	Glu	Thr	Leu	Glu	Gly	Ala	Phe	Lys	Asp
145				150				155					160	
Ser	Gly	Gly	Arg	Asp	Tyr	Phe	Gly	Gly	Gly	Ala	Ile	Gly	Phe	Val
			165				170					175		
Val	Val	Leu	Gly	Ser	Tyr	Leu	Gly	Trp	Phe	Lys	Val	Phe	Glu	Lys
			180				185					190		
Val	Gly	Val	Arg	Val	Leu	Asp	Val	Ala	Arg	Thr	Pro	Leu	Leu	Ala
			195			200					205			
Trp	Gly	Glu	Arg	Phe	Ala	Ala	Glu	Ala	Ala	Lys	Asp	Val	Leu	Pro
210				215							220			

Asp Asp Val Asp Lys Val Leu Glu Phe Leu Gln Lys Phe Leu Asp
225 230 235

(2) INFORMATION FOR SEQ ID NO:3999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3999:

```
Met Ala Ala Lys Gly Gly Asp Glu Leu Lys Leu Leu Gly Val Trp Asn
1      5      10      15
Ser Pro Tyr Val Asn Arg Val Gln Ile Val Leu Asn Leu Lys Gly Leu
20      25      30
Ser Tyr Glu Tyr Val Glu Glu Asp Leu Leu Ser Lys Ser Glu Leu Leu
35      40      45
Leu Lys Ser Asn Pro Val His Lys Lys Val Pro Val Leu Ile His Ala
50      55      60
Gly Lys Pro Val Ala Glu Ser Gln Ala Ile Ile Gln Tyr Leu Asp Glu
65      70      75      80
Ala Phe Pro Gly Gly Thr Phe Pro Ser Val Leu Pro Ala Asp Pro Tyr
85      90      95
Ala Arg Ala Thr Ala Arg Phe Trp Ala Ala Phe Val Asp Asp Lys Val
100      105      110
Gly Ser Pro Trp His Thr Val Leu Phe Ala Arg Asp His Gly Lys Lys
115      120      125
Ala Asp Ala Ala Ser Arg Ile Val Ala Ala Leu Glu Thr Leu Glu Gly
130      135      140
Ala Phe Lys Asp Cys Ser Gly Gly Arg Asp Tyr Phe Gly Gly Gly Ala
145      150      155      160
Ile Gly Phe Val Asp Val Val Leu Gly Ser Tyr Leu Gly Trp Phe Lys
165      170      175
Val Phe Glu Lys Met Val Gly Val Arg Val Leu Asp Val Ala Arg Thr
180      185      190
Pro Leu Leu Ala Ala Trp Gly Glu Arg Phe Ala Ala Glu Ala Ala
195      200      205
Lys Asp Val Leu Pro Asp Asp Val Asp Lys Val Leu Glu Phe Leu Gln
210      215      220
Lys Phe Leu Asp
225
```

(2) INFORMATION FOR SEQ ID NO:4000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4000:

```
acttcctccc ttctttacagc cgccgcgcgc gcattccagc ctccatcacc gtttcgcgtc 60
cggttgccatg ggtaagggtgc acggatcggt ggcgcgcgcgc gggaaggttc cggggcagac 120
cccccaagggtg gcgaagcgagg acaagaagaa gaagcccccgc ggcgcgcgcgc acaagaggat 180
gcagtaacaac cgccgcttcgc tcaccgcgcgt cgtcggcttc ggcaagaagc cggggcccaa 240
ctctcccgag aagtaggcgc cgctcggtc gtaccggtc ctcatccttc ctgctctccg 300
```

tatgcttatg ctcttgatgg tactagtttc gttgttcgca agcagaggaa gaacctttcg 360
tagattcggt tttgttgctc atgtgctcag atgggaactt gagattgtat gaatttgaga 420
tatggtgata tgagctgatg atttttatta tgctt

(2) INFORMATION FOR SEQ ID NO:4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4001:

Leu	Pro	Pro	Phe	Leu	Gln	Pro	Pro	Pro	Pro	His	Pro	Ser	Leu	His	His
1			5							10				15	
Arg	Phe	Arg	Leu	Val	Ala	Met	Gly	Lys	Val	His	Gly	Ser	Leu	Ala	Arg
			20					25					30		
Ala	Gly	Lys	Val	Arg	Gly	Gln	Thr	Pro	Lys	Val	Ala	Lys	Gln	Asp	Lys
		35					40					45			
Lys	Lys	Lys	Pro	Arg	Gly	Arg	Ala	His	Lys	Arg	Met	Gln	Tyr	Asn	Arg
		50				55					60				
Arg	Phe	Val	Thr	Ala	Val	Val	Gly	Phe	Gly	Lys	Lys	Arg	Gly	Pro	Asn
		65			70				75					80	
Ser	Ser	Glu	Lys												

(2) INFORMATION FOR SEQ ID NO:4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4002:

Phe	Leu	Pro	Ser	Tyr	Ser	Arg	Arg	Arg	Arg	Ile	Pro	Ala	Ser	Ile	Thr
1			5							10				15	
Val	Ser	Val	Ser	Leu	Pro	Trp	Val	Arg	Cys	Thr	Asp	Arg	Trp	Arg	Ala
			20					25					30		
Pro	Gly	Arg	Ser	Ala	Gly	Arg	Pro	Pro	Arg	Trp	Arg	Ser	Arg	Thr	Arg
		35					40					45			
Arg	Arg	Ser	Pro	Ala	Ala	Ala	Arg	Thr	Arg	Gly	Cys	Ser	Thr	Thr	Ala
		50				55					60				
Ala	Ser	Ser	Pro	Pro	Ser	Ser	Ala	Ser	Ala	Arg	Ser	Ala	Gly	Pro	Thr
		65			70				75					80	
Pro	Pro	Arg	Ser	Arg	Arg	Arg	Ser	Ala	Arg	Thr	Gly	Ser	Ser	Ser	Phe
			85					90					95		
Leu	Leu	Ser	Val	Cys	Leu	Cys	Ser								
															100

(2) INFORMATION FOR SEQ ID NO:4003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1579119
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4003:
Met Gly Lys Val His Gly Ser Leu Ala Arg Ala Gly Lys Val Arg Gly
1 5 10 15
Gln Thr Pro Lys Val Ala Lys Gln Asp Lys Lys Lys Val Pro Arg Gly
20 25 30
Arg Ala His Lys Arg Met Gln Tyr Asn Arg Arg Phe Val Thr Ala Val
35 40 45
Val Gly Phe Gly Lys Lys Arg Gly Pro Asn Ser Ser Glu Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:4004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..662

(D) OTHER INFORMATION: / Ceres Seq. ID 1579128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4004:

agtatccgggt aggggttttcc tctcgccgcg ccgcggaaca caacaccgca ccacactacc 60
cagcggaatc cgcaccaccg caccggaggc agaggagata tctcgcaagg gaaggaggga 120
gcgtcgagga agggaggagt ggtaaccagg gactacacca tcaacctcca caagcgctc 180
cacggctgca cattcaagaa gaaggcacc aacgccatca aggagatcag gaagtttgcg 240
cagaaggcca tggggaccac ggacattagg attgatgtga agctcaacaa gcacatctgg 300
acagcgggga tcaggagcgt gccgcggagg gtctgtgtga ggatcgcccg caagaggaaac 360
gacgaggagg atgccaaagg ggagctctac tcccttgtca ccgtcgcgga gatccccgcc 420
gagggcttaa aagggtctgg gaccaaggtc gttgacgata ccgattaaac tgtcgcgtta 480
tctacatctt tagagagttc ctagtttgta ttgcaacag caaaaccttt tgtattcaca 540
aagttgtcta tttccgcaac agaattgcat ggctagtttt cttttcattg ctgctGgcot 600
ccttttcttc attatcgccc cctgggaagt cgctgctcat gggacaagtt tggaaatctc 660
ct

(2) INFORMATION FOR SEQ ID NO:4005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4005:

Val Ser Gly Arg Val Phe Leu Ser Arg Arg Gly Thr Gln His Arg
1 5 10 15
Thr Thr Leu Pro Ser Gly Ile Arg Pro Pro Ala Pro Gly Ala Glu Glu
20 25 30
Ile Cys Arg Arg Gly Arg Glu Glu Arg Arg Gly Arg Arg Trp Ser
35 40 45
Pro Gly Ser Thr Pro Ser Thr Ser Thr Ser Ala Ser Thr Ala Ala His
50 55 60
Ser Arg Arg Arg His Pro Thr Pro Ser Arg Arg Ser Gly Ser Leu Arg
65 70 75 80
Arg Arg Pro Trp Ala Pro Arg Thr Leu Gly Leu Met
85 90

(2) INFORMATION FOR SEQ ID NO:4006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1579130
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4006:
Tyr Pro Val Gly Phe Ser Ser Arg Ala Ala Ala Glu His Asn Thr Ala
1 5 10 15
Pro His Tyr Pro Ala Glu Ser Ala His Pro His Pro Glu Gln Arg Arg
20 25 30
Tyr Val Ala Gly Glu Gly Arg Ser Val Glu Glu Gly Gly Gly His
35 40 45
Gln Gly Val His His Gln Pro Pro Gln Ala Pro Pro Arg Leu His Ile
50 55 60
Gln Glu Glu Gly Thr Gln Arg His Gln Gly Asp Gln Glu Val Cys Ala
65 70 75 80
Glu Gly His Gly His His Gly His
85
(2) INFORMATION FOR SEQ ID NO:4007:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1579131
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4007:
Met Ser Gln Gly Lys Gly Gly Ala Ser Arg Lys Glu Glu Val Thr
1 5 10 15
Arg Glu Tyr Thr Ile Asn Leu His Lys Arg Leu His Gly Cys Thr Phe
20 25 30
Lys Lys Lys Ala Pro Asn Ala Ile Lys Glu Ile Arg Lys Phe Ala Gln
35 40 45
Lys Ala Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu Asn Lys
50 55 60
His Ile Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val Arg Val
65 70 75 80
Arg Ile Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu Glu Leu
85 90 95
Tyr Ser Leu Val Thr Val Ala Glu Ile Pro Ala Glu Gly Leu Lys Gly
100 105 110
Leu Gly Thr Lys Val Val Asp Asp Thr Asp
115 120
(2) INFORMATION FOR SEQ ID NO:4008:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1051

(D) OTHER INFORMATION: / Ceres Seq. ID 1579182
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4008:

aatccaacga	actgaccaca	actacctaag	ctaaaaagcta	accaccgtac	ccccggccat	60
ggcgctcgcg	cccacctccg	ctgcggtgct	caagaccccg	ttctcgtggg	ccaggcgcg	120
gctcgccaag	cccgcgctcc	gccgcgcgct	cgctatcgcc	gccgcggccg	ccgccaaaga	180
gtcgtggatc	ccggccatca	agagcgacgc	cgagatcgtc	aaccgcacct	ggctcgacgg	240
ctcgctcccc	ggcgacttcg	ggctcgaccc	gctggggctg	ggcaaggagc	cgcgcttcct	300
caagtgggtac	cgggaggcgg	astgatccac	gggcggtggg	cgatggcgcc	cgtgctgggc	360
atcttcgttg	ggcaggcggt	gagcggcgtc	ccgtgggtcg	argccggcgc	ggacccgagc	420
gccatcgcg	ccttctCctt	cgggtcgctg	ctgggcaacg	agctgctgct	gatggggtgg	480
gtggagtoga	agcggtgggt	ggactttctt	aaccgcgaact	ccagggccgt	ggagtggggc	540
acgcgctgtg	cgcgaccgcg	tgagaaactc	gccaaactca	ccggcgagca	ggctaccgcc	600
ggcgacgaat	ttctcgaccc	gctcggcctc	gccggcacccg	tcaaggacgg	cgtctacatc	660
cccgacgtcg	acaagctcga	cgcggtcaag	ctggccgaga	tcaagcacgc	ccgcatcgcc	720
atgcttgcca	tgctcgctct	ctacttcgag	gccggggcagg	gcaagacgcc	gctcggcgcg	780
ctcgccctat	gattttgatg	ctgcggcgga	cagagtcagt	ttctcgattg	cgggggtggg	840
tgagctccta	gggagctacg	gctcgacggg	atcagacgcc	ttgctctgca	gattggaggc	900
gaaagaagag	cgtagacgca	atctactgtc	tgtgttggtg	gttttagcgt	cgtgaaccag	960
atggggtgtt	cctctctgtt	ttttctttct	ttcttttctg	tgtatgtatg	taccatgtaa	1020
tgatatagta	ggatcgattt	tcattgcatt	g			

(2) INFORMATION FOR SEQ ID NO:4009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1579183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4009:

Met	Ala	Leu	Ala	Pro	Thr	Ser	Ala	Ala	Val	Leu	Lys	Thr	Pro	Phe	Leu
1		5							10					15	
Gly	Ala	Arg	Arg	Ala	Leu	Ala	Lys	Pro	Ala	Pro	Arg	Arg	Ala	Leu	Val
		20							25					30	
Ile	Ala	Ala	Ala	Ala	Ala	Ala	Lys	Lys	Ser	Trp	Ile	Pro	Ala	Ile	Lys
		35							40					45	
Ser	Asp	Ala	Glu	Ile	Val	Asn	Pro	Pro	Trp	Leu	Asp	Gly	Ser	Leu	Pro
		50				55					60				
Gly	Asp	Phe	Gly	Phe	Asp	Pro	Leu	Gly	Leu	Gly	Lys	Asp	Pro	Ala	Phe
		65				70				75				80	
Leu	Lys	Trp	Tyr	Arg	Glu	Ala	Xaa								
						85									

(2) INFORMATION FOR SEQ ID NO:4010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4010:

Met	Ala	Ala	Val	Leu	Gly	Ile	Phe	Val	Gly	Gln	Ala	Trp	Ser	Gly	Ile
1				5						10				15	
Pro	Trp	Phe	Xaa	Ala	Gly	Ala	Asp	Pro	Ser	Ala	Ile	Ala	Pro	Phe	Ser
				20						25				30	
Phe	Gly	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Leu	Met	Gly	Trp	Val	Glu	

35	40	45
Ser Lys Arg Trp Val Asp Phe Asn Pro Asp Ser Gln Ala Val Glu		
50	55	60
Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn Phe Ala Asn Phe Thr		
65	70	75
Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe Asp Pro Leu Gly Leu		
85	90	95
Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro Asp Val Asp Lys Leu		
100	105	110
Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala Arg Ile Ala Met Leu		
115	120	125
Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln Gly Lys Thr Pro Leu		
130	135	140
Gly Ala Leu Gly Leu		

145

(2) INFORMATION FOR SEQ ID NO:4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4011:

Met Gly Trp Val Glu Ser Lys Arg Trp Val Asp Phe Asn Pro Asp	
1	5
Ser Gln Ala Val Glu Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn	
20	25
Phe Ala Asn Phe Thr Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe	
35	40
Asp Pro Leu Gly Leu Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro	
50	55
Asp Val Asp Lys Leu Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala	
65	70
Arg Ile Ala Met Leu Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln	
85	90
Gly Lys Thr Pro Leu Gly Ala Leu Gly Leu	
100	105

(2) INFORMATION FOR SEQ ID NO:4012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4012:

atgaggaggc aagtrcgacg gaggccaata aaaagaacaa gaaaaagaag gcacatgata	60
taagcagaag tgaaaagtcag gcagggaactg gacttgggtga gtcagatagc aaggaaccac	120
tccaaacacg gacgtttgccc aatggtatga tgattcagga gttagagatg gcgaacactg	180
atggtataaaa ggccagccgt gggaagaag tttctgttag atatattggc agcgtaaaga	240
atggcactat tttgactccc aacgtcagtg gaagaccttt tgagtttaga ctaggtgttg	300
ggcaggttat cagtggtgtg gcagttggcg tcaatgggat gcgggtggg gacaaaagga	360
gactcaccat tccaccttcc atgggggtatg ggagcaaaaag agtggggcag ataccacaga	420
actcaactct catcttcgat gtggagcttg tgaacgtaaa atgaagttag aagatccacg	480

agaaactgcg cgactttcac aaattttGct acgcatcatt ttctctgggc aatgctgttt 540
cgtaggcata ggggcatgtt aagtggattc atctctgtcg ctatcatact ttcgaaactga 600
gtttcagaag gaaaaaaact gtggactgtt gccatctggg ataattctcg ggctgcagca 660
ttcgccatcc ttctcccggt tccttcaggg tcattttgac attctgtga taccctcaga 720
accttttgaa ctgatgaat ggtaaagggt gagtacgtg

(2) INFORMATION FOR SEQ ID NO:4013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1579250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4013:

Glu Glu Ala Ser Xaa Gln Glu Ala Asn Lys Lys Asn Lys Lys Lys Lys
1 5 10 15
Ala His Asp Ile Ser Arg Ser Glu Ser Gln Ala Gly Thr Gly Leu Gly
20 25 30
Glu Ser Asp Ser Lys Glu Pro Leu Gln Thr Arg Thr Phe Ala Asn Gly
35 40 45
Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala
50 55 60
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn
65 70 75 80
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg
85 90 95
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly
100 105 110
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly
115 120 125
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile
130 135 140
Phe Asp Val Glu Leu Val Asn Val Lys
145 150

(2) INFORMATION FOR SEQ ID NO:4014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1579251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4014:

Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala
1 5 10 15
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn
20 25 30
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg
35 40 45
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly
50 55 60
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly
65 70 75 80
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile
85 90 95

Phe Asp Val Glu Leu Val Asn Val Lys
100 105

(2) INFORMATION FOR SEQ ID NO:4015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1579252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4015:

Met	Ile	Gln	Glu	Leu	Glu	Met	Gly	Lys	Pro	Asp	Gly	Lys	Lys	Ala	Ser
1		5						10						15	
Arg	Gly	Lys	Lys	Val	Ser	Val	Arg	Tyr	Ile	Gly	Lys	Leu	Lys	Asn	Gly
		20						25					30		
Thr	Ile	Phe	Asp	Ser	Asn	Val	Ser	Gly	Arg	Pro	Phe	Glu	Phe	Arg	Leu
		35					40					45			
Gly	Val	Gly	Gln	Val	Ile	Ser	Gly	Trp	Asp	Val	Gly	Val	Asn	Gly	Met
		50				55				60					
Arg	Val	Gly	Asp	Lys	Arg	Arg	Leu	Thr	Ile	Pro	Pro	Ser	Met	Gly	Tyr
		65			70					75				80	
Gly	Ser	Lys	Arg	Val	Gly	Gln	Ile	Pro	Gln	Asn	Ser	Thr	Leu	Ile	Phe
			85					90						95	

Asp Val Glu Leu Val Asn Val Lys
100

(2) INFORMATION FOR SEQ ID NO:4016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..525
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1579256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4016:

acacggatcg	aaaacgaatt	accnctcgGt	gccctccctc	tcggcggcgg	cggcgcaagt	60
ccccttcac	tccgcgcg	caaatggcag	cgcgagggtt	tgcacatgct	accctcaagt	120
gccccagcgt	ggtagaaggag	atcttcattg	gactgacctt	gggtctgata	gctggaggta	180
tgtggaagat	gcacacatgg	aacgagcaga	ggaataactag	atcctctctac	gacatgcttg	240
acaaggcgcca	gatcagcgct	gtcgtcgagg	accaggacga	ccagaagcaa	gagcagccgc	300
cgctgcgcgc	cgtatgatac	aaacccgatt	ccctgtctgt	actagctgct	actgctgcta	360
tgctgcacaaa	taaaagtcgt	tgctgcgtgt	cagtcagttac	tactgctctg	ctgctactat	420
ccatgtctcta	gtatattagt	atattataca	gtcctctctg	tgaataattga	atcgactcga	480
aaatcaaac	ccaccaatat	gagcttgcta	atattgtacc	tcctcg		

(2) INFORMATION FOR SEQ ID NO:4017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1579257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4017:

His Gly Ser Lys Thr Asn Tyr Xaa Ser Val Pro Ser Leu Ser Ala Ala
1 5 10 15
Ala Ala Gln Val Pro Phe Ile Ser Gly Ala Ala Asn Gly Arg Arg Gln
20 25 30
Gly Cys Thr Cys Tyr Pro Gln Gly Pro Gln Arg Gly Glu Gly Asp Leu
35 40 45
His Trp Thr Asp Pro Gly Ser Asp Arg Trp Arg Tyr Val Glu Asp Ala
50 55 60
Pro Leu Glu Arg Ala Glu Glu Asn
65 70

(2) INFORMATION FOR SEQ ID NO:4018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4018:

Thr Asp Arg Lys Arg Ile Thr Xaa Arg Cys Pro Pro Ser Arg Arg Arg
1 5 10 15
Arg Arg Lys Ser Pro Ser Ser Pro Ala Arg Gln Met Ala Gly Gly Arg
20 25 30
Val Ala His Ala Thr Leu Lys Gly Pro Ser Val Val Lys Glu Ile Phe
35 40 45
Ile Gly Leu Thr Leu Gly Leu Ile Ala Gly Gly Met Trp Lys Met His
50 55 60
His Trp Asn Glu Gln Arg Lys Thr Arg Ser Phe Tyr Asp Met Leu Asp
65 70 75 80
Lys Gly Gln Ile Ser Val Val Val Glu Asp Gln Asp Asp Gln Lys Gln
85 90 95
Glu Gln Pro Pro Leu Pro Pro Val
100

(2) INFORMATION FOR SEQ ID NO:4019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1579259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4019:

Met Ala Gly Gly Arg Val Ala His Ala Thr Leu Lys Gly Pro Ser Val
1 5 10 15
Val Lys Glu Ile Phe Ile Gly Leu Thr Leu Gly Leu Ile Ala Gly Gly
20 25 30
Met Trp Lys Met His His Trp Asn Glu Gln Arg Lys Thr Arg Ser Phe
35 40 45
Tyr Asp Met Leu Asp Lys Gly Gln Ile Ser Val Val Val Glu Asp Gln
50 55 60
Asp Asp Gln Lys Gln Glu Gln Pro Pro Leu Pro Pro Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:4020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 906 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..906
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1579263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4020:

attatctatt	tatctcgtag	tatctcttct	taacagaacc	cctataaatt	ccctacgac	60
gatcccttgg	ctccacctat	cacttttctc	tcgcgacaga	tcctctcagt	tatcatggcg	120
ggcgcgccct	tcaccgagaa	ggcggaagcaa	tatccgggga	agatgacggg	gttcgtcttc	180
ctcgccctgcc	tgtctgcctc	ctccggcgccg	ctcatcttgc	gatacgacat	tggcatctca	240
ggcgggcgta	cgctccatga	cccgcttctg	aagcgcttct	tcocgctcgg	gtacgccaag	300
gagcaggagg	tgggtggagac	caaccagtag	tgcaagttgc	acagcgtgct	gCtgacgctc	360
ttcacctctc	cgctctacct	cgcgggcgctc	gtcgccctccc	tccttcgcgg	ctacataccc	420
aagagggtgc	ggcgcaaggGt	gtccatgctc	ggcgcgcgcg	cCatcttctc	cgctggcgcc	480
gtcctcaacg	gcctcgccca	gaacgtggcc	atgtctcatca	tcggcaggat	ctttctcgcc	540
attggcgctg	gattcaagcaa	tcagcgggat	gcattggatct	gcgtcgcgat	ttatttttgg	600
aaccgtttct	ctgatcgctc	ggccttttta	gcgggcaact	gaacattgct	gccaagtggc	660
aacagagacc	aaactttccct	gcactgtaga	gtatgctgca	tgtgtttgtg	gcagccgac	720
ctggaagacg	atgcactgcc	agaagctcct	agattttatt	ntcactttacg	ttttttcagt	780
gctagccagt	atttcacatt	tctaacttacg	gttatttttg	aaccgtcatc	acaaatgggt	840
ttcttaagtc	aactgtcaat	aaaaatagca	ttttttattg	cggttttctt	tatgaaaccc	900

aagtgg

(2) INFORMATION FOR SEQ ID NO:4021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4021:

Met	Ala	Gly	Gly	Ala	Phe	Thr	Glu	Lys	Gly	Lys	Gln	Tyr	Pro	Gly	Lys
1		5						10						15	
Met	Thr	Val	Phe	Val	Phe	Leu	Ala	Cys	Leu	Val	Ala	Ser	Ser	Gly	Gly
		20						25					30		
Leu	Ile	Phe	Gly	Tyr	Asp	Ile	Gly	Ile	Ser	Gly	Gly	Val	Thr	Ser	Met
		35				40						45			
Asp	Pro	Phe	Leu	Lys	Arg	Phe	Pro	Ser	Val	Tyr	Ala	Lys	Glu	Gln	
		50				55					60				
Glu	Val	Val	Glu	Thr	Asn	Gln	Tyr	Cys	Lys	Phe	Asp	Ser	Val	Leu	Leu
		65				70				75				80	
Thr	Leu	Phe	Thr	Ser	Ser	Leu	Tyr	Leu	Ala	Ala	Leu	Val	Ala	Ser	Leu
			85					90					95		
Phe	Ala	Gly	Tyr	Ile	Thr	Lys	Arg	Cys	Gly	Arg	Arg	Val	Ser	Met	Leu
		100					105						110		
Gly	Gly	Gly	Ala	Ile	Phe	Leu	Val	Gly	Ala	Val	Leu	Asn	Gly	Leu	Ala
		115				120				125					
Gln	Asn	Val	Ala	Met	Leu	Ile	Ile	Gly	Arg	Ile	Phe	Leu	Gly	Ile	Gly
		130				135				140					
Val	Gly	Phe	Ser	Asn	Gln	Pro	Asp	Ala	Trp	Ile	Cys	Val	Ala	Ile	Tyr
		145			150					155				160	
Phe	Trp	Asn	Arg	Phe	Ser	Asp	Arg	Leu	Ala	Phe	Leu	Ala	Gly	Asn	
			165				170							175	

(2) INFORMATION FOR SEQ ID NO:4022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1579265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4022:

Met	Thr	Val	Phe	Val	Phe	Leu	Ala	Cys	Leu	Val	Ala	Ser	Ser	Gly	Gly
1			5						10					15	
Leu	Ile	Phe	Gly	Tyr	Asp	Ile	Gly	Ile	Ser	Gly	Gly	Val	Thr	Ser	Met
			20					25				30			
Asp	Pro	Phe	Leu	Lys	Arg	Phe	Phe	Pro	Ser	Val	Tyr	Ala	Lys	Glu	Gln
			35				40					45			
Glu	Val	Val	Glu	Thr	Asn	Gln	Tyr	Cys	Lys	Phe	Asp	Ser	Val	Leu	Leu
			50			55				60					
Thr	Leu	Phe	Thr	Ser	Ser	Leu	Tyr	Leu	Ala	Ala	Leu	Val	Ala	Ser	Leu
					70				75					80	
Phe	Ala	Gly	Tyr	Ile	Thr	Lys	Arg	Cys	Gly	Arg	Arg	Val	Ser	Met	Leu
				85					90					95	
Gly	Gly	Gly	Ala	Ile	Phe	Leu	Val	Gly	Ala	Val	Leu	Asn	Gly	Leu	Ala
			100					105				110			
Gln	Asn	Val	Ala	Met	Leu	Ile	Ile	Gly	Arg	Ile	Phe	Leu	Gly	Ile	Gly
			115			120					125				
Val	Gly	Phe	Ser	Asn	Gln	Pro	Asp	Ala	Trp	Ile	Cys	Val	Ala	Ile	Tyr
			130			135				140					
Phe	Trp	Asn	Arg	Phe	Ser	Asp	Arg	Leu	Ala	Phe	Leu	Ala	Gly	Asn	
145				150					155						

(2) INFORMATION FOR SEQ ID NO:4023:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..128

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4023:

Met	Asp	Pro	Phe	Leu	Lys	Arg	Phe	Phe	Pro	Ser	Val	Tyr	Ala	Lys	Glu
1			5						10					15	
Gln	Glu	Val	Val	Glu	Thr	Asn	Gln	Tyr	Cys	Lys	Phe	Asp	Ser	Val	Leu
			20					25				30			
Leu	Thr	Leu	Phe	Thr	Ser	Ser	Leu	Tyr	Leu	Ala	Ala	Leu	Val	Ala	Ser
			35				40					45			
Leu	Phe	Ala	Gly	Tyr	Ile	Thr	Lys	Arg	Cys	Gly	Arg	Arg	Val	Ser	Met
			50			55				60					
Leu	Gly	Gly	Gly	Ala	Ile	Phe	Leu	Val	Gly	Ala	Val	Leu	Asn	Gly	Leu
65				70					75					80	
Ala	Gln	Asn	Val	Ala	Met	Leu	Ile	Ile	Gly	Arg	Ile	Phe	Leu	Gly	Ile
				85					90				95		
Gly	Val	Gly	Phe	Ser	Asn	Gln	Pro	Asp	Ala	Trp	Ile	Cys	Val	Ala	Ile
			100					105				110			
Tyr	Phe	Trp	Asn	Arg	Phe	Ser	Asp	Arg	Leu	Ala	Phe	Leu	Ala	Gly	Asn
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:4024:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..783
(D) OTHER INFORMATION: / Ceres Seq. ID 1579270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4024:

atgtgtgtgt	cccaacagct	gagtggcatg	gacatggacc	aaaggcttca	gtgcattgtt	60
aagagagtcc	gggagacctt	cgacgctgcg	acagaaggca	tcaagacaaa	ctactatggc	120
ataaagcatg	tgatcgaagc	cttgctgcct	ctgcttcaag	cttctccgga	tgggaggatc	180
gttaacgtct	cctctgagtt	cggcctgcta	aggctgatca	acaacgagga	gctaaggcag	240
gagctaaacg	acgtgggagan	gctcaccgar	gagargctgg	acgargtgct	ggccgcgctac	300
ctgaragact	tgcagcccvr	cnargtkggg	gcrccgggtg	kgccggttga	ctctctggcc	360
tacaargtgg	ccaaggtggc	catgaacgcg	tacacgagga	tcttagcgag	gaggcaccct	420
gggtgtgcgcg	tcaactgcgc	gcaccccgcc	tacgtgagca	cgacatgac	cgtccacacc	480
gggcytytca	cgccccgagca	aggcgccggc	aacgtcgtga	agggtggcgt	gatgccggag	540
ggcgcccgca	cgccgcgcgta	cttcgcgttg	ggagaggagg	cgtcctttgt	gtgacgaaag	600
caccgtctgc	gttaagtctg	tcgttgttgc	ccaactccct	gtcagtcgat	ttctaaatcg	660
acgtacaatg	aaatcatatca	tcgctgcgaa	ctcacaaatg	aaaacagtta	agggaaacct	720
ttgtagcaaa	aaaaaaagtg	gacagaataa	tgaataatca	tgtaaatat	cgcttgagta	780

tct

(2) INFORMATION FOR SEQ ID NO:4025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..197
(D) OTHER INFORMATION: / Ceres Seq. ID 1579271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4025:

Met	Cys	Val	Ser	Gln	Gln	Leu	Ser	Gly	Met	Asp	Met	Asp	Gln	Arg	Leu
1			5					10					15		
Gln	Cys	Met	Phe	Lys	Arg	Val	Arg	Glu	Thr	Tyr	Asp	Ala	Ala	Thr	Glu
			20					25					30		
Gly	Ile	Lys	Thr	Asn	Tyr	Tyr	Gly	Ile	Lys	His	Val	Ile	Glu	Ala	Leu
			35					40				45			
Leu	Pro	Leu	Leu	Gln	Ala	Ser	Ser	Asp	Gly	Arg	Ile	Val	Asn	Val	Ser
			50					55				60			
Ser	Glu	Phe	Gly	Leu	Leu	Arg	Leu	Ile	Asn	Asn	Glu	Glu	Leu	Arg	Gln
			65					70			75				80
Glu	Leu	Asn	Asp	Val	Glu	Xaa	Leu	Thr	Xaa	Glu	Xaa	Leu	Asp	Xaa	Val
				85				90					95		
Leu	Ala	Ala	Tyr	Leu	Xaa	Asp	Phe	Asp	Ala	Xaa	Xaa	Xaa	Gly	Xaa	Arg
			100					105					110		
Gly	Xaa	Pro	Val	Asp	Phe	Ser	Ala	Tyr	Xaa	Val	Ala	Lys	Val	Ala	Met
			115					120				125			
Asn	Ala	Tyr	Thr	Arg	Ile	Leu	Ala	Arg	Arg	His	Xaa	Gly	Xaa	Arg	Val
			130					135				140			
Asn	Cys	Ala	His	Pro	Gly	Tyr	Val	Ser	Thr	Asp	Met	Thr	Val	His	Thr
			145					150			155				160
Gly	Xaa	Xaa	Thr	Pro	Glu	Gln	Gly	Ala	Ala	Asn	Val	Val	Lys	Val	Ala
			165					170					175		
Leu	Met	Pro	Glu	Gly	Gly	Pro	Thr	Gly	Ala	Tyr	Phe	Ala	Leu	Gly	Glu
			180					185					190		

Glu Ala Ser Phe Val
195

(2) INFORMATION FOR SEQ ID NO:4026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4026:

Met Asp Met Asp Gln Arg Leu Gln Cys Met Phe Lys Arg Val Arg Glu
1 5 10 15
Thr Tyr Asp Ala Ala Thr Glu Gly Ile Lys Thr Asn Tyr Tyr Gly Ile
20 25 30
Lys His Val Ile Glu Ala Leu Leu Pro Leu Leu Gln Ala Ser Ser Asp
35 40 45
Gly Arg Ile Val Asn Val Ser Ser Glu Phe Gly Leu Leu Arg Leu Ile
50 55 60
Asn Asn Glu Glu Leu Arg Gln Glu Leu Asn Asp Val Glu Xaa Leu Thr
65 70 75 80
Xaa Glu Xaa Leu Asp Xaa Val Leu Ala Ala Tyr Leu Xaa Asp Phe Asp
85 90 95
Ala Xaa Xaa Xaa Gly Xaa Arg Gly Xaa Pro Val Asp Phe Ser Ala Tyr
100 105 110
Xaa Val Ala Lys Val Ala Met Asn Ala Tyr Thr Arg Ile Leu Ala Arg
115 120 125
Arg His Xaa Gly Xaa Arg Val Asn Cys Ala His Pro Gly Tyr Val Ser
130 135 140
Thr Asp Met Thr Val His Thr Gly Xaa Xaa Thr Pro Glu Gln Gly Ala
145 150 155 160
Ala Asn Val Val Lys Val Ala Leu Met Pro Glu Gly Gly Pro Thr Gly
165 170 175
Ala Tyr Phe Ala Leu Gly Glu Glu Ala Ser Phe Val
180 185
190

(2) INFORMATION FOR SEQ ID NO:4027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..655
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4027:

cactaccacc agtaccacac cactccgcgc tastaggac ggtacagcgg cacagaggtg 60
cgacgtacga cgacgacgac gcargcgcca cacatggcat ccagctctc cgccgcgcgtg 120
ccccggttcc aggcctcccg gggtacgccc gcgcccaggt ccgcggtggc agcgtgccc 180
tccgtgaggg tgggcaggaa gaggtcgctc tcgcagggca tccgctgcga ctacatybgC 240
tccgccacca acctgatcat ggtgacgacg acgacgctga tgcgtgttcg rggcggttc 300
ggcgtggCgc cgtcggCgaa ccgcaaggcg acggcgggcg tgaagctgga ggcgcgcgac 360
tccgcctcgc agacgggtga cccgcgcggg ttcacctcg ccgacacgct gGcctcgggc 420
gcgcgtcgcc acatcctcgg cgtcggcatc gtgcctggcg tcaagaacac gcgcgccttc 480
gaccagatca tcggctagat cctacgctcg tcgttgttaa gatcagactc agcacctcg 540
atcgcgccgc cggccggcag gtgcctcgag gtggtgactt tgtaacgctg gtgcgtgcgt 600
acgtgtacat tgcattccat ttggttccaa tggacatata gctcctgttg ctcct

(2) INFORMATION FOR SEQ ID NO:4028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4028:

Leu Pro Pro Val Pro His His Ser Ala Leu Xaa Arg Thr Val Gln Arg
1 5 10 15
His Arg Gly Ala Thr Tyr Asp Asp Asp Ala Xaa Ala Thr His Gly
20 25 30
Ile Pro Ala Leu Arg Arg Arg Ala Pro Val Pro Arg Pro Pro Gly Leu
35 40 45
Arg Arg Ala Gln Val Arg Gly Gly Ser Ala Ala Val Arg Glu Gly Gly
50 55 60
Gln Glu Glu Val Val Val Ala Gly His Pro Leu Arg Leu His Xaa Leu
65 70 75 80
Arg His Gln Pro Asp His Gly Asp Asp Asp Asp Ala Asp Ala Val Arg
85 90 95
Xaa Ala Val Arg Ala Gly Ala Val Gly Glu Pro Gln Gly Asp Gly Gly
100 105 110
Ala Glu Ala Gly Gly Ala Arg Leu Arg Pro Ala Asp Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:4029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4029:

Met Ala Ser Gln Leu Ser Ala Ala Val Pro Arg Phe His Gly Leu Arg
1 5 10 15
Gly Tyr Ala Ala Pro Arg Ser Ala Val Ala Ala Leu Pro Ser Val Arg
20 25 30
Val Gly Arg Lys Arg Ser Ser Ser Gln Gly Ile Arg Cys Asp Tyr Xaa
35 40 45
Xaa Ser Ala Thr Asn Leu Ile Met Val Thr Thr Thr Leu Met Leu
50 55 60
Phe Xaa Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr
65 70 75 80
Ala Gly Leu Lys Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp
85 90 95
Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Ala Val Gly
100 105 110
His Ile Leu Gly Val Gly Ile Val Leu Gly Leu Lys Asn Thr Gly Ala
115 120 125
Leu Asp Gln Ile Ile Gly
130

(2) INFORMATION FOR SEQ ID NO:4030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1579277
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4030:
Met Val Thr Thr Thr Leu Met Leu Phe Xaa Gly Arg Phe Gly Leu
1 5 10 15
Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu Lys Leu Glu Ala
20 25 30
Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly Phe Thr Leu Ala
35 40 45
Asp Thr Leu Ala Cys Gly Ala Val Gly His Ile Leu Gly Val Gly Ile
50 55 60
Val Leu Gly Leu Lys Asn Thr Gly Ala Leu Asp Gln Ile Ile Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:4031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..851
(D) OTHER INFORMATION: / Ceres Seq. ID 1579278
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4031:

ctccccaatc cccaggtcct catcggccto ctctctctcg gtctcgccag atctccccac 60
ggaaccttac ccgagcatca gccatggcaa tcgcggcgcg cgccctgcgc cgctcccgcg 120
ttcaccctctc cccctcgatc tcccgctcct tctgcgcggt ttcccccggc ccgcctcgg 180
ctacctcggc ccccgccgccc gcgtcccgca aggtcgctga ccgcatcggt cgcgctctcg 240
ccatcgatcc cgacggggcg cgccgcgatg tggctcgccct ctccggggcag acactccctc 300
gcgctctggc caacgcggggG ctcatcgagc cggcctccca ccgctcggag gatatcgagc 360
cgtgTccgcg cgagtgcgag gtccacatcg cgcaggagtg gcttgacaag ctgccaccac 420
cgctctacga ggagcgatac gtgctcaagc gcgcgtccag gaaccgcgag ctcaacaagy 480
acgcgcgcct gggtgcgccag gtgctctcgc ccgcggagct gcagggggatg gtgctgcgca 540
tcgccgagcc taagccgtgg gacatcccat aatggcctgc cgacgaaag taaggctcgag 600
cttttgagcg tgtgagcctt ccttaattcc cttggctcgg tcaagctgtg cgccgtgtgc 660
atcccttttt atattgttag gatttagtga agaataataa tttgatgagc aaactgtggc 720
attggttaac ttttgttctc agtatatgga tgctctaagt tggaaatcct ttgcaactac 780
cgcagtttaa tgttttcattg tttgaagttt tgtacattgt gatgaatggt tgattaatct 840
tttcatttcc t

(2) INFORMATION FOR SEQ ID NO:4032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..204
(D) OTHER INFORMATION: / Ceres Seq. ID 1579279
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4032:

Leu Pro Asn Pro Gln Val Leu Ile Gly Leu Leu Ser Leu Gly Leu Ala
1 5 10 15
Arg Ser Pro His Gly Thr Leu Pro Glu His Gln Pro Trp Gln Ser Arg

Arg	Ala	Pro	Cys	Ala	Ala	Ser	Arg	Phe	Thr	Ser	Pro	Pro	Arg	Ser	Pro	20	25	30
																35	40	45
Ala	Pro	Ser	Ala	Arg	Phe	Pro	Arg	Pro	Pro	Pro	Arg	Leu	Pro	Arg	Pro	50	55	60
Pro	Pro	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr	Ala	Ser	Cys	Ala	Ser	Ser	65	70	75
Pro	Ser	Ile	Pro	Thr	Gly	Arg	Ala	Ala	Met	Trp	Ser	Ala	Ser	Arg	Gly	85	90	95
Arg	His	Ser	Phe	Ala	Leu	Trp	Pro	Thr	Arg	Gly	Ser	Ser	Ser	Arg	Pro	100	105	110
Pro	Thr	Ala	Ser	Arg	Ile	Ser	Thr	Arg	Ala	Pro	Pro	Ser	Ala	Arg	Ser	115	120	125
Thr	Ser	Arg	Arg	Ser	Gly	Leu	Thr	Ser	Cys	His	His	Arg	Pro	Thr	Arg	130	135	140
Ser	Asp	Thr	Cys	Ser	Arg	Ala	Arg	Pro	Gly	Thr	Ala	Ser	Ser	Thr	Xaa	145	150	155
Thr	Arg	Ala	Trp	Ala	Ala	Arg	Ser	Ser	Ser	Arg	Arg	Ser	Cys	Arg	Gly	165	170	175
Trp	Ser	Ser	Pro	Ser	Pro	Ser	Leu	Ser	Arg	Gly	Thr	Ser	His	Asn	Gly	180	185	190
Leu	Pro	Thr	Lys	Gly	Lys	Val	Arg	Leu	Leu	Thr	Leu					195	200	

(2) INFORMATION FOR SEQ ID NO:4033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1579280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4033:

Pro	Gln	Ser	Pro	Gly	Pro	His	Arg	Pro	Pro	Leu	Ser	Arg	Ser	Arg	Gln	1	5	10	15
Ile	Ser	Pro	Arg	Asn	Pro	Thr	Arg	Ala	Ser	Ala	Met	Ala	Ile	Ala	Ala	20	25	30	
Arg	Ala	Leu	Arg	Arg	Leu	Pro	Leu	His	Leu	Ser	Pro	Ser	Ile	Ser	Arg	35	40	45	
Ser	Phe	Cys	Ala	Val	Ser	Pro	Ala	Ala	Ala	Ser	Ala	Thr	Ser	Ala	Pro	50	55	60	
Ala	Ala	Ala	Ser	Ala	Lys	Val	Ala	Asp	Arg	Ile	Val	Arg	Val	Leu	Ala	65	70	75	80
Ile	Asp	Pro	Asp	Gly	Ala	Arg	Arg	Asp	Val	Val	Gly	Leu	Ser	Gly	Gln	85	90	95	
Thr	Leu	Leu	Arg	Ala	Leu	Ala	Asn	Ala	Gly	Leu	Ile	Glu	Pro	Ala	Ser	100	105	110	
His	Arg	Leu	Glu	Asp	Ile	Asp	Ala	Cys	Ser	Ala	Glu	Cys	Glu	Val	His	115	120	125	
Ile	Ala	Gln	Glu	Trp	Leu	Asp	Lys	Leu	Pro	Pro	Pro	Ser	Tyr	Glu	Glu	130	135	140	
Arg	Tyr	Val	Leu	Thr	Arg	Ala	Ser	Arg	Asn	Arg	Glu	Leu	Asn	Lys	Xaa	145	150	155	160
Ala	Arg	Leu	Gly	Cys	Gln	Val	Val	Leu	Ala	Pro	Glu	Leu	Gln	Gly	Met	165	170	175	
Val	Val	Ala	Ile	Pro	Glu	Pro	Lys	Pro	Trp	Asp	Ile	Pro				180	185		

(2) INFORMATION FOR SEQ ID NO:4034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1579281
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4034:
Met Ala Ile Ala Ala Arg Ala Leu Arg Arg Leu Pro Leu His Leu Ser
1 5 10 15
Pro Ser Ile Ser Arg Ser Phe Cys Ala Val Ser Pro Ala Ala Ala Ser
20 25 30
Ala Thr Ser Ala Pro Ala Ala Ala Ser Ala Lys Val Ala Asp Arg Ile
35 40 45
Val Arg Val Leu Ala Ile Asp Pro Asp Gly Ala Arg Arg Asp Val Val
50 55 60
Gly Leu Ser Gly Gln Thr Leu Leu Arg Ala Leu Ala Asn Ala Gly Leu
65 70 75 80
Ile Glu Pro Ala Ser His Arg Leu Glu Asp Ile Asp Ala Cys Ser Ala
85 90 95
Glu Cys Glu Val His Ile Ala Gln Glu Trp Leu Asp Lys Leu Pro Pro
100 105 110
Pro Ser Tyr Glu Glu Arg Tyr Val Leu Thr Arg Ala Ser Arg Asn Arg
115 120 125
Glu Leu Asn Lys Xaa Ala Arg Leu Gly Cys Gln Val Val Leu Ala Pro
130 135 140
Glu Leu Gln Gly Met Val Val Ala Ile Pro Glu Pro Lys Pro Trp Asp
145 150 155 160
Ile Pro

(2) INFORMATION FOR SEQ ID NO:4035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1579303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4035:

tcttcaccca cattataaag attctccact tcgcactttc gccgcgcgct ctctccttcc 60
cgagcaggag gcggacaagg taagcagcaa tcgcaggaaac cctagcgcgc ccgcaccgcc 120
aggaatgggt atcgacctcg tcgcccgtgg gaggrkaag aagaccaagc gcaactgcgcc 180
caagtctgac gatgtctacc tcAagctcct cgtcaagctc taccgtttcN ttggtcagga 240
ggaccaagag caatttcaac gctgtcattc tcaagaggct tttcatgagt aaaaccaaac 300
gaccaccaat ctccatgcgc cgctttgtca agtttatgga aggaaaggag aagaacattg 360
ctgtcatgtt tggcacagtc acagatgaca aaaggatcca ggagggtcca gcaatgaagg 420
ttaetgacct gaggttcaag gagacagcaa gggccaggat tgtcaatgct ggtggcgagt 480
gcctcacatt tgaccagctt gctcttcgtg ctccacttgg cgagacaacg gtccctcttga 540
ggggccccc aaatgcccggt gaggcagtga ggcactttgg caaggctcct ggagtgccgc 600
acagccacac caagccggtat tgcgcgtcca aggggaaggaa gttcgagaag gtctgtggca 660
ggaggaacag ccgtggattc aagggttaaa acaaattgtg gccctccgtg ttscatcagc 720
catmstgcaa ccgtgtgtgt tgatcagtcg acagtaatta gtcatactc tgtaccgaga 780
ttmstaggac aatttgttgt cctgtytga attytsgaag atatttgatg tcgtctccyt 840
att

(2) INFORMATION FOR SEQ ID NO:4036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..165
(D) OTHER INFORMATION: / Ceres Seq. ID 1579304
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4036:
Met Ser Thr Ser Ser Ser Ser Ser Ser Ser Thr Val Xaa Leu Val Arg
1 5 10 15
Arg Thr Lys Ser Asn Phe Asn Ala Val Ile Leu Lys Arg Leu Phe Met
20 25 30
Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys Phe
35 40 45
Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val Thr
50 55 60
Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala Leu
65 70 75 80
Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly Glu
85 90 95
Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu Asn
100 105 110
Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg His
115 120 125
Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr Val
130 135 140
Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn Ser
145 150 155 160
Arg Gly Phe Lys Val
165
(2) INFORMATION FOR SEQ ID NO:4037:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1579305
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4037:
Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1 5 10 15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
20 25 30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala
35 40 45
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly
50 55 60
Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu
65 70 75 80
Asn Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg
85 90 95
His Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr
100 105 110
Val Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn
115 120 125
Ser Arg Gly Phe Lys Val

130

(2) INFORMATION FOR SEQ ID NO:4038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4038:

Met	Arg	Arg	Leu	Val	Lys	Phe	Met	Glu	Gly	Lys	Glu	Lys	Asn	Ile	Ala
1			5						10					15	
Val	Ile	Val	Gly	Thr	Val	Thr	Asp	Asp	Lys	Arg	Ile	Gln	Glu	Val	Pro
			20					25					30		
Ala	Met	Lys	Val	Thr	Ala	Leu	Arg	Phe	Thr	Glu	Thr	Ala	Arg	Ala	Arg
			35					40					45		
Ile	Val	Asn	Ala	Gly	Gly	Glu	Cys	Leu	Thr	Phe	Asp	Gln	Leu	Ala	Leu
			50				55				60				
Arg	Ala	Pro	Leu	Gly	Glu	Asn	Thr	Val	Leu	Leu	Arg	Gly	Pro	Lys	Asn
65						70					75			80	
Ala	Arg	Glu	Ala	Val	Arg	His	Phe	Gly	Lys	Ala	Pro	Gly	Val	Pro	His
						85								95	
Ser	His	Thr	Lys	Pro	Tyr	Val	Arg	Ser	Lys	Gly	Arg	Lys	Phe	Glu	Lys
			100					105						110	
Ala	Arg	Gly	Arg	Arg	Asn	Ser	Arg	Gly	Phe	Lys	Val				
			115					120							

(2) INFORMATION FOR SEQ ID NO:4039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4039:

aaatcccccac	gaaaacccta	aaccttcgct	accggcgggc	ggctacaagc	tcttcgtcgg	60
ttcagcacca	tgargccacc	ggctagagga	ggacgtgggt	ggagggggtg	caggttcgat	120
ggcgggcgcc	tctgtcgcgg	cgggcgttgc	atcgtccctc	gcctcaccgt	tctcttcctt	180
ctcgcgctcg	cgggcttcct	cctctggccc	cgggaccggg	acatctccct	ggccgccttc	240
caactagcgc	acgtctccgt	cgtggcaacg	cctgcgcgtg	cogtcaatat	atCcgccaag	300
ctcaagggtc	cggttcgcaa	tctcgaccct	ttcgcgcgtg	actacacccg	cctcgacgtc	360
gctatcggtt	aCcgcggtgc	Ggggcttgcc	cggttaacat	ccggcgggcg	acgggttcgg	420
gcgcgcgctg	tctcgtacgt	cgacgcacaac	ctgcagctcg	acggcatacg	cgtcgtcgag	480
gacgcgatgt	acctgcgtcg	ggaccttcgc	caaggatccg	tgccttcga	caccatcgcc	540
gaggtcgagg	gccacctcca	cttccttttc	ctcagcatcc	cggtcaaggg	gagaatatct	600
tgcgtaatgc	atattaatcc	acacaaccaa	accatagtac	atcaggactg	ctatcctgag	660
gtaattgctt	atggcgtgga	aattgtggaag	ggtgtaagct	atgttgcctt	gcgaatggat	720
cgtttgattt	gtttctaacc	tttgcttcca	gtcgtgggtg	taaaagtaag	aaccaactaa	780
ggggtgtttg	aatgtaatta	agctaatagt	tagttcgtc			

(2) INFORMATION FOR SEQ ID NO:4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1579308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4040:

```
Met Xaa Pro Pro Ala Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Phe
 1           5           10           15
Asp Gly Gly Gly Leu Cys Arg Gly Gly Arg Cys Ile Val Pro Cys Leu
 20           25           30
Thr Val Leu Phe Leu Leu Ala Leu Ala Gly Phe Leu Leu Trp Pro Ala
 35           40           45
Asp Pro Asp Ile Ser Leu Ala Arg Leu His Leu Ala His Val Ser Val
 50           55           60
Val Ala Arg Pro Ala Val Ala Val Thr Ile Ser Ala Thr Leu Lys Val
 65           70           75           80
Arg Val Arg Asn Pro Asp Leu Phe Ala Leu Asp Tyr Thr Arg Leu Asp
 85           90           95
Val Ala Ile Gly Tyr Arg Gly Ala Gly Leu Gly Arg Val Thr Ser Gly
 100          105          110
Gly Gly Arg Val Arg Ala Arg Ala Val Ser Tyr Val Asp Ala Asn Leu
 115          120          125
Gln Leu Asp Gly Ile Arg Val Val Glu Asp Ala Met Tyr Leu Leu Glu
 130          135          140
Asp Leu Ala Gln Gly Ser Val Pro Phe Asp Thr Ile Ala Glu Val Glu
 145          150          155          160
Gly His Leu His Phe Leu Phe Leu Ser Ile Pro Val Lys Gly Arg Ile
 165          170          175
Ser Cys Val Met His Ile Asn Pro His Asn Gln Thr Ile Val His Gln
 180          185          190
Asp Cys Tyr Pro Glu
 195
```

(2) INFORMATION FOR SEQ ID NO:4041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 628 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..628

(D) OTHER INFORMATION: / Ceres Seq. ID 1579351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4041:

```
ataaaagcgt gttcttctcc cctcatcgca tacggcatac cacactagaa ccgccgccgc 60
tgccgttttc gcacccgtac cctagccctc gtcagcggcg gcttcgagct cctccagcca 120
tgacgttcaa gcggaggaat ggccgacgca acaagcacgg gcgcggccac gtcaagtaca 180
tcgcgtgctc caactgcgcc aagtgtctgc ccaaggataa ggctatcaag cggtctcttg 240
tgaggaaacat tgttgagcag gctgcccgtga gagatgtgca ggaggccgtg gtacatgatg 300
gatatgttct acccaaatgg tatgcaaagg ttcatactgt tgtctcatgc gcaatccatg 360
cgacatttgc ccgtgtccgc tctcgtgaga acaggaggaa ccgtgagccc ccgcagcgct 420
tcagacgcgg ggatgatggc ccaaggccgt gtcaggggccc gccgcgccca ggcggtgcag 480
ctctctCagc tgcagctgtc gctgctcttc gtacctaatg tctggaatta gtttcggggc 540
ttaattttgt gaaacattac ctgttttgag aaaccattgt tactgtatcc ccttgatgtc 600
aaacttttta gcacaatttg tggttctg
```

(2) INFORMATION FOR SEQ ID NO:4042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..171
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579352
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4042:

```

Lys Lys Leu Phe Phe Ser Pro His Arg Ile Arg His Thr Thr Leu Glu
1      5      10      15
Pro Pro Pro Leu Pro Phe Arg Ala Pro Tyr Pro Ser Pro Arg Gln Arg
      20      25      30
Arg Leu Arg Ala Pro Pro Ala Met Thr Phe Lys Arg Arg Asn Gly Gly
      35      40      45
Arg Asn Lys His Gly Arg Gly His Val Lys Tyr Ile Arg Cys Ser Asn
50      55      60
Cys Ala Lys Cys Cys Pro Lys Asp Lys Ala Ile Lys Arg Phe Leu Val
65      70      75
Arg Asn Ile Val Glu Gln Ala Ala Val Arg Asp Val Gln Glu Ala Cys
      85      90      95
Val His Asp Gly Tyr Val Leu Pro Lys Leu Tyr Ala Lys Val His His
      100      105      110
Cys Val Ser Cys Ala Ile His Ala His Ile Val Arg Val Arg Ser Arg
      115      120      125
Glu Asn Arg Arg Asn Arg Glu Pro Pro Gln Arg Phe Arg Arg Arg Asp
130      135      140
Asp Gly Pro Arg Pro Gly Gln Gly Pro Pro Arg Pro Gly Gly Ala Ala
145      150      155      160
Pro Ala Ala Ala Ala Ala Ala Pro Arg Thr
      165      170

```

(2) INFORMATION FOR SEQ ID NO:4043:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4043:

```

Met Thr Phe Lys Arg Arg Asn Gly Gly Arg Asn Lys His Gly Arg Gly
1      5      10      15
His Val Lys Tyr Ile Arg Cys Ser Asn Cys Ala Lys Cys Cys Pro Lys
      20      25      30
Asp Lys Ala Ile Lys Arg Phe Leu Val Arg Asn Ile Val Glu Gln Ala
35      40      45
Ala Val Arg Asp Val Gln Glu Ala Cys Val His Asp Gly Tyr Val Leu
50      55      60
Pro Lys Leu Tyr Ala Lys Val His His Cys Val Ser Cys Ala Ile His
65      70      75      80
Ala His Ile Val Arg Val Arg Ser Arg Glu Asn Arg Arg Asn Arg Glu
      85      90      95
Pro Pro Gln Arg Phe Arg Arg Arg Asp Asp Gly Pro Arg Pro Gly Gln
      100      105      110
Gly Pro Pro Arg Pro Gly Gly Ala Ala Pro Ala Ala Ala Ala Ala Ala
115      120      125
Ala Pro Arg Thr
130

```

(2) INFORMATION FOR SEQ ID NO:4044:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579354
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4044:
Met Cys Arg Arg Pro Val Tyr Met Met Asp Met Phe Tyr Pro Asn Cys
1 5 10 15
Met Gln Arg Phe Ile Thr Val Ser His Ala Gln Ser Met Arg Thr Leu
 20 25 30
Ser Val Ser Ala Leu Val Arg Thr Gly Gly Thr Val Ser Pro Arg Ser
 35 40 45
Ala Ser Asp Ala Gly Met Met Ala Gln Gly Leu Val Arg Ala Arg Arg
 50 55 60
Ala Gln Ala Val Gln Leu Leu Gln Leu Gln Leu Leu Leu Val
65 70 75 80
Pro Lys Phe Trp Asn
 85

(2) INFORMATION FOR SEQ ID NO:4045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..804

(D) OTHER INFORMATION: / Ceres Seq. ID 1579355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4045:

tttgctgaag tacaccaaac aaggcatact cctgtacagt ctacagatttg ggtcgggtgtg 60
gttgccagcag tcatggccagg cctctttaat gtgcgtgtgc tctcacatat tctttccgtc 120
ggcactctga ccggttattc agttgtatat gcttgtgtga tcacactaag atggaatgac 180
aaaggaacta gtcgtcgctc ccttggaagt atgtcaattt ggcaagaggg tgttctaagt 240
cttgccatag ttgctctttg tggttttata gtgggacttt gctatcgctt taactatgtg 300
atagccttta tggttgtagc ttttgtgata gctgttgctg ccagtttccg tctccagttt 360
cgtcaggctc atgtggatcc acctggcctt tcttgtccctg gggtagccgtt gggtcccat 420
attttctgtt tcttcaacat ggtcctgttt gtcacagctac atgaagaagc gtggtataga 480
tttgccatcc ttagtctcat cgctgtggga gttTatgccg gctatgtcca gtacaatgct 540
gttccttcca gctcagaaca ctctactatt ggttaccatg cggttccctc tgaagccgca 600
tgagctatgt tcatccccgg agttcttcga acatactgta cggtaccacac atacaccatg 660
gtcaccgaag ttgtgaacctg ttgctttttt cttgatgttt tgcacagtcg atactcttgt 720
agttacgctt agtactccta tatgtagaca gtgaatttcg cagcctgtgt tgtgccacc 780
acaccattcg tcaggaagct tgcc

(2) INFORMATION FOR SEQ ID NO:4046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1579356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4046:

Phe Ala Glu Val His Pro Thr Arg His Thr Pro Val Gln Ser Gln Ile
1 5 10 15

Trp	Val	Gly	Cys	Val	Ala	Ala	Val	Met	Ala	Gly	Leu	Phe	Asn	Val	Arg	
		20						25					30			
Val	Leu	Ser	His	Ile	Leu	Ser	Val	Gly	Thr	Leu	Thr	Gly	Tyr	Ser	Val	
		35					40					45				
Val	Ser	Ala	Cys	Val	Ile	Thr	Leu	Arg	Trp	Asn	Asp	Lys	Gly	Thr	Ser	
		50					55				60					
Arg	Arg	Ser	Leu	Gly	Ser	Met	Ser	Ile	Trp	Gln	Glu	Gly	Val	Leu	Ser	
		65					70				75				80	
Leu	Val	Ile	Val	Ala	Leu	Cys	Gly	Phe	Ile	Val	Gly	Leu	Cys	Tyr	Arg	
				85					90					95		
Phe	Asn	Tyr	Ala	Ile	Ala	Phe	Met	Val	Val	Ala	Phe	Val	Ile	Ala	Val	
		100						105					110			
Ala	Ala	Ser	Phe	Ala	Leu	Gln	Phe	Arg	Gln	Val	Tyr	Val	Asp	Pro	Pro	
		115					120					125				
Gly	Phe	Ser	Cys	Pro	Gly	Val	Pro	Leu	Val	Pro	Ile	Ile	Ser	Val	Phe	
		130				135					140					
Phe	Asn	Met	Val	Leu	Phe	Ala	Gln	Leu	His	Glu	Glu	Ala	Trp	Tyr	Arg	
		145				150					155				160	
Phe	Val	Ile	Leu	Ser	Leu	Ile	Ala	Val	Gly	Val	Tyr	Ala	Gly	Tyr	Gly	
				165					170					175		
Gln	Tyr	Asn	Ala	Val	Pro	Ser	Ser	Ser	Glu	His	Ser	Thr	Ile	Gly	Tyr	
				180				185						190		
His	Gly	Val	Pro	Ser	Glu	Ala	Ala									
		195				200										

(2) INFORMATION FOR SEQ ID NO:4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4047:

Met	Ala	Gly	Leu	Phe	Asn	Val	Arg	Val	Leu	Ser	His	Ile	Leu	Ser	Val	
			5						10					15		
Gly	Thr	Leu	Thr	Gly	Tyr	Ser	Val	Val	Ser	Ala	Cys	Val	Ile	Thr	Leu	
			20					25					30			
Arg	Trp	Asn	Asp	Lys	Gly	Thr	Ser	Arg	Arg	Ser	Leu	Gly	Ser	Met	Ser	
		35					40				45					
Ile	Trp	Gln	Glu	Gly	Val	Leu	Ser	Leu	Val	Ile	Val	Ala	Leu	Cys	Gly	
		50					55				60					
Phe	Ile	Val	Gly	Leu	Cys	Tyr	Arg	Phe	Asn	Tyr	Ala	Ile	Ala	Phe	Met	
		65				70				75				80		
Val	Val	Ala	Phe	Val	Ile	Ala	Val	Ala	Ala	Ser	Phe	Ala	Leu	Gln	Phe	
			85					90						95		
Arg	Gln	Val	Tyr	Val	Asp	Pro	Pro	Gly	Phe	Ser	Cys	Pro	Gly	Val	Pro	
		100						105					110			
Leu	Val	Pro	Ile	Ile	Ser	Val	Phe	Phe	Asn	Met	Val	Leu	Phe	Ala	Gln	
		115					120					125				
Leu	His	Glu	Glu	Ala	Trp	Tyr	Arg	Phe	Val	Ile	Leu	Ser	Leu	Ile	Ala	
		130				135					140					
Val	Gly	Val	Tyr	Ala	Gly	Tyr	Gly	Gln	Tyr	Asn	Ala	Val	Pro	Ser	Ser	
		145				150				155				160		
Ser	Glu	His	Ser	Thr	Ile	Gly	Tyr	His	Gly	Val	Pro	Ser	Glu	Ala	Ala	
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:4048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1579358
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4048:
Met Ser Ile Trp Gln Glu Gly Val Leu Ser Leu Val Ile Val Ala Leu
1 5 10 15
Cys Gly Phe Ile Val Gly Leu Cys Tyr Arg Phe Asn Tyr Ala Ile Ala
20 25 30
Phe Met Val Val Ala Phe Val Ile Ala Val Ala Ala Ser Phe Ala Leu
35 40 45
Gln Phe Arg Gln Val Tyr Val Asp Pro Pro Gly Phe Ser Cys Pro Gly
50 55 60
Val Pro Leu Val Pro Ile Ile Ser Val Phe Phe Asn Met Val Leu Phe
65 70 75 80
Ala Gln Leu His Glu Glu Ala Trp Tyr Arg Phe Val Ile Leu Ser Leu
85 90 95
Ile Ala Val Gly Val Tyr Ala Gly Tyr Gly Gln Tyr Asn Ala Val Pro
100 105 110
Ser Ser Ser Glu His Ser Thr Ile Gly Tyr His Gly Val Pro Ser Glu
115 120 125
Ala Ala
130

(2) INFORMATION FOR SEQ ID NO:4049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..650
(D) OTHER INFORMATION: / Ceres Seq. ID 1579359
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4049:
attatttttt cggtgctcga ggttcagggt tcacgcagkc ggcgagagct ggcagccatg 60
aagargggga gcccatggtc gctgcggctg ctaatttgct gcgcggcaat ggtggccatc 120
gcgcttctcc cccaacaagg aggcaggccc gcttgtttcg tgcgcagccc ggtgccagct 180
ccggcaaccgc cggctctcct cgcgcagcaac acgaacgact cctccgctgc tctctgccca 240
gccaagccca gcgcattccc acccccattg tacggtgtgt tcacccccgg cagtcctccg 300
ccacacgagtg cggcgccggc gtcgcggggg cgggtgctcg gcagcggcga ccagaagccg 360
tgccctctct tctgcgcgcaa gtvctgcgcg gctgacctgt gcgtgcgcgc gggcacctac 420
ggcaacaaga acacctgcgc ctgctacaac aactggaaga ccaagcgggg agggcccaag 480
tgccctctct agccctctct ctggtgtctac ttgatgagat cttctgttca aaaaatcaaa 540
aggtaagaat ctgttttaac atcttttagat ttcaacaata aaacaggttt caatttatct 600
ttgtagtcaa acgcttgcga ctcagtgtgt aatctcatcc aatattagt

(2) INFORMATION FOR SEQ ID NO:4050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1579360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4050:

Ile	Ile	Leu	Ser	Val	Leu	Glu	Val	Gln	Val	Ser	Arg	Xaa	Arg	Arg	Glu	
1			5						10						15	
Leu	Ala	Ala	Met	Lys	Xaa	Gly	Ser	Pro	Trp	Ser	Leu	Arg	Leu	Leu	Ile	
			20					25						30		
Cys	Cys	Ala	Ala	Met	Val	Ala	Ile	Ala	Leu	Leu	Pro	Gln	Gln	Gly	Gly	
			35				40					45				
Gln	Ala	Ala	Cys	Phe	Val	Pro	Thr	Pro	Gly	Pro	Ala	Pro	Ala	Pro	Pro	
			50			55					60					
Gly	Ser	Ser	Ala	Thr	Asn	Thr	Asn	Asp	Ser	Ser	Ala	Ala	Pro	Arg	Pro	
65				70					75					80		
Ala	Lys	Pro	Ser	Ala	Phe	Pro	Pro	Pro	Met	Tyr	Gly	Gly	Val	Thr	Pro	
				85					90					95		
Gly	Ser	Leu	Gln	Pro	His	Glu	Cys	Gly	Gly	Arg	Cys	Ala	Gly	Arg	Cys	
			100				105						110			
Ser	Ala	Thr	Ala	Tyr	Gln	Lys	Pro	Cys	Leu	Phe	Phe	Cys	Arg	Lys	Xaa	
			115				120					125				
Cys	Ala	Ala	Cys	Leu	Cys	Val	Pro	Pro	Gly	Thr	Tyr	Gly	Asn	Lys	Asn	
			130			135					140					
Thr	Cys	Pro	Cys	Tyr	Asn	Asn	Trp	Lys	Thr	Lys	Arg	Gly	Gly	Pro	Lys	
145					150					155				160		
Cys	Pro															

(2) INFORMATION FOR SEQ ID NO:4051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1579361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4051:

Tyr	Phe	Ile	Gly	Ala	Arg	Gly	Ser	Gly	Phe	Thr	Gln	Xaa	Ala	Arg	Ala	
1			5						10						15	
Gly	Ser	His	Glu	Xaa	Gly	Glu	Pro	Met	Val	Ala	Ala	Ala	Ala	Asn	Leu	
			20					25						30		
Leu	Arg	Gly	Asn	Gly	Gly	His	Arg	Ala	Ser	Pro	Pro	Thr	Arg	Arg	Pro	
			35			40						45				
Gly	Arg	Leu	Phe	Arg	Ala	Asp	Ala	Gly	Ser	Ser	Ser	Gly	Thr	Ala	Arg	
			50			55					60					
Leu	Leu	Arg	Asp	Glu	His	Glu	Arg	Leu	Leu	Arg	Cys	Ser	Ser	Ala	Ser	
65				70					75					80		
Gln	Ala	Gln	Arg	Ile	Pro	Thr	Pro	Asn	Val	Arg	Trp	Cys	His	Pro	Arg	
				85					90					95		
Gln	Ser	Pro	Ala	Thr	Arg	Val	Arg	Arg	Pro	Val	Arg	Gly	Ala	Val	Leu	
			100				105						110			
Gly	Asp	Gly	Val	Pro	Glu	Ala	Val	Pro	Leu	Leu	Leu	Pro	Gln	Xaa	Leu	
			115				120					125				
Arg	Gly	Val	Pro	Val	Arg	Ala	Ala	Gly	His	Leu	Arg	Gln	Gln	Glu	His	
			130			135					140					
Leu	Pro	Leu	Leu	Gln	Gln	Leu	Glu	Asp	Gln	Ala	Gly	Arg	Pro	Gln	Val	
145				150					155					160		
Pro	Leu	Val	Ala	Leu	Pro	Leu	Gly	Leu	Leu	Asp	Glu	Ile	Phe	Cys	Ser	
				165					170					175		
Lys	Asn	Gln	Lys	Val	Arg	Ile	Cys	Leu	Thr	Ile	Phe	Arg	Phe	His	Lys	
				180				185						190		

(2) INFORMATION FOR SEQ ID NO:4052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4052:

Met Val Ala Ala Ala Ala Asn Leu Leu Arg Gly Asn Gly Gly His Arg
1 5 10 15
Ala Ser Pro Pro Thr Arg Arg Pro Gly Arg Leu Phe Arg Ala Asp Ala
20 25 30
Gly Ser Ser Ser Gly Thr Ala Arg Leu Leu Arg Asp Glu His Glu Arg
35 40 45
Leu Leu Arg Cys Ser Ser Ala Ser Gln Ala Gln Arg Ile Pro Thr Pro
50 55 60
Asn Val Arg Trp Cys His Pro Arg Gln Ser Pro Ala Thr Arg Val Arg
65 70 75 80
Arg Pro Val Arg Gly Ala Val Leu Gly Asp Gly Val Pro Glu Ala Val
85 90 95
Pro Leu Leu Leu Pro Gln Xaa Leu Arg Gly Val Pro Val Arg Ala Ala
100 105 110
Gly His Leu Arg Gln Gln Glu His Leu Pro Leu Leu Gln Gln Leu Glu
115 120 125
Asp Gln Ala Gly Arg Pro Gln Val Pro Leu Val Ala Leu Pro Leu Gly
130 135 140
Leu Leu Asp Glu Ile Phe Cys Ser Lys Asn Gln Lys Val Arg Ile Cys
145 150 155 160
Leu Thr Ile Phe Arg Phe His Lys
165

(2) INFORMATION FOR SEQ ID NO:4053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4053:

ggagcgattt attaaagcorr cctccgccaa ccgcactctg ccgcgccaaa gcgtcgctcg 60
gccactctgc actcgcgcg cctcaaaaga tgcacaggca gctcagcctc tcgcgccagcm 120
cgaagcagca gcagccgcct cctgamggca ccacaccgg angcggcgac gcggcgcgga 180
agcgcatggc gcgcggcgag gacgagtcgt cgccctcgca ctccagctcc aaggccagca 240
gggggtggtc ggccggggac gagagggcca tccactcgt ccgcgtgctc acctctctct 300
gcttcctcct gctcttctc tgctccacag acccgctccc cgccgatatg tcgagCttcg 360
ctggaggcgg cgccgggagga ggaggagcga gatctgggaa ccggagggtta aggatgcttt 420
agtgtgcgta ttacctacc attggagtat tattatcgcg atgcggatgt tgtactgttc 480
cagcagtaac caagtatggg accaaagtat gtcaccatac aaacactctt tgctgtggta 540
atactaccaa cctacatcag catgtctcgt

(2) INFORMATION FOR SEQ ID NO:4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..139
(D) OTHER INFORMATION: / Ceres Seq. ID 1579367
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4054:
Thr His Leu Leu Ser Xaa Pro Pro Pro Thr Ala Leu Cys Pro Pro Lys
1 5 10 15
Ala Ser Ser Gly His Leu Ala Leu Ala Arg Ala Ser Lys Met His Arg
20 25 30
Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro Pro Pro Xaa
35 40 45
Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Lys Ala Met Ala Ala
50 55 60
Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Lys Ala Ser Arg
65 70 75 80
Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val Pro Leu Leu
85 90 95
Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His Asp Pro Ser
100 105 110
Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly Gly Gly
115 120 125
Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu
130 135
(2) INFORMATION FOR SEQ ID NO:4055:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1579368
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4055:
Met His Arg Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro
1 5 10 15
Pro Pro Xaa Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Ala Lys Ala
20 25 30
Met Ala Ala Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Ser Lys
35 40 45
Ala Ser Arg Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val
50 55 60
Pro Leu Leu Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His
65 70 75 80
Asp Pro Ser Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly
85 90 95
Gly Gly Gly Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu
100 105 110
(2) INFORMATION FOR SEQ ID NO:4056:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1579369
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4056:
Met Ala Ala Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Lys
1 5 10 15
Ala Ser Arg Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val
20 25 30
Pro Leu Leu Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His
35 40 45
Asp Pro Ser Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly
50 55 60
Gly Gly Gly Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:4057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..618

(D) OTHER INFORMATION: / Ceres Seq. ID 1579382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4057:

agcaatsecc aacagcgcca ctgtccagtg cgcgcgtsaa gcttgcttag stagccgccca 60
tggtccctcc cgcgcgcgtc tccgtgaagc ccgtggccat caaggggtctc gcgcgcagct 120
ctatctccgg aaggaagctc gccgtcgcca gCgcgtcggc ccgctccatc cgcagggccc 180
gcgcagcCgc cgtggtggcc aagtcacggc acaagagcgt ctacttcgac ctgcagacaca 240
ctcgcaacac caccggacag tgggacctct acggctctga cgcgcctcgc cctacaacac 300
cgctacagag caagttcttc gagacgtttc cggtccggtt caccagagaga ggtctgctgc 360
tcaagttcct gctgctgggc ggccggtcac ttctggccta cgtcagcgcg tcggcgctcac 420
cggacctcct gccgatcaag aagggaacctc aggagccgcc gcagcctggc ccgcgcggca 480
agatctaaag tcagctactc catttgcagt gtctagtagt agcttgcgtt gtactstagg 540
gcgcgtcgat ccgtcgcaat cgtcatggat catctctcta tcttgtgttt acgctgttca 600
taatttggtg tattcgcc

(2) INFORMATION FOR SEQ ID NO:4058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4058:

Ala Xaa Pro Asn Ser Ala Thr Val Gln Cys Ala Arg Xaa Ala Cys Leu
1 5 10 15
Xaa Ser Arg His Gly Leu Pro Arg Arg Arg Leu Arg Glu Ala Arg Gly
20 25 30
His Gln Gly Ser Arg Arg Gln Leu Tyr Leu Arg Lys Glu Ala Arg Arg
35 40 45
Arg Gln Ala Val Gly Pro Leu His Pro Gln Ala Pro Arg Ser Arg Arg
50 55 60
Gly Gly Gln Val Arg Arg Gln Glu Arg Leu Leu Arg Pro Arg Arg His
65 70 75 80
Arg Gln His Arg Thr Val Gly Pro Leu Arg Leu
85 90

(2) INFORMATION FOR SEQ ID NO:4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4059:

Met	Ala	Ser	Leu	Ala	Ala	Val	Ser	Val	Lys	Pro	Val	Ala	Ile	Lys	Gly	
1			5						10					15		
Leu	Ala	Gly	Ser	Ser	Ile	Ser	Gly	Arg	Lys	Leu	Ala	Val	Ala	Arg	Pro	
			20					25						30		
Ser	Ala	Arg	Ser	Ile	Arg	Arg	Pro	Arg	Ala	Ala	Ala	Val	Val	Ala	Lys	
			35					40						45		
Tyr	Gly	Asp	Lys	Ser	Val	Tyr	Phe	Asp	Leu	Asp	Asp	Ile	Gly	Asn	Thr	
			50				55					60				
Thr	Gly	Gln	Trp	Asp	Leu	Tyr	Gly	Ser	Asp	Ala	Pro	Ser	Pro	Tyr	Asn	
			65			70			75					80		
Pro	Leu	Gln	Ser	Lys	Phe	Phe	Glu	Thr	Phe	Ala	Ala	Pro	Phe	Thr	Lys	
			85					90						95		
Arg	Gly	Leu	Leu	Lys	Phe	Leu	Leu	Gly	Gly	Gly	Ser	Leu	Leu			
			100				105							110		
Ala	Tyr	Val	Ser	Ala	Ser	Ala	Ser	Pro	Asp	Leu	Leu	Pro	Ile	Lys	Lys	
			115				120							125		
Gly	Pro	Gln	Glu	Pro	Pro	Gln	Pro	Gly	Pro	Arg	Gly	Lys	Ile			
			130			135								140		

(2) INFORMATION FOR SEQ ID NO:4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4060:

atcacaaattc	acagcgctca	agttctcgcg	cccagagcca	aattttttctc	cactcaaatca	60
ctgcagccat	gnacgccagc	ngascggtag	caagcggaag	aagggggcg	ctggcgccaa	120
ggctggcgccg	cccaggaaga	agtcggtgtc	gcggtccgct	aagggccggc	tgcagttccc	180
cgctgcgcggg	atcgggcgct	acctcaagaa	gggcgcgtac	gcgcagcgCG	tgggcaccgg	240
cgcccccgctc	tatctcgccg	ccgtgcttga	gtacctcgcc	gcgaggtgc	tggagctggc	300
cggaacgcg	gcgaaggaca	acaagaagac	gcgcatcgct	ccgcgccagc	tgctcctggc	360
gatccgcgaac	gacgttgagc	tcggcaagct	gctggctggc	gtcaccatcg	cgcacggcgg	420
tgctctccccc	aacatcaacc	cggttctctc	gcccaagaag	gtggcggaga	aggcgtctag	480
cgggcgccagc	aaggagagca	agtcctccaa	gaaggccgcc	aagtccccaa	agaaggcagc	540
caagtccccc	aagaagcgct	agaaattagt	cactccacta	gcgctctgct	gtagcatggt	600
cggtgtttaga	tctgtggatg	ttatgtgttc	cggcctaatt	tcctctttgc	ctgtgtgctt	660
ctgatattgtt	catcgccgat	tttgccgtgt	tgtgtttcct	tggtctgatt	ttgcaattca	720
tcattctgtt	gaatgaactt	actatcgga	aatgaagcat	aataacgatg	c	

(2) INFORMATION FOR SEQ ID NO:4061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1579399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4061:

Ser Gln Phe Thr Ala Leu Lys Phe Ser Arg Pro Glu Pro Asn Phe Ser
1 5 10 15
Pro Leu Asn His Cys Ser His Xaa Arg Gln Xaa Xaa Gly Ser Lys Ala
20 25 30
Lys Lys Gly Ala Ala Gly Arg Lys Ala Gly Gly Pro Arg Lys Lys Ser
35 40 45
Val Ser Arg Ser Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile
50 55 60
Gly Arg Tyr Leu Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly
65 70 75 80
Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val
85 90 95
Leu Glu Leu Ala Gly Asn Ala Ala Lys Asp Asn Lys Lys Thr Arg Ile
100 105 110
Val Pro Arg His Val Leu Leu Ala Ile Arg Asn Asp Val Glu Leu Gly
115 120 125
Lys Leu Leu Ala Gly Val Thr Ile Ala His Gly Gly Val Leu Pro Asn
130 135 140
Ile Asn Pro Val Leu Leu Pro Lys Lys Val Ala Glu Lys Ala Ser Ser
145 150 155 160
Gly Gly Ser Lys Glu Ser Lys Ser Pro Lys Lys Ala Ala Lys Ser Pro
165 170 175
Lys Lys Ala Ala Lys Ser Pro Lys Lys Ala
180 185

(2) INFORMATION FOR SEQ ID NO:4062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1579400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4062:

His Asn Ser Gln Arg Ser Ser Ser Arg Ala Gln Ser Gln Ile Phe Leu
1 5 10 15
His Ser Ile Thr Ala Ala Met Xaa Ala Ser Xaa Xaa Val Ala Arg Arg
20 25 30
Arg Arg Gly Arg Leu Gly Ala Arg Leu Ala Ala Pro Gly Arg Ser Arg
35 40 45
Cys Arg Gly Pro Ser Arg Pro Gly Cys Ser Ser Pro Ser Ala Gly Ser
50 55 60
Gly Ala Thr Ser Arg Arg Ala Gly Thr Arg Ser Ala Trp Ala Pro Ala
65 70 75 80
Pro Pro Ser Ile Ser Pro Pro Cys Leu Ser Thr Ser Pro Pro Arg Cys
85 90 95
Trp Ser Trp Pro Ala Thr Arg Arg Arg Thr Thr Arg Arg Arg Ala Ser
100 105 110
Ser Arg Ala Thr Cys Ser Trp Arg Ser Ala Thr Thr Leu Ser Ser Ala
115 120 125
Ser Cys Trp Leu Ala Ser Pro Ser Arg Thr Ala Val Ser Ser Pro Thr
130 135 140
Ser Thr Arg Phe Ser Cys Pro Arg Arg Trp Arg Arg Arg Leu Ala

145 150 155 160
Ala Ala Ala Arg Arg Ala Ser Pro Leu Arg Arg Pro Pro Ser Pro Gln
165 170 175
Arg Arg Gln Pro Ser Pro Arg Arg Arg Leu Arg Asn
180 185

(2) INFORMATION FOR SEQ ID NO:4063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4063:

Met Xaa Ala Ser Xaa Xaa Val Ala Arg Arg Arg Gly Arg Leu Gly
1 5 10 15
Ala Arg Leu Ala Ala Pro Gly Arg Ser Arg Cys Arg Gly Pro Ser Arg
20 25 30
Pro Gly Cys Ser Ser Pro Ser Ala Gly Ser Gly Ala Thr Ser Arg Arg
35 40 45
Ala Gly Thr Arg Ser Ala Trp Ala Pro Ala Pro Pro Ser Ile Ser Pro
50 55 60
Pro Cys Leu Ser Thr Ser Pro Pro Arg Cys Trp Ser Trp Pro Ala Thr
65 70 75 80
Arg Arg Arg Thr Thr Arg Arg Arg Ala Ser Ser Arg Ala Thr Cys Ser
85 90 95
Trp Arg Ser Ala Thr Thr Leu Ser Ser Ala Ser Cys Trp Leu Ala Ser
100 105 110
Pro Ser Arg Thr Ala Val Ser Ser Pro Thr Ser Thr Arg Phe Ser Cys
115 120 125
Pro Arg Arg Trp Arg Arg Arg Leu Ala Ala Ala Arg Arg Ala
130 135 140
Ser Pro Leu Arg Arg Pro Pro Ser Pro Gln Arg Arg Gln Pro Ser Pro
145 150 155 160
Arg Arg Arg Leu Arg Asn
165

(2) INFORMATION FOR SEQ ID NO:4064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4064:

asattcaagcc cacaagcaca taacaacata gcacccccc taggggttcca caacatatgt 60
accctctcgc gcaaacactc ctctttccgc rcmgcctccc ctcccgcaca ctgtctccgc 120
cgccgcggcc accgcgcgcg caccgcagca gccagtcagc agatcgtaac catggcggat 180
tctaaggccg ctgcggcggt gacctccgc acgcgcgaagt tcatgaccaa ccgcctcttc 240
tcocgcaagc agttcgtgct cgaGgtcact caccocggcc gccccaactg ctccaaggcg 300
gaGbtcaagg agaggctggc gaagatctac gaggtgaagg acccaaaactg catcttcgtc 360
tccaagtttc ggaccaactt cggaggcggc aagtccaccg gcttcgggtc catctcacag 420
aaccttgagg cgcgcaagaa gtttcgagccc aagtaccgcc tcatcaggaa cggccttgct 480
accaaggtag agaagtcacg aaagcagatg aaggaaacgta agracagggc gaagaaatc 540
cgtggtgtga agaagacaaa agcggggagat gcccaagaaga agtaaggag gaagtactt 600

gccttgccat ttctcatott aggottttggg ttgttttaggg tgggctcctt ccggccaatgc 660
tgaatgtgtt tagttagaag tagagaagat ttgtccaatc acccattacg ttgagtttct 720
cgttgcacct ttctgtcagt ttgtaggcac ttgtcagac acaagaatat atatactgg 780
tc

(2) INFORMATION FOR SEQ ID NO:4065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4065:

Xaa	Phe	Ser	Pro	Gln	Ala	His	Asn	Asn	Ile	Ala	Pro	Pro	Leu	Gly	Phe	
1				5						10				15		
His	Asn	Ile	Cys	Thr	Leu	Ser	Arg	Lys	His	Ser	Ser	Phe	Arg	Xaa	Ala	
			20					25					30			
Ser	Pro	Pro	Ala	His	Leu	Leu	Arg	Arg	Arg	Gly	His	Arg	Arg	Arg	Thr	
			35				40					45				
Ala	Ala	Ala	Ser	Gln	Gln	Ile	Val	Thr	Met	Ala	Asp	Ser	Lys	Ala	Ala	
			50			55					60					
Ala	Ala	Val	Thr	Leu	Arg	Thr	Arg	Lys	Phe	Met	Thr	Asn	Arg	Leu	Leu	
			65			70				75				80		
Ser	Arg	Lys	Gln	Phe	Val	Leu	Glu	Val	Ile	His	Pro	Gly	Arg	Pro	Asn	
			85					90						95		
Val	Ser	Lys	Ala	Glu	Xaa	Lys	Glu	Arg	Leu	Ala	Lys	Ile	Tyr	Glu	Val	
			100					105					110			
Lys	Asp	Pro	Asn	Cys	Ile	Phe	Val	Phe	Lys	Phe	Arg	Thr	Asn	Phe	Gly	
			115				120					125				
Gly	Gly	Lys	Ser	Thr	Gly	Phe	Gly	Leu	Ile	Tyr	Asp	Asn	Leu	Glu	Ala	
			130				135				140					
Ala	Lys	Lys	Phe	Glu	Pro	Lys	Tyr	Arg	Leu	Ile	Arg	Asn	Gly	Leu	Ala	
			145			150				155				160		
Thr	Lys	Val	Glu	Lys	Ser	Arg	Lys	Gln	Met	Lys	Glu	Arg	Lys	Xaa	Arg	
			165					170						175		
Ala	Lys	Lys	Ile	Arg	Gly	Val	Lys	Lys	Thr	Lys	Ala	Gly	Asp	Ala	Lys	
			180					185						190		
Lys	Lys															

(2) INFORMATION FOR SEQ ID NO:4066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4066:

Met	Ala	Asp	Ser	Lys	Ala	Ala	Ala	Ala	Val	Thr	Leu	Arg	Thr	Arg	Lys	
1				5					10					15		
Phe	Met	Thr	Asn	Arg	Leu	Leu	Ser	Arg	Lys	Gln	Phe	Val	Leu	Glu	Val	
			20					25					30			
Ile	His	Pro	Gly	Arg	Pro	Asn	Val	Ser	Lys	Ala	Glu	Xaa	Lys	Glu	Arg	
			35			40				45						
Leu	Ala	Lys	Ile	Tyr	Glu	Val	Lys	Asp	Pro	Asn	Cys	Ile	Phe	Val	Phe	

50		55		60
Lys Phe Arg Thr Asn Phe Gly Gly Lys Ser Thr Gly Phe Gly Leu				
65	70	75	80	
Ile Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg				
	85	90	95	
Leu Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln				
	100	105	110	
Met Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys				
	115	120	125	
Thr Lys Ala Gly Asp Ala Lys Lys Lys				
130	135			

(2) INFORMATION FOR SEQ ID NO:4067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4067:

Met Thr Asn Arg Leu Leu Ser Arg Lys Gln Phe Val Leu Glu Val Ile	
1	5 10 15
His Pro Gly Arg Pro Asn Val Ser Lys Ala Glu Xaa Lys Glu Arg Leu	
	20 25 30
Ala Lys Ile Tyr Glu Val Lys Asp Pro Asn Cys Ile Phe Val Phe Lys	
	35 40 45
Phe Arg Thr Asn Phe Gly Gly Gly Lys Ser Thr Gly Phe Gly Leu Ile	
	50 55 60
Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg Leu	
	65 70 75 80
Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln Met	
	85 90 95
Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys Thr	
	100 105 110
Lys Ala Gly Asp Ala Lys Lys Lys	
	115 120

(2) INFORMATION FOR SEQ ID NO:4068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..650
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4068:

attcacgcgtc	cacgtttccat	atgggttcct	gcaggatgac	actcctcctt	ggcttgctgc	60
tgctagttagt	agcttcgccc	gcgatcgcgt	atgacgactc	cggtatctac	taccagctgg	120
ctcttatgtg	gcaggagaca	tactcgcagc	agaccagcgc	tgggtgctgc	aaGccgacca	180
ccggcgctctc	gccgacgcgc	gacttctaca	taacgggctt	caccgtcctt	aacgcgacca	240
ccgacgctgc	agtgacggga	tgacgaacca	aagttcctta	cgaccctaac	ctgattaccg	300
gcataccaag	cctgaatcag	tactggagca	acatcaggtg	ccccagcaac	aacgggcaga	360
gcagctggaa	gaacgcctgg	aagaaggccg	gcgcctgata	ttgtcccgaa	gggtgtgttt	420
gggaattggg	agggggaaaa	aaagaggaaa	ttgtgcata	gagtcagacg	gtgtatacgc	480
ttgtacgcca	tcaatcaagt	gctgtaaaaa	tgccctggaa	ataattgggg	acctggattt	540
gaataagatt	tgagttgttg	ggggcggaag	tgctacatta	ggccttggtc	ggtttattct	600

aataccttcg gtgcaataaaa ggaatcatc ttgcgcgtga ccgagcgtgc

(2) INFORMATION FOR SEQ ID NO:4069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4069:

Ser	Pro	Ser	Thr	Phe	His	Met	Ala	Ser	Cys	Arg	Met	Ala	Leu	Leu	Leu
1					5				10					15	
Gly	Leu	Leu	Leu	Val	Val	Ala	Ser	Pro	Ala	Ile	Ala	Asp	Asp	Asp	
				20				25				30			
Ser	Gly	Ile	Tyr	Tyr	Gln	Leu	Ala	Leu	Met	Trp	Pro	Gly	Ala	Tyr	Cys
				35				40				45			
Glu	Gln	Thr	Ser	Ala	Gly	Cys	Cys	Lys	Pro	Thr	Thr	Gly	Val	Ser	Pro
				50			55					60			
Xaa	Arg	Asp	Phe	Tyr	Ile	Thr	Gly	Phe	Thr	Val	Leu	Asn	Ala	Thr	Thr
65					70				75					80	
Asp	Ala	Ala	Val	Thr	Gly	Cys	Ser	Asn	Lys	Val	Pro	Tyr	Asp	Pro	Asn
				85					90					95	
Leu	Ile	Thr	Gly	Ile	Gln	Gly	Leu	Asn	Gln	Tyr	Trp	Ser	Asn	Ile	Arg
				100				105					110		
Cys	Pro	Ser	Asn	Asn	Gly	Gln	Ser	Ser	Trp	Lys	Asn	Ala	Trp	Lys	Lys
				115			120						125		
Ala	Gly	Ala													
				130											

(2) INFORMATION FOR SEQ ID NO:4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4070:

Met	Ala	Ser	Cys	Arg	Met	Ala	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	
1				5					10				15		
Val	Ala	Ser	Pro	Ala	Ile	Ala	Asp	Asp	Asp	Ser	Gly	Ile	Tyr	Tyr	Gln
				20					25				30		
Leu	Ala	Leu	Met	Trp	Pro	Gly	Ala	Tyr	Cys	Glu	Gln	Thr	Ser	Ala	Gly
				35				40				45			
Cys	Cys	Lys	Pro	Thr	Thr	Gly	Val	Ser	Pro	Xaa	Arg	Asp	Phe	Tyr	Ile
				50			55				60				
Thr	Gly	Phe	Thr	Val	Leu	Asn	Ala	Thr	Thr	Asp	Ala	Ala	Val	Thr	Gly
65					70				75					80	
Cys	Ser	Asn	Lys	Val	Pro	Tyr	Asp	Pro	Asn	Leu	Ile	Thr	Gly	Ile	Gln
				85				90					95		
Gly	Leu	Asn	Gln	Tyr	Trp	Ser	Asn	Ile	Arg	Cys	Pro	Ser	Asn	Asn	Gly
				100				105					110		
Gln	Ser	Ser	Trp	Lys	Asn	Ala	Trp	Lys	Lys	Ala	Gly	Ala			
				115			120						125		

(2) INFORMATION FOR SEQ ID NO:4071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1579409
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4071:
Met Ala Leu Leu Leu Gly Leu Leu Leu Val Val Ala Ser Pro Ala
1 5 10 15
Ile Ala Asp Asp Asp Ser Gly Ile Tyr Tyr Gln Leu Ala Leu Met Trp
20 25 30
Pro Gly Ala Tyr Cys Glu Gln Thr Ser Ala Gly Cys Cys Lys Pro Thr
35 40 45
Thr Gly Val Ser Pro Xaa Arg Asp Phe Tyr Ile Thr Gly Phe Thr Val
50 55 60
Leu Asn Ala Thr Thr Asp Ala Ala Val Thr Gly Cys Ser Asn Lys Val
65 70 75 80
Pro Tyr Asp Pro Asn Leu Ile Thr Gly Ile Gln Gly Leu Asn Gln Tyr
85 90 95
Trp Ser Asn Ile Arg Cys Pro Ser Asn Asn Gly Gln Ser Ser Trp Lys
100 105 110
Asn Ala Trp Lys Lys Ala Gly Ala
115 120

(2) INFORMATION FOR SEQ ID NO:4072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 635 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..635
(D) OTHER INFORMATION: / Ceres Seq. ID 1579440
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4072:
atttataatt atttattgct gccgcgtcca cgcgcgtcc ccaaaccccta ccgcagtcgc 60
cgccaccgtc tccctcctg atccaatcca atggcgcgcc tccacctcgt ggccgtggga 120
atgggcttgc tcttggcctt gacgacggcg caggcaccgg gcgcgtccac gatgcccgCg 180
cccatggcgC agntccggcg acctcggcgc ctctcgtcc cgccgcattcc ccgaccaga 240
agaccgtcc agctccggcg cccaatgccca cggtaccgcg ccccgccctcG ccgcggcgcg 300
cgagctctat cgggcagacg ccgaccgagg cgcgcgtcctc cctccgcgcg ccagcgccg 360
cgtcacgcgt tgctccgcg ttgtacgtgg Nccgcgcgcta tggcgGctgt cgtgtttttt 420
ttctgaggtc ggtaactcgc gccgatggat ccgcgcgcta tggataggta cggtgccgtg 480
tggatttgac acgatggctc ccGcgtaccg ctggctcagat ttgcttatta ggatactagt 540
agttaattaa tagttgggtt gatcagatca gatctagcgt ttttgttgag tggggatatt 600
attttctcta cggatctgca cactagggtt atgtc

(2) INFORMATION FOR SEQ ID NO:4073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..178
(D) OTHER INFORMATION: / Ceres Seq. ID 1579441
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4073:

Leu Tyr Leu Phe Ile Ala Ala Ala Ser Thr Val Arg Pro Gln Thr Leu
1 5 10 15
Pro Gln Ser Pro Pro Ser Pro Leu Leu Ile Gln Ser Asn Gly Ala
20 25 30
Pro Pro Pro Arg Gly Arg Gly Asn Gly Leu Ala Leu Gly Leu Asp Asp
35 40 45
Gly Ala Gly Thr Gly Arg Val His Asp Ala Arg Ala His Gly Ala Xaa
50 55 60
Pro Ala Thr Ser Ala Pro Pro Arg Pro Ala Pro Ser Pro Thr Gln Lys
65 70 75 80
Thr Ala Pro Ala Pro Ala Pro Asn Ala Thr Val Pro Ala Pro Ala Ser
85 90 95
Pro Pro Ala Pro Ser Ser Ile Gly Gln Thr Pro Thr Glu Ala Pro Ser
100 105 110
Ser Pro Pro Pro Pro Ser Ala Ala Ser Ser Val Ala Ser Ala Leu Tyr
115 120 125
Val Xaa Arg Arg Tyr Gly Gly Cys Arg Val Phe Leu Leu Arg Ser Val
130 135 140
Leu Gly Ala Asp Gly Ser Ala Ala Tyr Gly Met Val Arg Cys Gly Val
145 150 155 160
Asp Leu Thr Arg Trp Leu Pro Ala Thr Ala Gly Arg Val Cys Leu Leu
165 170 175
Gly Tyr

(2) INFORMATION FOR SEQ ID NO:4074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1579442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4074:

Met Ala Arg Leu His Leu Val Ala Val Ala Met Gly Leu Leu Leu Ala
1 5 10 15
Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser Thr Met Pro Ala Pro Met
20 25 30
Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu Val Pro Arg His Pro Arg
35 40 45
Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro Met Pro Arg Tyr Pro Pro
50 55 60
Pro Pro Arg Arg Arg Arg Ala Leu Ser Gly Arg Arg Arg Pro Arg
65 70 75 80
Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro Arg Pro Ala Leu Pro Pro
85 90 95
Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala Val Val Phe Phe Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:4075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1579443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4075:
Met Gly Leu Leu Leu Ala Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser
1 5 10 15
Thr Met Pro Ala Pro Met Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu
20 25 30
Val Pro Arg His Pro Arg Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro
35 40 45
Met Pro Arg Tyr Pro Pro Pro Pro Arg Arg Arg Arg Arg Ala Leu Ser
50 55 60
Gly Arg Arg Arg Pro Arg Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro
65 70 75 80
Arg Pro Ala Leu Pro Pro Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala
85 90 95
Val Val Phe Phe Phe
100

(2) INFORMATION FOR SEQ ID NO:4076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4076:

actcagccca	ctacettica	gatttttcc	catctgccgc	cgctgcacc	caacaagcct	60
ctcgacgcta	gtcatggcgc	cttccaacgg	cgccgcscgc	tcgacgagac	cgctcgccgc	120
accgactccg	tgcaggagcc	tcaccaaga	atctccaaga	tctctccct	gctcaagggtg	180
aagaagctct	ccgagaagcc	cgctgctgcc	tcgcccggtc	ccgctctcgc	cgccggctac	240
gacctctcga	gcgcgcagga	gatggtggtg	ccggcgcggtg	gcaaggcgct	cgctgccgacc	300
gacctcagcg	tgcccatccc	gcacggaaac	taacgcgcga	tcgcGCCcgc	gtcggggctg	360
gcgctgaagc	actccatcga	cgctggcgcc	ggcggtgatc	acgcggacta	ccgaggccccc	420
gtcggcgctca	tcctcttcaa	ccactccgac	gcgcgacttc	ccgtgaagcc	cgcgacaggg	480
atcgcgcgaga	tgatcatcga	ggtgatcgcg	acgcccaggg	tcgcggagggt	ggaggacctc	540
gacgccaccg	tcctggggga	cggaggggtc	gggtccaccg	gcgtctgaag	ggattcggtg	600
tctaggttag	gatggcgatg	caagccttgc	tgtcttttgt	tggctctaa	aaatcgatga	660
gttcaaccatc	actatcctgc	tatcgataat	tagtatttag	attagtagct	aggttgcgta	720
gttagctcga	tgacgctact	attgtcgaga	actcgctatt	ctgtgatggt	gaaaatgtct	780

(2) INFORMATION FOR SEQ ID NO:4077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4077:

Thr Gln Pro Thr Thr Phe Gln Ile Phe Pro His Leu Pro Pro Pro Ala
1 5 10 15
Pro Asn Lys Pro Leu Asp Ala Ser His Gly Arg Phe Gln Arg Arg Arg
20 25 30
Xaa Val Asp Glu Thr Val Ala Ala Thr Asp Ser Val Gln Glu Pro Pro
35 40 45
Gln Lys Ile Ser Lys Ile Ser Pro Leu Leu Lys Val Lys Lys Leu Ser
50 55 60

Glu Lys Ala Val Leu Pro Ser Arg Gly Ser Ala Leu Ala Ala Gly Tyr
65 70 75 80
Asp Leu Ser Ser Ala Glu Glu Met Val Val Pro Ala Arg Gly Lys Ala
85 90 95
Leu Val Pro Thr Asp Leu Ser Val Ala Ile Pro His Gly Thr Tyr Ala
100 105 110
Arg Ile Ala Pro Arg Ser Gly Leu Ala Leu Lys His Ser Ile Asp Val
115 120 125
Gly Ala Gly Val Ile Asp Ala Asp Tyr Arg Gly Pro Val Gly Val Ile
130 135 140
Leu Phe Asn His Ser Asp Ala Asp Phe Ala Val Lys Pro Gly Asp Arg
145 150 155 160
Ile Ala Gln Met Ile Ile Glu Val Ile Ala Thr Pro Glu Val Ala Glu
165 170 175
Val Glu Asp Leu Asp Ala Thr Val Arg Gly Asp Gly Gly Phe Gly Ser
180 185 190
Thr Gly Val
195

(2) INFORMATION FOR SEQ ID NO:4078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4078:

Met Val Val Pro Ala Arg Gly Lys Ala Leu Val Pro Thr Asp Leu Ser
1 5 10 15
Val Ala Ile Pro His Gly Thr Tyr Ala Arg Ile Ala Pro Arg Ser Gly
20 25 30
Leu Ala Leu Lys His Ser Ile Asp Val Gly Ala Gly Val Ile Asp Ala
35 40 45
Asp Tyr Arg Gly Pro Val Gly Val Ile Leu Phe Asn His Ser Asp Ala
50 55 60
Asp Phe Ala Val Lys Pro Gly Asp Arg Ile Ala Gln Met Ile Ile Glu
65 70 75 80
Val Ile Ala Thr Pro Glu Val Ala Glu Val Glu Asp Leu Asp Ala Thr
85 90 95
Val Arg Gly Asp Gly Gly Phe Gly Ser Thr Gly Val
100 105

(2) INFORMATION FOR SEQ ID NO:4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4079:

atccgttgct catctcacca gaagcgaaGc cggaggaggg aggaaggaga tcgcgagcag 60
cggaggccgg aggcCgagag gatgaagacg ttgcaccggt gcccggtctt ctccgcggcg 120
gagtggaagc gcaactggcc ctctccacag gggttcgcca tcaccggtt catcatcacc 180
aagatgacgg ccaacttcac cgaggaggac ctcaagaact ccaagttcgt ccaggaacac 240
aagaagcgct gaccaaccgg gagtcgtccg aatcgctcgc ggatgaaaaa ttagcccccct 300

attttatcttg tctttttttt tatctagatg cgtgcactct attgtaataa tgtaataaga 360
ggcaattgga ttgatccaac agcaaccggc ttctgatttt gaTcygcttc gctgacataa 420
tatgtgcctt ttttttgat gttggattgc atctaactct gttgaattg

(2) INFORMATION FOR SEQ ID NO:4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1579455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4080:

Ile	Arg	Cys	Ser	Ser	His	Gln	Lys	Arg	Ser	Arg	Arg	Arg	Glu	Glu	Gly
1			5							10				15	
Asp	Arg	Glu	Gln	Pro	Glu	Pro	Glu	Ala	Glu	Arg	Met	Lys	Thr	Phe	Asp
			20						25				30		
Pro	Trp	Pro	Val	Phe	Phe	Arg	Arg	Glu	Trp	Lys	Arg	Asn	Trp	Pro	Phe
			35				40					45			
Leu	Thr	Gly	Phe	Ala	Ile	Thr	Gly	Phe	Ile	Ile	Thr	Lys	Met	Thr	Ala
			50			55					60				
Asn	Phe	Thr	Glu	Glu	Asp	Leu	Lys	Asn	Ser	Lys	Phe	Val	Gln	Glu	His
					70					75				80	
Lys	Lys	Arg													

(2) INFORMATION FOR SEQ ID NO:4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1579456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4081:

Pro	Leu	Leu	Ile	Ser	Pro	Glu	Ala	Lys	Pro	Glu	Glu	Gly	Gly	Arg	Arg
1			5							10				15	
Ser	Arg	Ala	Ala	Gly	Ala	Gly	Gly	Arg	Glu	Asp	Glu	Asp	Val	Arg	Pro
			20					25					30		
Val	Ala	Gly	Leu	Leu	Pro	Pro	Gly	Val	Glu	Ala	Gln	Leu	Ala	Leu	Pro
			35				40					45			
His	Gly	Val	Arg	His	His	Arg	Leu	His	His	His	Gln	Asp	Asp	Gly	Gln
			50			55					60				
Leu	His	Arg	Gly	Gly	Pro	Gln	Glu	Leu	Gln	Val	Arg	Pro	Gly	Thr	Gln
					70					75				80	
Glu	Ala	Leu	Thr	Asn	Arg	Glu	Ser	Ser	Glu	Ser	Pro	Ala	Asp	Glu	Lys
				85					90				95		
Leu	Ala	Pro	Tyr	Leu	Ser	Cys	Leu	Phe	Phe	Tyr	Leu	Asp	Ala	Cys	Thr
			100					105					110		
Leu	Leu														

(2) INFORMATION FOR SEQ ID NO:4082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1579457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4082:

```
cctttcttccc ccaactgtcgc cgctcctcgt ettcactct etccaatttg ctgctctcttc 60
tcccttattta atgctcgtgg gctcctatga tccgcccctcc gccgcgggtt tcttgatcca 120
tccccggcccc aagggaagcgg accccggcga acactcctga cagattcgcc cCgtccgcgc 180
ctccctcgtat tcgggtccCTt ccccgtcagc ggcaggtgtt taggGacctc tgcagcatag 240
catctgggtcc gtccctggag atgtccggcg tacaggagca gttcgagatc aagtctccggG 300
ctgccggagc gcaccgacat cggaccNcag gcggttcccg ccgrogctca ccgtcgccac 360
gtccaaggag accatcatcc cccagtggcc cgatgatgtt gaaggctctg cagcgcaagc 420
cggcgatgta tactggcgcc ggcggcgccg gcgagcaaa gcggaggagc agctggtgag 480
gagattgaga ctgtggtgtt gcgtggcggt tactgttcat cgttcagaca gatgaactgc 540
tggccCatgc tgtgggctca ggaactgctt ettcacagt gcgatgttct gatctgtaat 600
gcacgaagca cgatactatt tttgtatat gtatgtatgt gtaactacag ataagattag 660
gaacgggtgt aaagaataaa gaaaccgatg gaataagtga tttgggaaca atctcagaat 720
caatttatgc agtcctttag g
```

(2) INFORMATION FOR SEQ ID NO:4083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1579458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4083:

```
Leu Leu Pro Pro Leu Ser Pro Leu Leu Val Phe His Ser Leu His Phe
1 5 10 15
Ala Ala Ser Ser Pro Leu Leu Met Leu Val Gly Ser Tyr Asp Pro Pro
20 25 30
Ser Ala Ala Gly Phe Leu Ile His Pro Arg Pro Lys Glu Ala Asp Pro
35 40 45
Gly Glu His Ser
50
```

(2) INFORMATION FOR SEQ ID NO:4084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4084:

```
Met Ser Gly Val Gln Glu Gln Phe Glu Ile Lys Phe Arg Ala Ala Gly
1 5 10 15
Arg His Arg His Arg Thr Xaa Gly Gly Ser Arg Xaa Arg Pro Pro Ser
20 25 30
Pro Arg Ser Arg Arg Pro Ser Ser Pro Ser Gly Pro Met Met Val Lys
35 40 45
Ala Leu Gln Arg Lys Pro Ala Met Tyr Thr Gly Gly Gly Gly Gly
50 55 60
Glu Gln Ser Gly Arg Ser Ser Trp
65 70
```


(2) INFORMATION FOR SEQ ID NO:4088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4088:

Met	Ser	Cys	Asn	Cys	Gly	Ser	Ser	Cys	Gly	Cys	Gly	Ser	Ser	Cys	Lys
1			5						10						15
Cys	Gly	Lys	Lys	Tyr	Pro	Asp	Leu	Glu	Glu	Thr	Ser	Thr	Ala	Ala	Gln
			20					25					30		
Ala	Thr	Val	Val	Leu	Gly	Val	Ala	Pro	Glu	Lys	Lys	Ala	Ala	Pro	Glu
			35				40					45			
Phe	Val	Glu	Ala	Ala	Ala	Glu	Ser	Gly	Glu	Ala	Ala	His	Asp	Leu	Arg
			50			55					60				
Leu	Arg														
65															

(2) INFORMATION FOR SEQ ID NO:4089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4089:

actctcccaa	accctagccc	agagcagccg	catcgaactc	tacctgcctt	tctctcgccc	60
ctggcggcgg	cggcaggatg	gcggcttcta	ctgcgaggac	ggtgaaggat	gtgaaccccc	120
acgagtttgt	caaggcctac	tccgcccata	tcaaacgctc	cggcaagatg	gagcttccctg	180
agtggttgga	cattgtgaag	actgcgaggt	tcaaggagct	ccctccctat	gacctgact	240
ggtactacat	cagggtctga	tctgtagcaa	ggaagatcta	cttgagacaa	ggcattgggtg	300
tgtgtggcct	ccagaagatt	tatggtggcc	gccagaggaa	tgGctcacgc	ccacctcaact	360
tctgcaagag	cagtgggtgcc	atttcacgca	acatcctcca	gcagctgcag	gagatgggca	420
ctatgatgtg	cgatcccaag	ggtggacggc	gcatacactc	ccaggggaag	cgtgatctgg	480
accaggtggc	tggaagggtt	gctgttgaag	cttgagcaat	ctcatatttg	gtttctatga	540
tgctatgttt	gattgttgag	atggctacac	tttatttgca	ctttggatta	ggattttttg	600
gttaagagaa	ctcaaggcat	tetagtctatg	tttcacactg	tattttccct	gagtaacctat	660
ttatcaaaac	ctattc					

(2) INFORMATION FOR SEQ ID NO:4090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4090:

Met	Ala	Ala	Ser	Thr	Ala	Arg	Thr	Val	Lys	Asp	Val	Asn	Pro	His	Glu
1			5						10						15
Phe	Val	Lys	Ala	Tyr	Ser	Ala	His	Leu	Lys	Arg	Ser	Gly	Lys	Met	Glu

20	25	30
Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys Glu Leu		
35	40	45
Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser Val Ala		
50	55	60
Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe Gln Lys		
65	70	75
Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His Phe Cys		
85	90	95
Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu Gln Glu		
100	105	110
Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile Thr Ser		
115	120	125
Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala Val Glu		
130	135	140

Ala
145

(2) INFORMATION FOR SEQ ID NO:4091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4091:

Met Glu Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys	
1	5
Glu Leu Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser	
20	25
Val Ala Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe	
35	40
Gln Lys Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His	
50	55
Phe Cys Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu	
65	70
Gln Glu Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile	
85	90
Thr Ser Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala	
100	105
Val Glu Ala	
115	

(2) INFORMATION FOR SEQ ID NO:4092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4092:

Met Val Ala Ala Arg Gly Met Ala His Ala His Leu Thr Ser Ala Arg	
1	5
Ala Val Val Pro Phe His Ala Thr Ser Ser Ser Ser Cys Arg Arg Trp	
20	25
	30

Ala Ser Leu Met Ser Ile Pro Arg Val Asp Gly Ala Ser Pro Pro Arg
35 40 45
Glu Gly Val Ile Trp Thr Arg Trp Leu Glu Gly Leu Leu Lys Leu
50 55 60
Glu Gln Ser His Ile Trp Phe Leu
65 70

(2) INFORMATION FOR SEQ ID NO:4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4093:

aaataggaca	cgccggctag	tactgcgcc	gccCactcca	gcgctgaagg	ctgcagcgc	60
cagcgacgcg	cytctctgct	actgtgncgt	ctgacgcgcg	tggggtgtga	gccaaactgcg	120
agctgctgcc	accctctgtg	ccgcgkctga	ccgccgcgcc	cggaccgcaga	tggacgctcg	180
gtggggcggtg	ctgcctgcgc	tgctgggtcgc	cagcgggcgc	gtccgtgtct	gcgcgcgcgc	240
tgkggccaag	ggcgccaact	ggctgggcgcg	gtgagccgc	gcgtcgttcc	ccaaaggggtt	300
cggtgttcggg	acggcgacgt	c				

(2) INFORMATION FOR SEQ ID NO:4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4094:

Asn Arg Thr Arg Arg Leu Val Leu Arg Gln Pro Thr Pro Ala Leu Lys	
1 5 10 15	
Ala Cys Ser Ala Ser Ala Ala Xaa Leu Cys Tyr Cys Xaa Cys	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4095:

Met Asp Ala Arg Trp Ala Val Leu Leu Ala Leu Leu Val Ala Ser Gly	
1 5 10 15	
Gly Val Arg Val Cys Ala Ala Ala Xaa Ala Lys Gly Ala Asn Trp Leu	
20 25 30	
Gly Gly Leu Ser Arg Ala Ser Phe Pro Lys Gly Phe Val Phe Gly Thr	
35 40 45	

Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:4096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..344
(D) OTHER INFORMATION: / Ceres Seq. ID 1579493
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4096:
gagcccatcc atctccattt ccgcgcgcc ccgcgcgaga gaccccaacc ccaccocatcc 60
accaccatgt ggcgcgcgct ccacacccta gcccccgcct tgcgcaggGc taccgcgcgc 120
gcgcgcgggg cccctgcgcg gtccgcctcc tctgcagccc gcgcgcgcc gctctcctcg 180
gcgcgcgcgc ctttcgcgcg caccagcccg ctctaccttt ggattagggt ttggtacccc 240
tgtgttccc tttgtttgct cccgctatga aacgagacga gagaagaatg agcaaggttt 300
ttgttcgag ctatttttgc ccaatgatat tgatatgttg ttct
(2) INFORMATION FOR SEQ ID NO:4097:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1579494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4097:
Glu Pro Ile His Leu His Phe Arg Arg Pro Ala Ala Glu Arg Pro Gln
1 5 10 15
Pro His Pro Ser Thr Thr Met Trp Arg Arg Leu His Thr Leu Ala Pro
20 25 30
Ala Leu Arg Arg Ala Thr Ala Ala Ala Gly Ala Pro Ala Ala Ser
35 40 45
Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser Ala Ala Ala
50 55 60
Phe Arg Arg Thr Ser Pro Leu Tyr Leu Trp Ile Arg Cys Trp Tyr Pro
65 70 75 80
Cys Cys Ser Leu Cys Leu Leu Pro Leu
85
(2) INFORMATION FOR SEQ ID NO:4098:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..74
(D) OTHER INFORMATION: / Ceres Seq. ID 1579495
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4098:
Ala His Pro Ser Pro Phe Pro Pro Pro Arg Arg Glu Thr Pro Thr
1 5 10 15
Pro Pro Ile His His His Val Ala Pro Pro Pro His Pro Ser Pro Arg
20 25 30
Leu Ala Gln Gly Tyr Arg Arg Arg Arg Gly Pro Cys Gly Val Arg
35 40 45
Leu Leu Cys Ser Pro Arg Arg Pro Ala Leu Leu Gly Gly Arg Arg Phe
50 55 60

Pro Pro His Gln Pro Ala Leu Pro Leu Asp
65 70

(2) INFORMATION FOR SEQ ID NO:4099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1579496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4099:

Met Trp Arg Arg Leu His Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr
1 5 10 15
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ala Ala Arg
20 25 30
Ala Ala Pro Leu Ser Ser Ala Ala Ala Ala Phe Arg Arg Thr Ser Pro
35 40 45
Leu Tyr Leu Trp Ile Arg Cys Trp Tyr Pro Cys Cys Ser Leu Cys Leu
50 55 60
Leu Pro Leu
65

(2) INFORMATION FOR SEQ ID NO:4100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 737 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..737

(D) OTHER INFORMATION: / Ceres Seq. ID 1579503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4100:

atagaaagt gaaaggatga agtttagagga tctcgttcca ctgcgctacg agacggcgac 60
gctcgcggaac aacaatggcg atgatgcctc ctgcagcggc gtcacccctc gcctccactc 120
cccgcggcat cgcgcgtccg cctaactcgca cggcatccct gtgcatccgc ttagggtgtcg 180
tgacggcgac gctgttcgct ggactggcgg cggcgtcgca gccagtgagg cgtcacgccg 240
cggtggtggt cgcgatggcg aagaggggag aggagctgga ggggatccag gccatgacga 300
cggaacagct ggagaggagg gtggtagacc tcaaggggga gcttttctgt cctccgcctta 360
agcgcctcgc cgcgccaggag ttcaagaaca gcgagttcgg ccgcatgcgc aagagagattg 420
ctcgtatggt gactgtgaaa agagagcggg aaactgaaca aggaataaac aagagattgt 480
ccagggagct tgataggaaa tggaaacagg gcattgtggt cagaccacca ccatctctaa 540
gggagaacaa agaggagtag agagctgcaa aagaagcaat ctgcaaaagt cgtttcatgc 600
aagagtgttg caagaagggt cctttgtgat tccaaacttt atttcattgt tacgtattcc 660
atgtttacat tttactaagc attgctatcc gaatctgaat ttcagtcgtt agtctcttct 720
gtaaatttga tttatct

(2) INFORMATION FOR SEQ ID NO:4101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1579504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4101:

```

Met Ala Met Met Pro Pro Ala Ala Ala Ser Ser Leu Ala Ser Thr Pro
1      5      10
Arg Gly Ile Ala Ala Pro Pro Thr Arg Thr Ala Ser Leu Cys Ile Arg
      20      25      30
Leu Gly Val Val Thr Ala Thr Leu Phe Ala Gly Leu Ala Ala Ser
      35      40      45
Gln Pro Val Glu Arg His Ala Ala Val Val Ala Met Ala Lys Arg
      50      55      60
Glu Gln Glu Leu Glu Gly Ile Gln Ala Met Thr Thr Glu Gln Leu Glu
      65      70      75      80
Glu Glu Val Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys
      85      90      95
Arg Ser Ala Arg Gln Glu Phe Lys Asn Ser Glu Phe Gly Arg Met Arg
      100      105      110
Lys Arg Ile Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Thr Glu
      115      120      125
Gln Gly Ile Asn Lys Arg Leu Ser Arg Glu Leu Asp Arg Lys Trp Lys
      130      135      140
Gln Gly Ile Val Val Arg Pro Pro Ser Leu Arg Glu Asn Lys Glu
      145      150      155      160
Glu

```

(2) INFORMATION FOR SEQ ID NO:4102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1579505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4102:

```

Met Met Pro Pro Ala Ala Ala Ser Ser Leu Ala Ser Thr Pro Arg Gly
1      5      10      15
Ile Ala Ala Pro Pro Thr Arg Thr Ala Ser Leu Cys Ile Arg Leu Gly
      20      25      30
Val Val Thr Ala Thr Leu Phe Ala Gly Leu Ala Ala Ser Gln Pro
      35      40      45
Val Glu Arg His Ala Ala Val Val Val Ala Met Ala Lys Arg Glu Gln
      50      55      60
Glu Leu Glu Gly Ile Gln Ala Met Thr Thr Glu Gln Leu Glu Glu
      65      70      75      80
Val Val Asp Leu Lys Gly Glu Leu Phe Leu Arg Leu Lys Arg Ser
      85      90      95
Ala Arg Gln Glu Phe Lys Asn Ser Glu Phe Gly Arg Met Arg Lys Arg
      100      105      110
Ile Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Thr Glu Gln Gly
      115      120      125
Ile Asn Lys Arg Leu Ser Arg Glu Leu Asp Arg Lys Trp Lys Gln Gly
      130      135      140
Ile Val Val Arg Pro Pro Ser Leu Arg Glu Asn Lys Glu Glu
      145      150      155

```

(2) INFORMATION FOR SEQ ID NO:4103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1579506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4103:

```
Met Pro Pro Ala Ala Ala Ser Ser Leu Ala Ser Thr Pro Arg Gly Ile
1      5      10      15
Ala Ala Pro Pro Thr Arg Thr Ala Ser Leu Cys Ile Arg Leu Gly Val
20      25      30
Val Thr Ala Thr Leu Phe Ala Gly Leu Ala Ala Ala Ser Gln Pro Val
35      40      45
Glu Arg His Ala Ala Val Val Val Ala Met Ala Lys Arg Glu Gln Glu
50      55      60
Leu Glu Gly Ile Gln Ala Met Thr Thr Glu Gln Leu Glu Glu Val
65      70      75      80
Val Asp Leu Lys Gly Glu Leu Phe Leu Arg Leu Lys Arg Ser Ala
85      90      95
Arg Gln Glu Phe Lys Asn Ser Glu Phe Gly Arg Met Arg Lys Arg Ile
100     105     110
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Thr Glu Gln Gly Ile
115     120     125
Asn Lys Arg Leu Ser Arg Glu Leu Asp Arg Lys Trp Lys Gln Gly Ile
130     135     140
Val Val Arg Pro Pro Pro Ser Leu Arg Glu Asn Lys Glu Glu
145     150     155
```

(2) INFORMATION FOR SEQ ID NO:4104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..456
(D) OTHER INFORMATION: / Ceres Seq. ID 1579543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4104:

```
agccgtcatc gtttcgcgtc tgccctcagcc cgccgcgaagg agaggagaca tcttcgagaa      60
gctgaaatgg ctctctaaagc tgctcctgcc aagaagggtg atgccaaagc ccaggcccttg      120
aagggtgccca aggcgtgtgaa gtctgtggggc gccaaagaaga agaccaagaag gatccgcacg      180
tctgtgacat ttcaccgcgcc caccgacctg aagaaggcta gggaccoccaa gtaccacacga      240
atcagcacta ccggaaggaag caagccttgat cagtaccaaa ttctcaagta cccctctacc      300
acagaatcag cgatgaagaa gattgaagat aacaacactc tggttctcat tgttgacctc      360
aaggcgagaca agaagaagat caaggctgcc gtcaagaaga tgtatgacat ccaggcaaa      420
aaggtaaca ccttgatcag gccctgatgg aagaag
```

(2) INFORMATION FOR SEQ ID NO:4105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1579544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4105:

```
Ser Arg His Arg Phe Ala Ser Ala Ser Ala Arg Arg Lys Glu Arg Arg
1      5      10      15
His Leu Arg Glu Ala Glu Met Ala Pro Lys Ala Pro Ala Lys Lys
20      25      30
```

Gly Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser
35 40 45
Gly Ala Ala Lys Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe
50 55 60
His Arg Pro Thr Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg
65 70 75 80
Ile Ser Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys
85 90 95
Tyr Pro Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn
100 105 110
Thr Leu Val Phe Ile Val Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys
115 120 125
Ala Ala Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr
130 135 140
Leu Ile Arg Pro Asp Gly Lys Lys
145 150

(2) INFORMATION FOR SEQ ID NO:4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4106:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln
1 5 10 15
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ala Ala Lys Lys Lys
20 25 30
Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Thr Thr Leu
35 40 45
Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg
50 55 60
Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu
65 70 75 80
Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val
85 90 95
Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys Ala Ala Val Lys Lys Met
100 105 110
Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly
115 120 125
Lys Lys
130

(2) INFORMATION FOR SEQ ID NO:4107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..445
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4107:

aaaaaaaaacc tactaacccg gtctctctc cagcgccgcg cgtgcgccgc gccctctctc 60
tggtcccgcc gtccgtcgag gtcacatgat tgagggtcag tgtgctcaac gatgcgctca 120
agtccatgta caatgcagag aagaggggca agaggcaggt catgatcagg ccgtcgctcca 180

```
aggatgatcat caagttcctg acggtcatcg agcgtcatgg ttagtctcca atctcgtgcc 240
ccatttcaat tggcagcatt ccgaggatcac gtacctgatt agtgctatat tattaggata 300
cattggcgag ttcgagtacg tggatgacca cagagctggg aagattgtgg tggaaactgaa 360
cggcagacta aacaatgcg gtgtaattag cccccggttt gatgtgggg taaaggaat 420
cgaaggctgg actgcgagcg tgctt
```

(2) INFORMATION FOR SEQ ID NO:4108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4108:

```
Lys Asn Pro Thr Asn Arg Val Ser Ser Pro Ala Pro Ala Val Ala Ala
1          5          10          15
Ala Leu Leu Leu Val Pro Pro Ser Val Glu Val Ile Met Val Arg Val
20          25          30
Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn Ala Glu Lys Arg
35          40          45
Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys Val Ile Ile Lys
50          55          60
Phe Leu Thr Val Met Gln Arg His Gly
65          70
```

(2) INFORMATION FOR SEQ ID NO:4109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4109:

```
Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn
1          5          10          15
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys
20          25          30
Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly
35          40          45
```

(2) INFORMATION FOR SEQ ID NO:4110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4110:

```
accgcacaag gcttttggca gctacaaacc accccaaagc cacccccaga aaccggcggt 60
ccttgggtgt tcgggatctg agccagcagc tgagaagagg atgagcgccg tggcgccatg 120
gcgacgtcgt cgtgtaaccc caacgcgcgc ctcttcaccc cggcggcgta ccggcaggtg 180
gaggaattct cgcccagagt gtatgagctc gtcaacacca ccgcctgggt ccgggaccac 240
```

tggttcgcgc agcaccagca ccacgaggcc gccttcgcgc ccgcgcgcga cgcgcagctc 300
gacgtgcgcg cgctctctcc cgacgactcc gtcgacctcc tcgacaccga cgacctcttc 360
tacgcgcctg acgtccacca cccccacaac gccaaagccgg cgctgctgcc cgggtacgac 420
ctcgacatgc tcagggcgct gaggctcagc tccccccggg ccg

(2) INFORMATION FOR SEQ ID NO:4111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4111:

Met Ala Thr Ser Ser Leu Asn Pro Asn Ala Pro Leu Phe Ile Pro Ala
1 5 10 15
Ala Tyr Arg Gln Val Glu Glu Phe Ser Pro Glu Trp Tyr Glu Leu Val
20 25 30
Asn Thr Thr Ala Trp Phe Arg Asp His Trp Phe Arg Gln His Gln His
35 40 45
His Glu Ala Ala Phe Ala Ala Ala Asp Ala Glu Leu Asp Val Ala
50 55 60
Ala Leu Leu Pro Asp Asp Ser Val Asp Leu Leu Asp Thr Asp Asp Leu
65 70 75 80
Phe Tyr Ala Pro Asp Val His His Pro His Asn Ala Lys Pro Ala Leu
85 90 95
Leu Pro Gly Tyr Asp Leu Asp Met Leu Arg Ala Leu Ser Leu Ser Ser
100 105 110
Pro Arg Ala
115

(2) INFORMATION FOR SEQ ID NO:4112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1579571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4112:

Met Ser Ser Ser Thr Pro Pro Pro Gly Ser Gly Thr Thr Gly Ser Ala
1 5 10 15
Ser Thr Ser Thr Thr Arg Pro Pro Ser Pro Pro Pro Pro Thr Pro Ser
20 25 30
Ser Thr Ser Pro Arg Ser Ser Pro Thr Thr Pro Ser Thr Ser Ser Thr
35 40 45
Pro Thr Thr Ser Ser Thr Arg Leu Thr Ser Thr Thr Pro Thr Thr Pro
50 55 60
Ser Arg Arg Cys Cys Pro Gly Thr Thr Ser Thr Cys Ser Gly Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:4113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1579576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4113:

aaaaaaaaacgc	ccaccaacgcc	gccactcgca	accgcacacc	agccctcgca	acccaccacc	60
acgtccgaga	cgctccgagat	ggagttcttc	gcgcgctacc	tgctgccgtg	ctcgggcgcc	120
ggcccgccccc	ccacgctccc	gaccaaggac	gacgtgcgtc	gcacctgag	atccgtcagc	180
gcgcgaggtgg	aggaggaccg	cctcgacctg	gtcttcgcc	tcctagaggt	taaggacatc	240
gcgcgagctga	tcgccacggg	cggggagcat	ctgcctacg	cgccgtcagg	agccgctgct	300
gcgcgtcgttg	ccactctctg	cgctgccgag	gtcgaggagg	aggccacgaa	ggaggaggat	360
gaggacatcg	ccctcttcaa	cctcttcgac	tgatcgtgca	accctaogtg	gaccgatoga	420
tgccatctctc	gtccttgcct	gctgcggttt	gcttggtgct	ctgattgtac	attgtagt	

(2) INFORMATION FOR SEQ ID NO:4114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4115:

Lys	Lys	Thr	Pro	Thr	Thr	Pro	Pro	Leu	Ala	Thr	Ala	His	Gln	Pro	Ser	
1			5					10				15				
Gln	Pro	Thr	Thr	Thr	Ser	Glu	Thr	Ser	Glu	Met	Glu	Phe	Leu	Ala	Ala	
			20					25				30				
Tyr	Leu	Leu	Pro	Cys	Leu	Gly	Ala	Gly	Pro	Ala	Pro	Thr	Leu	Pro	Thr	
		35				40					45					
Lys	Asp	Asp	Val	Arg	Arg	Ile	Leu	Arg	Ser	Val	Ser	Ala	Glu	Val	Glu	
	50				55						60					
Glu	Asp	Arg	Leu	Asp	Leu	Val	Phe	Ala	Leu	Leu	Glu	Val	Lys	Asp	Ile	
	65			70						75			80			
Ala	Glu	Leu	Ile	Ala	Thr	Gly	Gly	Glu	His	Leu	Ala	Tyr	Ala	Pro	Ser	
			85					90					95			
Gly	Ala	Ala	Ala	Ala	Val	Val	Ala	Thr	Pro	Ala	Ala	Ala	Glu	Val	Glu	
			100					105					110			
Glu	Glu	Ala	Thr	Lys	Glu	Glu	Asp	Glu	Asp	Ile	Ala	Leu	Phe	Asn	Leu	
			115				120						125			
Phe	Asp															
	130															

(2) INFORMATION FOR SEQ ID NO:4115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1579578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4115:

Lys	Asn	Ala	His	His	Ala	Ala	Thr	Arg	Asn	Arg	Thr	Pro	Ala	Leu	Ala	
1			5					10				15				
Thr	His	His	His	Val	Arg	Asp	Val	Arg	Asp	Gly	Val	Pro	Arg	Arg	Val	
			20					25				30				
Pro	Ala	Ala	Val	Pro	Gly	Arg	Arg	Pro	Gly	Pro	His	Ala	Pro	Asp	Gln	
			35				40					45				

Gly Arg Arg Ala Ser His Pro Glu Ile Arg Gln Arg Arg Gly Gly Gly
50 55 60
Gly Pro Pro Arg Pro Gly Leu Arg Pro Pro Arg Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:4116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4116:

Met Glu Phe Leu Ala Ala Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro
1 5 10 15
Ala Pro Thr Leu Pro Thr Lys Asp Asp Val Arg Arg Ile Leu Arg Ser
20 25 30
Val Ser Ala Glu Val Glu Glu Asp Arg Leu Asp Leu Val Phe Ala Leu
35 40 45
Leu Glu Val Lys Asp Ile Ala Glu Leu Ile Ala Thr Gly Gly Glu His
50 55 60
Leu Ala Tyr Ala Pro Ser Gly Ala Ala Ala Val Val Ala Thr Pro
65 70 75 80
Ala Ala Ala Glu Val Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp
85 90 95
Ile Ala Leu Phe Asn Leu Phe Asp
100

(2) INFORMATION FOR SEQ ID NO:4117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..448
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4117:

gctgtctttc ttctgtctct ccatacgccg agtggtttga gaagctggtc ggcgctccta 60
gatcccttcg cctctctcgc gttcgaggct aggtagccgc caccatgagc cgctcggggc 120
agccctccgga tctcaagaag tacatggaca agaagcttca gattaagctg aatgcacaac 180
gtgtgtttat tggcacactt cggggattcg accagttcat gaatctggtg atcgacaaca 240
ctgtggaggt caatggaaat gacaagacag atattggaat ggtgtgttgc aggggaaaca 300
gtgtgtgcat gatcgaggca ctggagccag ttgccaaagtc gcagtgaaac cttatttttc 360
agctgatata gtccgagcat gaaaactgat gtaaatgcta tgagtgaacc ctgttgtact 420
tgcatttgta attgaagtct gtcgcttt

(2) INFORMATION FOR SEQ ID NO:4118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4118:

Met	Ser	Arg	Ser	Gly	Gln	Pro	Pro	Asp	Leu	Lys	Lys	Tyr	Met	Asp	Lys
1			5					10					15		
Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile	Gly	Thr	Leu
			20					25					30		
Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn	Thr	Val	Glu
		35				40					45				
Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val	Ile	Arg	Gly
		50				55					60				
Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala	Lys	Ser	Gln
65				70					75					80	

(2) INFORMATION FOR SEQ ID NO:4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4119:

Met	Asp	Lys	Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile
1			5					10					15		
Gly	Thr	Leu	Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn
			20					25					30		
Thr	Val	Glu	Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val
		35				40					45				
Ile	Arg	Gly	Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala
		50				55					60				
Lys	Ser	Gln													
65															

(2) INFORMATION FOR SEQ ID NO:4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4120:

Met	Asn	Leu	Val	Ile	Asp	Asn	Thr	Val	Glu	Val	Asn	Gly	Asn	Asp	Lys
1			5					10					15		
Thr	Asp	Ile	Gly	Met	Val	Val	Ile	Arg	Gly	Asn	Ser	Val	Val	Met	Ile
			20					25					30		
Glu	Ala	Leu	Glu	Pro	Val	Ala	Lys	Ser	Gln						
		35				40									

(2) INFORMATION FOR SEQ ID NO:4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1579596

cgtgtaaaccc	aagcgcctcc	ttctcccgcg	cacgagacacc	atcgcggaatg	gaagtgtgtct	60
ctgcggtgaa	gcaacccctc	ccctatggcg	agggcgccaa	ctcccgctct	ttctccacca	120
ctctctctct	gacctcgccc	tggccgcgcg	cgccgtcccc	gccgcgcgcg	cagcagcagt	180
cgcagtcgca	ggcgccgctg	cgccgcgcatc	tcgacacac	gcctctcccc	accactcttg	240
tgagagcgca	cacggccgac	ttccaaaggag	tgctccaaag	ctgcacgcg	tcgcgacacg	300
cgccgcctcg	ccagaagccc	gccgaagctcc	acgcgccaca	ccaccaccac	cacggcgctcg	360
cgccgctcgg	cccaagaagc	cgccgaatca	agctctacga	cgccggatcg	ggcaagaaca	420
actccaagat	gatcgcgccg	cttcggggggc	cgtcgccgcg	gaagcgcgcg	cgggagatcg	480
tatcccgca	catactgaac	ttgcgcgc				

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:4122:

Arg	Glu	Thr	Asn	Ala	Pro	Leu	Ser	Pro	Arg	Thr	Arg	Pro	Ile	Ala	Asn
1			5					10					15		
Gly	Ser	Cys	Ser	Cys	Gly	Glu	Ala	Thr	Pro	Pro	His	Gly	Ala	Gly	Pro
			20					25					30		
Gln	Leu	Pro	Val	Leu	Leu	His	His	Leu	Leu	Leu	Ala	Leu	Ala	Leu	Gly
		35					40					45			
Arg	Arg	Ala	Val	Pro	Ala	Ala	Ala	Pro	Ala	Ala	Val	Ala	Val	Ala	Gly
		50				55					60				
Ala	Arg	Ala	Ala	His	His	Arg	His	His	Ala	Leu	Pro	His	His	Leu	Arg
65				70						75				80	
Ala	Gly	Arg	His	Gly	Gln	Leu	Gln	Gly	Gly	Arg	Pro	Glu	Ala	His	Arg
				85				90						95	
Leu	Arg	His	Ala	Ala	Cys	Pro	Glu	Glu	Ala	Arg	Gln	Asp	Pro	Arg	Pro
		100					105					110			
Pro	Pro	Pro	Pro	Pro	Arg	Arg	Arg	Arg	Arg	Arg	Ala	Gln	Glu	Ala	Gly
		115				120						125			
Leu	Gln	Ala	Leu	Arg	Ala	Pro	Asp	Arg	Gln	Glu	Gln	Pro	Gln	Asp	Asp
		130				135					140				
Arg	Ala	Ala	Gly	Gly	Ala	Val	Ala	Ala	Glu	Gly	Gly	Ala	Gly	Gly	Ala
145				150					155					160	
Val	Ala	Gln	Arg	Ala	Arg	Leu	Pro	Phe	Xaa	Trp	Arg				
				165					170						

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4123:

Val Lys Pro Thr Pro Leu Ser Pro Arg Ala Arg Asp Pro Ser Arg Met
1 5 10 15

Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly Pro
20 25 30
Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser Ala
35 40 45
Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln Ala
50 55 60
Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe Val
65 70 75 80
Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr Gly
85 90 95
Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly His
100 105 110
His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro Ala
115 120 125
Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met Ile
130 135 140
Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val Leu
145 150 155 160
Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly
165 170

(2) INFORMATION FOR SEQ ID NO:4124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1579599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4124:

Met Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly
1 5 10 15
Pro Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser
20 25 30
Ala Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln
35 40 45
Ala Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe
50 55 60
Val Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr
65 70 75 80
Gly Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly
85 90 95
His His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro
100 105 110
Ala Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met
115 120 125
Ile Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val
130 135 140
Leu Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:4125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1579610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4125:

attccgagtc	tactattgta	cctctccgtg	ggggcgatcc	gccatttgtg	ccaattctag	60
catcacgctc	cgatcgacca	ggagtgtgaa	gtaggtgtgg	gagatcaagg	gcacgagcga	120
cccgcccaag	tttagtgtgg	attttaaaat	caagttcctt	acagttgtgtg	gaaagaaact	180
aaagttgaca	atatgggata	ccgctggcca	ggagagggtt	aggacaataa	ctagttctta	240
ctacagaggt	gctcagggaa	ttattttagt	atatgatgtc	acaaagagag	agagtttctc	300
aaatttgct	gatgtttgga	ctaaggaat	agaagcaaac	tcaacaaaca	aagactgcat	360
aaaaatgctt	gttggaaaca	aagttgacaa	ggatgatgaa	agaatgggtca	cagaagaaga	420
aggctctgct	tttgctgaag	aatctggttg	tctgtttctt	gagagcagtg	caaaacacga	480
gaaaatg						

(2) INFORMATION FOR SEQ ID NO:4126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..30

(D) OTHER INFORMATION: / Ceres Seq. ID 1579611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4126:

Phe	Arg	Val	Tyr	Cys	Thr	Ser	Pro	Trp	Gly	Arg	Ser	Ala	Ile	Cys	
1			5				10					15			
Ala	Asn	Ser	Ser	Ile	Ser	Val	Arg	Ser	Thr	Arg	Ser	Val	Lys		
			20				25					30			

(2) INFORMATION FOR SEQ ID NO:4127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1579612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4127:

Met	Leu	Val	Gly	Asn	Lys	Val	Asp	Lys	Asp	Glu	Arg	Met	Val	Thr	
1			5				10					15			
Glu	Glu	Glu	Gly	Leu	Ala	Phe	Ala	Glu	Glu	Ser	Gly	Cys	Leu	Phe	Leu
			20				25					30			
Glu	Ser	Ser	Ala	Lys	His	Glu	Lys	Met							
			35				40								

(2) INFORMATION FOR SEQ ID NO:4128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1579613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4128:

Met	Met	Lys	Glu	Trp	Ser	Gln	Lys	Lys	Lys	Val	Leu	Leu	Leu	Leu	Lys
1			5				10					15			
Asn	Leu	Val	Val	Cys	Phe	Leu	Arg	Ala	Val	Gln	Asn	Thr	Arg	Lys	

20 25 30

(2) INFORMATION FOR SEQ ID NO:4129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1579614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4129:

agtggcgccc	cgtgtcgtgt	agtgtgtagt	cgcagcagct	agcgcccgcc	cgccagctcg	60
agtgaagtcca	tctctccatcg	ccatcccaatg	gccgccaccg	cctgagcatg	agcatctctcc	120
gcgcgcgcgc	gccctgcttc	tcgtcccccac	tcaggctcag	ggtcgcgggt	gccaaagccgc	180
tggcgccccc	catgcggcgc	cagctgctgc	gcgcgcaggc	cacctacaac	gtgaagctga	240
tcacgcggga	ggggagaggtg	gagctgcagg	tgcccagcga	cgtctacaac	ctggactctg	300
ccgaggagga	aggcatcgac	ctgcccttct	cctgcccgtgc	ggggtcctgc	tcctcctgag	360
ccggcaaggt	cgtctctggc	tccgtcgacc	agtcgcacca	gagcttctct	aacgacaacc	420
aggtcgcgca	cggttgggtg	ctcactgcgc	tgctaccacc	acctccgacg	tcgtcatcga	480
gacgcacaag						

(2) INFORMATION FOR SEQ ID NO:4130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1579615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4130:

Met	Ser	Ile	Leu	Arg	Ala	Pro	Pro	Pro	Cys	Phe	Ser	Ser	Pro	Leu	Arg	
1				5					10					15		
Leu	Arg	Val	Ala	Val	Ala	Lys	Pro	Leu	Ala	Ala	Pro	Met	Arg	Arg	Gln	
				20					25					30		
Leu	Leu	Arg	Ala	Gln	Ala	Thr	Tyr	Asn	Val	Lys	Leu	Ile	Thr	Pro	Glu	
				35				40					45			
Gly	Glu	Val	Glu	Leu	Gln	Val	Pro	Asp	Asp	Val	Tyr	Ile	Leu	Asp	Phe	
				50				55				60				
Ala	Glu	Glu	Glu	Gly	Ile	Asp	Leu	Pro	Phe	Ser	Cys	Arg	Ala	Gly	Ser	
				65				70				75		80		
Cys	Ser	Ser	Cys	Ala	Gly	Lys	Val	Val	Ser	Gly	Ser	Val	Asp	Gln	Ser	
				85				90					95			
Asp	Gln	Ser	Phe	Leu	Asn	Asp	Asn	Gln	Val	Ala	Asp	Gly	Trp	Val	Leu	
				100				105					110			
Thr	Ala	Leu	Arg	Thr	Pro	Pro	Pro	Thr	Ser	Ser	Ser	Arg	Arg	Thr		
				115				120					125			

(2) INFORMATION FOR SEQ ID NO:4131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1579616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4131:
Met Arg Arg Gln Leu Leu Arg Ala Gln Ala Thr Tyr Asn Val Lys Leu
1 5 10 15
Ile Thr Pro Glu Gly Glu Val Glu Leu Gln Val Pro Asp Asp Val Tyr
20 25 30
Ile Leu Asp Phe Ala Glu Glu Glu Gly Ile Asp Leu Pro Phe Ser Cys
35 40 45
Arg Ala Gly Ser Cys Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser
50 55 60
Val Asp Gln Ser Asp Gln Ser Phe Leu Asn Asp Asn Gln Val Ala Asp
65 70 75 80
Gly Trp Val Leu Thr Ala Leu Arg Thr Pro Pro Thr Ser Ser Ser
85 90 95
Arg Arg Thr

(2) INFORMATION FOR SEQ ID NO:4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4132:

acacaaatttc	accgaaatcc	tccaaatacc	caccctacga	atcttctctt	cgggtctctt	60
ctgcgccatc	tctgggtc	agaagcgcg	cctcatgcgc	ggctctca	tcttcaatga	120
gtctcatctc	cgggacgagg	gcctccaactg	cgacttcg	tgctctctt	atgacctct	180
tccggggcaag	ctcgatgagt	cccgcgtccg	cgagatcgtt	gccgacgcgc	tcgacatcga	240
cgctgagttc	gtttgcgacg	cgctcccg	cgcgctggtc	ggaatgaacg	gcgggctcat	300
gagccagttac	atcgagttcg	tgcgcgaccg	cctgctcatg	gcgctggggc	acaggaagat	360
gtacaacgctg	gccaaaccc	tgcactggat	ggagctcatt	tcctgcagg	ccaaagacta	420
acttctttga	gaagcgcgtc	gggwagtacc	agaaggcgtc	cgtaatgt		

(2) INFORMATION FOR SEQ ID NO:4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4133:

His Asn Phe Thr Glu Ile Leu Gln Tyr Pro Thr Leu Arg Ile Phe Phe	
1 5 10 15	
Ser Gly Ser Phe Cys Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met	
20 25 30	
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu	
35 40 45	
His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys Leu	
50 55 60	
Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile Glu	
65 70 75 80	
Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met Asn	
85 90 95	
Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu Leu	
100 105 110	

Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe Asp
115 120 125
Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp
130 135

(2) INFORMATION FOR SEQ ID NO:4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4134:

Thr Ile Ser Pro Lys Ser Ser Asn Thr Pro Pro Tyr Glu Ser Ser Ser
1 5 10 15
Arg Ala Pro Ser Ala Pro Ser Ser Gly Ser Arg Ser Ala Ala Ser Cys
20 25 30
Arg Ala Ser Leu Ser Leu Met Ser Ser Ser Pro Gly Thr Arg Ala Ser
35 40 45
Thr Ala Thr Ser Pro Ala Ser Phe Met Thr Ser Phe Gly Ala Ser Ser
50 55 60
Met Ser Pro Ala Ser Ala Arg Ser Leu Pro Thr Thr Ser Ser
65 70 75 80
Val Ser Ser Phe Ala Thr Arg Ser Pro Ser Arg Trp Ser Glu
85 90

(2) INFORMATION FOR SEQ ID NO:4135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4135:

Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly
1 5 10 15
Leu His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys
20 25 30
Leu Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile
35 40 45
Glu Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met
50 55 60
Asn Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu
65 70 75 80
Leu Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe
85 90 95
Asp Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp
100 105

(2) INFORMATION FOR SEQ ID NO:4136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..445
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4136:

aaggccagtc	tgagttgtg	gtcgttcgc	ttgtgtctg	ca gctagggttt	agagggtttc	60
tggggcgga	gcggggagg	gcggcggtc	tggtgtcgc	ggaggaggag	atcgcggtga	120
aggagccgct	ggatctgata	cgctcagcc	tcgacgagc	catctacgtc	aagctccgat	180
ccgaccgga	gctgcgggc	aagctccatg	cgtatgatca	acatttaaac	atgatacttg	240
gagatgttga	agagggtcgtg	acaactgttg	agatagatga	tgaacatat	gaagaattg	300
tgccgataa	tctttgcaga	ccaacgaac	cactatcccc	tttcttttg	tccgaggtga	360
tggtgtcata	ttggtttctc	cacccttcg	tacggcayga	astttgaagt	tagatcatgc	420
tggtgtgtaa	ttatgataac	tggtg				

(2) INFORMATION FOR SEQ ID NO:4137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4137:

Gly	Gln	Ser	Glu	Cys	Ala	Phe	Asp	Ser	Leu	Val	Leu	Gln	Leu	Gly	Phe
1			5						10					15	
Arg	Gly	Phe	Leu	Gly	Ala	Glu	Arg	Glu	Ala	Ala	Ala	Met	Ala	Ala	
			20					25				30			
Ala	Glu	Glu	Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	Ile	Arg	Leu
			35				40				45				
Ser	Leu	Asp	Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Arg	Glu	Leu
			50			55				60					
Arg	Gly	Lys	Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met	Ile	Leu	Gly
			65		70				75				80		
Asp	Val	Glu	Glu	Val	Thr	Thr	Val	Glu	Ile	Asp	Asp	Glu	Thr	Tyr	
			85				90					95			
Glu	Glu	Ile	Val	Arg	Asp	Asn	Leu	Cys	Arg	Pro	Arg	Asn	Ala	Leu	Ser
			100				105					110			
Pro	Phe	Phe	Leu	Ser	Glu	Val	Met	Val	Ser	Tyr	Trp	Phe	Leu	His	Pro
			115			120						125			
Phe	Val	Arg	Xaa	Glu	Xaa										
			130												

(2) INFORMATION FOR SEQ ID NO:4138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4138:

Met	Ala	Ala	Ala	Glu	Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	
1				5				10					15		
Ile	Arg	Leu	Ser	Leu	Asp	Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp
			20				25					30			
Arg	Glu	Leu	Arg	Gly	Lys	Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met
			35				40					45			

Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp
50 55 60
Glu Thr Tyr Glu Glu Ile Val Arg Asp Asn Leu Cys Arg Pro Arg Asn
65 70 75 80
Ala Leu Ser Pro Phe Phe Leu Ser Glu Val Met Val Ser Tyr Trp Phe
85 90 95
Leu His Pro Phe Val Arg Xaa Glu Xaa
100 105

(2) INFORMATION FOR SEQ ID NO:4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4139:

atataaaagc tgccctcgcg acctagcacc agccctgccca ctccactcct accccacaca	60
gaagcggcgg cgcgaggaga aasgcaggcg aaggcgaggg tgtgagggaa ggagcaccag	120
ccatgggtgca cgtcaacttc taccgcaact atggttaagac gttcaagaaa ccaagcgctc	180
cttatgagaa ggagcgtctt gatgctgaac tgaagctggt cggtgagtat gggtcgaggt	240
gcaagcgtga gctttggagg gtccagtatg cactgagcag gatccgtaat gctgcaaggc	300
acttgctcac ccttgacgag aagaaccccc gtcttatctt tgagggtgag gcgctttctt	360
gccgcgatga ccgctatggg ctgcttgctg agggtcagaa caagcttg	

(2) INFORMATION FOR SEQ ID NO:4140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4140:

Tyr Lys Ser Cys Pro Arg Asp Leu Ala Pro Ala Leu Pro Leu His Ser	
1 5 10 15	
Tyr Pro Thr Gln Lys Arg Arg Arg Arg Ser Lys Xaa Arg Arg Arg Arg	
20 25 30	
Gly Cys Glu Gly Arg Ser Thr Ser His Gly Ala Arg Gln Leu Leu Pro	
35 40 45	
Gln Leu Trp	
50	

(2) INFORMATION FOR SEQ ID NO:4141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4141:

Met Val His Val Asn Phe Tyr Arg Asn Tyr Gly Lys Thr Phe Lys Lys	
1 5 10 15	

Pro Arg Arg Pro Tyr Glu Lys Glu Arg Leu Asp Ala Glu Leu Lys Leu
20 25 30
Val Gly Glu Tyr Gly Leu Arg Cys Lys Arg Glu Leu Trp Arg Val Gln
35 40 45
Tyr Ala Leu Ser Arg Ile Arg Asn Ala Ala Arg His Leu Leu Thr Leu
50 55 60
Asp Glu Lys Asn Pro Arg Arg Ile Phe Glu Gly Glu Ala Leu Leu Arg
65 70 75 80
Arg Met Asn Arg Tyr Gly Leu Leu Ala Glu Gly Gln Asn Lys Leu
85 90 95

(2) INFORMATION FOR SEQ ID NO:4142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..467

(D) OTHER INFORMATION: / Ceres Seq. ID 1579635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4142:

cgaaaaatcc atcgagctgc ccgcgcgcgc cagttaagct cacacatcag ctagnetacc	60
ttggacggcc gaccaggtac gttgcgagcg atggcgggat acaaaacgtc ggcgcggcac	120
gcgcctcgcg tcgtctctggc tgttgccgcg ctctctcgcg cggcgcgat gccggtggac	180
gacgagcaca tgtaccactg gaagtgcctc aactcgtgca cggggaagtg ccgcgacgag	240
gacgcctttg acgacggcca ccgttcgggg gattcgaaac tctcttcgt cgtctctggc	300
ggcaagtgcg acaacagggt cctcagcgag tgcttcgagg acctgcgcgc catctgctac	360
caccagtgcg tcgtcagcaa gtgcctctgc ttcaccacct ttacgaaga gaaaacgatg	420
tgcatgaaga gctgctgcaa caagtgcctc caccacggcc cgccagc	

(2) INFORMATION FOR SEQ ID NO:4143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1579636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4143:

Met Ala Gly Tyr Lys Ala Ser Gly Gly Thr Ala Leu Gly Val Val Leu	
1 5 10 15	
Ala Val Ala Ala Leu Leu Ala Ala Ala Met Ala Val Asp Asp Glu	
20 25 30	
His Met Tyr His Trp Lys Cys Phe Asn Ser Cys Thr Gly Lys Cys Arg	
35 40 45	
Asp Glu Asp Ala Phe Asp Asp Gly His Arg Ser Gly Asp Ser Asn Val	
50 55 60	
Ser Ser Val Val Ser Gly Gly Lys Cys Asn Asn Arg Cys Leu Ser Glu	
65 70 75 80	
Cys Phe Glu Asp Leu Pro Ala Ile Cys Tyr His Gln Cys Val Val Ser	
85 90 95	
Lys Cys Leu Cys Phe Pro Pro Phe Ser Lys Glu Lys Thr Met Cys Met	
100 105 110	
Lys Ser Cys Cys Asn Lys Cys Phe His His Gly Pro Pro	
115 120 125	

(2) INFORMATION FOR SEQ ID NO:4144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1579637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4144:
Met Ala Val Asp Asp Glu His Met Tyr His Trp Lys Cys Phe Asn Ser
1 5 10 15
Cys Thr Gly Lys Cys Arg Asp Glu Asp Ala Phe Asp Asp Gly His Arg
20 25 30
Ser Gly Asp Ser Asn Val Ser Ser Val Val Ser Gly Gly Lys Cys Asn
35 40 45
Asn Arg Cys Leu Ser Glu Cys Phe Glu Asp Leu Pro Ala Ile Cys Tyr
50 55 60
His Gln Cys Val Val Ser Lys Cys Leu Cys Phe Pro Pro Phe Ser Lys
65 70 75 80
Glu Lys Thr Met Cys Met Lys Ser Cys Cys Asn Lys Cys Phe His His
85 90 95
Gly Pro Pro

(2) INFORMATION FOR SEQ ID NO:4145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1579638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4145:
Met Tyr His Trp Lys Cys Phe Asn Ser Cys Thr Gly Lys Cys Arg Asp
1 5 10 15
Glu Asp Ala Phe Asp Asp Gly His Arg Ser Gly Asp Ser Asn Val Ser
20 25 30
Ser Val Val Ser Gly Gly Lys Cys Asn Asn Arg Cys Leu Ser Glu Cys
35 40 45
Phe Glu Asp Leu Pro Ala Ile Cys Tyr His Gln Cys Val Val Ser Lys
50 55 60
Cys Leu Cys Phe Pro Pro Phe Ser Lys Glu Lys Thr Met Cys Met Lys
65 70 75 80
Ser Cys Cys Asn Lys Cys Phe His His Gly Pro Pro
85 90

(2) INFORMATION FOR SEQ ID NO:4146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..450
(D) OTHER INFORMATION: / Ceres Seq. ID 1579643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4146:
atccgggtccg gacacccgag taccgacctg cttgtctcatc gcgcgcaccc gccaaagcaa 60
ccaaccgcc catcgctccc gtccgtgttc ggcaggcagc cgctcccgcct cccgtccccc 120

cacccccactc cccctcgcgc ggcgcgttct cagatccccc gcccggttgg caccggcacc 180
ccggtccgaa atgcgaggag cctttagcgc cctcggagca cgacaggaaat cgcgcgcgat 240
gcattccaaag cccgagggcg gcggcgacga cgacggggcc gcccgaggag tgggctcccc 300
ggcggtccggc taecttcggc agcggagcat gcacgcgcgc gcccgccgag cggatccgga 360
ggcgcgcgcg cggcgcgttc acgtcgagaa cccgccttgc tccgcgcgag gggggtcgcg 420
gccagcgagt ccgtcaccaa gctggagtcg

(2) INFORMATION FOR SEQ ID NO:4147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1579644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4147:

Ile Arg Ser Gly His Pro Ser Thr Asp Leu Leu Ala His Arg Ala His
1 5 10 15
Pro Pro Lys Gln Pro Thr Ala Pro Ser Ser Pro Ser Cys Ser Gly Arg
20 25 30
Gln Pro Leu Pro Leu Pro Leu Pro His Pro Thr Pro Pro Arg Ala Ala
35 40 45
Arg Ser Gln Ile Pro Arg Pro Val Gly Thr Gly Thr Pro Val Arg Asn
50 55 60
Ala Arg Ser Leu Val Ala Pro Arg Ser Thr Asp Gly Ile Ala Pro His
65 70 75 80
Ala Ser Gln Ala Arg Gly Arg Arg Arg Arg Arg Gly Arg Arg Gly
85 90 95
Gly Gly Leu Pro Ala Val Arg Leu Leu Pro Ala Ala Glu His Ala Arg
100 105 110
Arg Arg Arg Arg Arg Gly Ser Gly Gly Gly Ala Pro Ala Val Pro Arg
115 120 125
Arg Glu Pro Ala Leu Leu Arg Arg Arg Gly Ala Ala Ala Ser Glu Ser
130 135 140
Val Thr Lys Leu Glu Ser
145 150

(2) INFORMATION FOR SEQ ID NO:4148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4148:

Pro Val Arg Thr Pro Glu Tyr Arg Pro Ala Cys Ser Ser Arg Ala Pro
1 5 10 15
Ala Lys Ala Thr Asn Arg Pro Ile Val Pro Val Leu Phe Arg Gln Ala
20 25 30
Ala Ala Pro Ala Pro Ala Pro Pro His Ser Pro Ser Arg Gly Ala
35 40 45
Phe Ser Asp Pro Pro Pro Gly Trp His Arg His Pro Gly Pro Lys Cys
50 55 60
Glu Glu Pro Cys Ser Ala Ser Glu His Gly Arg Asn Arg Ala Ala Cys
65 70 75 80
Ile Glu Ser Pro Arg Ala Ala Ala Thr Thr Gly Pro Pro Arg Arg

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1579648
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4151:
Met Lys Glu His Trp Asp Glu Leu Phe Thr Arg Cys Phe Gln Arg Leu
1 5 10 15
Asp Asp Glu Val Ser Gly Gln Ala Ser Arg Leu Val Gly Gly Val Gln
20 25 30
Glu Thr Arg Pro Val Ala Ala Glu Asn Val Gly Ser Thr Ala Val Val
35 40 45
Ala Val Val Cys Ser Ser His Val Val Val Ala Asn Cys Gly Asp Ser
50 55 60
Arg Val Val Leu Cys Arg Gly Lys Glu Pro Leu Glu Leu Ser Ile Asp
65 70 75 80
His Lys Val Ser Phe Phe Val Ala Lys Leu Glu Leu
85 90

(2) INFORMATION FOR SEQ ID NO:4152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..420
(D) OTHER INFORMATION: / Ceres Seq. ID 1579700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4152:

aaaaaaaaaca cagcgtaacg gcttctcttc ctcgcttgcc gccgcgcgcg ccgcccgcgat 60
ggaaaaaggag aagctctcgt tctccatata ctctcgaag cagcggccccc ccaagcctcc 120
cgacacgacct gggcgccgcg cagacgacga tgacctccgc tccgcgcgcc ctccgggccca 180
gcagtagctc accgagttcg atccgtccca aaccctagcc gccgcctcgc cggcgcgcgc 240
cgctcatcgcg ccgctccccca actccggcaa ctgcctcacc caccgccacc gcaaacgctc 300
ctcgctcccc acccctgagc aggaggccgc cctcgccgcg gaatccgcgc gctggggccc 360
ccgcttcgctc ctcgacacct cgaaccgctcc cgaagaccca tcattcaaaa tcggctacgc 420

(2) INFORMATION FOR SEQ ID NO:4153:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..139
(D) OTHER INFORMATION: / Ceres Seq. ID 1579701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4153:

Lys Lys Thr His Gly Thr Arg Phe Ser Ser Leu Ala Ala Ala Ala
1 5 10 15
Ala Ala Ala Met Glu Lys Glu Lys Leu Ser Phe Ser Ile Ser Ser Ser
20 25 30
Lys Gln Arg Pro Pro Lys Pro Pro Ala Arg Pro Ala Ala Ala Asp
35 40 45
Asp Asp Asp Leu Arg Ser Ala Pro Ala Pro Gly Gln Gln Tyr Val Thr

50 55 60
Glu Phe Asp Pro Ser Gln Thr Leu Ala Ala Ala Cys Ala Ala Arg Ala
65 70 75 80
Val Ile Ala Pro Leu Pro Asn Ser Gly Asn Xaa Leu Thr His Arg Pro
85 90 95
Arg Lys Pro Ser Ser Leu Pro Thr Pro Glu Glu Glu Ala Ala Leu Ala
100 105 110
Ala Glu Ser Gly Gly Trp Gly Pro Xaa Phe Val Leu Asp Thr Ser Thr
115 120 125
Ala Pro Glu Asp Pro Ser Ser Lys Ile Gly Tyr
130 135

(2) INFORMATION FOR SEQ ID NO:4154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1579702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4154:

Lys Lys His Thr Val Arg Ala Ser Pro Pro Arg Leu Pro Pro Pro Pro
1 5 10 15
Pro Pro Arg Trp Lys Arg Arg Ser Ser Arg Ser Pro Tyr Pro Pro Arg
20 25 30
Ser Ser Gly Pro Pro Ser Leu Pro His Asp Leu Arg Pro Pro Gln Thr
35 40 45
Thr Met Thr Ser Ala Pro Arg Pro Leu Arg Ala Ser Ser Thr Ser Pro
50 55 60
Ser Ser Ile Arg Pro Lys Pro
65 70

(2) INFORMATION FOR SEQ ID NO:4155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1579703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4155:

Met Glu Lys Glu Lys Leu Ser Phe Ser Ile Ser Ser Ser Lys Gln Arg
1 5 10 15
Pro Pro Lys Pro Pro Ala Arg Pro Ala Ala Ala Ala Asp Asp Asp Asp
20 25 30
Leu Arg Ser Ala Pro Ala Pro Gly Gln Gln Tyr Val Thr Glu Phe Asp
35 40 45
Pro Ser Gln Thr Leu Ala Ala Ala Cys Ala Ala Arg Ala Val Ile Ala
50 55 60
Pro Leu Pro Asn Ser Gly Asn Xaa Leu Thr His Arg Pro Arg Lys Pro
65 70 75 80
Ser Ser Leu Pro Thr Pro Glu Glu Glu Ala Leu Ala Ala Glu Ser
85 90 95
Gly Gly Trp Gly Pro Xaa Phe Val Leu Asp Thr Ser Thr Ala Pro Glu
100 105 110
Asp Pro Ser Ser Lys Ile Gly Tyr
115 120

(2) INFORMATION FOR SEQ ID NO:4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4156:

atgctgtgaga	tgatgataat	gatgatgatg	atgatgaacc	tcctcttaat	gaagacgaac	60
acgaggagatt	agatgaacctt	gagcaagggg	aggatgaacc	tmacacacaa	catcttgtac	120
ttgcacaaatt	tgataaaagt	tcaaggacca	agaatcgttg	gaagtgcacc	ttgaaggatg	180
gaatcatgca	tttgaatggc	agggatgtcc	tttttaacaa	ggcgacaggt	gagtttgatt	240
tttgattttt	tggatgaaga	tgagctattt	tagaagcagc	tgatggaca	tatctttgtc	300
ttgacataag	gacagggagg	tgacagtgtt	cttgggtggg	tcctggcagc	atgactgcgt	360
cgtgttttct	ttcctattga	atcttctgtc	caccctcttg	tttgtcaccg	caactgttat	420
cgctgtaaag	aagttaactgc	ttgtgctgtg	c			

(2) INFORMATION FOR SEQ ID NO:4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4157:

Ala	Gly	Asp	Asp	Asp	Asn	Asp	Asp	Asp	Asp	Asp	Glu	Pro	Pro	Leu	Asn	
1			5						10					15		
Glu	Asp	Asp	Asp	Glu	Glu	Leu	Asp	Asp	Leu	Glu	Gln	Gly	Glu	Asp	Glu	
			20						25					30		
Pro	Xaa	Thr	Gln	His	Leu	Val	Leu	Ala	Gln	Phe	Asp	Lys	Val	Ser	Arg	
			35						40					45		
Thr	Lys	Asn	Arg	Trp	Lys	Cys	Thr	Leu	Lys	Asp	Gly	Ile	Met	His	Leu	
			50						55					60		
Asn	Gly	Arg	Asp	Val	Leu	Phe	Asn	Lys	Ala	Thr	Gly	Glu	Phe	Asp	Phe	
65					70					75				80		

(2) INFORMATION FOR SEQ ID NO:4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4158:

aggactctag	gagaaactggg	acgacagcag	cgccggggcga	cggggatgag	aacctgtac	60
tgtatttcgt	cgactcttgc	catggcgtcg	tcgatgatga	gttctcgcgc	ggcgccggcg	120
gcggccggag	gaggagaaca	ccgcgcctcag	cacgtcaccc	tgccgtgcgg	tgggctgaac	180
cgcccgagta	ccaggcccgct	gccggggcgca	gctggccccc	ggcccgggac	gccagggccc	240
cgggggacctg	ctgcagctcg	ggcggggtccc	tcgtcttcgt	cgccgacggg	gcgcgccggg	300

ccggagtgcactgtgtggg gcgtgcccgc cggcagcagg cgaacccgag cgggtcgagg 360
agcggcaggg ccgcggggcg gcgcgtgccc acgggcaagg ggaacccgca gctggtgaga 420
cgggcgtcga cgcgcggccc

(2) INFORMATION FOR SEQ ID NO:4159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1579712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4159:

Arg Thr Leu Gly Glu Leu Gly Arg Gln Gln Arg Arg Ala Thr Gly Met
1 5 10 15
Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser Met
20 25 30
Met Ser Ser Arg Ala Gly Ala Ala Ala Gly Gly Gly Glu His Arg
35 40 45
Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser Thr
50 55 60
Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg Pro
65 70 75 80
Arg Gly Pro Ala Ala Ala Ala Gly Gly Ser Ser Ser Ser Pro Thr
85 90 95
Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg Gln
100 105 110
Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala Arg
115 120 125
Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Ala Leu Thr
130 135 140
Pro Ala
145

(2) INFORMATION FOR SEQ ID NO:4160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1579713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4160:

Asp Ser Arg Arg Thr Gly Thr Thr Ala Ala Ala Gly Asp Gly Asp Glu
1 5 10 15
Asn Pro Val Leu Tyr Phe Val Asp Leu Cys His Gly Val Val Asp Asp
20 25 30
Glu Phe Ser Arg Gly Arg Gly Gly Gly Arg Arg Arg Arg Thr Pro Pro
35 40 45
Ser Ala Arg His Arg Gly Val Arg Trp Ala Asp Ala Ala Glu Tyr Gln
50 55 60
Ala Arg Ala Gly Arg Ser Trp Pro Thr Ala Arg Asp Ala Glu Ala Ala
65 70 75 80
Gly Thr Cys Cys Ser Cys Gly Arg Leu Leu Val Phe Val Ala Asp Gly
85 90 95
Ala Arg Gly Ala Gly Val Gln Leu Val Gly Arg Cys Arg Ala Ala Ala
100 105 110

Gly Asp Ala Glu Ala Val Glu Glu Arg Gln Gly Arg Gly Arg Ala Arg
115 120 125
Ala His Gly Gln Gly Glu Pro Arg Ala Gly Glu Thr Gly Ala His Ala
130 135 140
Gly Pro
145

(2) INFORMATION FOR SEQ ID NO:4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4161:

Met Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser
1 5 10 15
Met Met Ser Ser Arg Ala Gly Ala Ala Ala Ala Gly Gly Gly Glu His
20 25 30
Arg Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser
35 40 45
Thr Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg
50 55 60
Pro Arg Gly Pro Ala Ala Ala Gly Gly Ser Ser Ser Ser Ser Pro
65 70 75 80
Thr Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg
85 90 95
Gln Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala
100 105 110
Arg Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Arg Ala Leu
115 120 125
Thr Pro Ala
130

(2) INFORMATION FOR SEQ ID NO:4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..434
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4162:

ccaattagcc ttgtttaaga ccaacagaaa ggatagcatg ttgtctgacc gggtatttga 60
cttgttttgac acgaaacaca atggaattct cgagtttgag gaatttgctc gagccctttc 120
tgtgtttccat ccgagtgcac caatcgattt caaaattgat ttgtcttcca aattgtatga 180
tctcaagcaa carggtttca ttgaaaagca ggaggtcaaag caaatggtgg tcgcaacact 240
tgctgaayca ggaatgaatc ttctcagatga tattattgaa ggcattattg ataagacatt 300
tgaggaagca gwatacaaaag caccwtggca aaattgataw ggaggattgg ccgagccttg 360
tcttgaggca tccattctctg ttaaaaaata tgacctctcc atatctccgg gatataccca 420
caacwtttcm aagc

(2) INFORMATION FOR SEQ ID NO:4163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579725
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4163:
Gln Leu Ala Leu Phe Lys Thr Asn Arg Lys Asp Ser Met Phe Ala Asp
1 5 10 15
Arg Val Phe Asp Leu Phe Asp Thr Lys His Asn Gly Ile Leu Glu Phe
 20 25 30
Glu Glu Phe Ala Arg Ala Leu Ser Val Phe His Pro Ser Ala Pro Ile
 35 40 45
Asp Phe Lys Ile Asp Phe Ala Phe Lys Leu Tyr Asp Leu Lys Gln Xaa
50 55 60
Gly Phe Ile Glu Lys Gln Glu Val Lys Gln Met Val Val Ala Thr Leu
65 70 75 80
Ala Glu Xaa Gly Met Asn Leu Ser Asp Asp Ile Ile Glu Gly Ile Ile
 85 90 95
Asp Lys Thr Phe Glu Glu Ala Xaa Tyr Lys Ala Xaa Trp Gln Asn
 100 105 110
(2) INFORMATION FOR SEQ ID NO:4164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..99
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579726
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4164:
Met Phe Ala Asp Arg Val Phe Asp Leu Phe Asp Thr Lys His Asn Gly
1 5 10 15
Ile Leu Glu Phe Glu Glu Phe Ala Arg Ala Leu Ser Val Phe His Pro
 20 25 30
Ser Ala Pro Ile Asp Phe Lys Ile Asp Phe Ala Phe Lys Leu Tyr Asp
 35 40 45
Leu Lys Gln Xaa Gly Phe Ile Glu Lys Gln Glu Val Lys Gln Met Val
50 55 60
Val Ala Thr Leu Ala Glu Xaa Gly Met Asn Leu Ser Asp Asp Ile Ile
65 70 75 80
Glu Gly Ile Ile Asp Lys Thr Phe Glu Glu Ala Xaa Tyr Lys Ala Xaa
 85 90 95
Trp Gln Asn
(2) INFORMATION FOR SEQ ID NO:4165:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579727
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4165:
Met Glu Phe Ser Ser Leu Arg Asn Leu Leu Glu Pro Phe Leu Cys Ser
1 5 10 15

Ile Arg Val His Gln Ser Ile Ser Lys Leu Ile Leu Leu Ser Asn Cys
20 25 30
Met Ile Ser Ser Asn Xaa Val Ser Leu Lys Ser Arg Arg Ser Ser Lys
35 40 45
Trp Trp Ser Gln His Leu Leu Xaa Gln Glu
50 55

(2) INFORMATION FOR SEQ ID NO:4166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4166:

aaatggaggc	ggaggcctcc	accgacggag	cagggcaggga	caggttgcat	ttgcatctga	60
gttcctgatt	gttgatcccc	agtttcttct	gtgagtgga	tcgcgaggaa	gaaggatgtc	120
gtgctgcgga	ggcaactgcg	ggtgcggcgc	cggctgcaag	tcgcgcagcg	gctgcggagg	180
gtgcaagatg	tacccgagca	tgccagagca	ggtgaccacc	accagactg	tcacatcatggg	240
tgttgcacca	tccaaggcgc	ggttcgagcg	ggccgccgga	gctgagaatg	gcgggtgcaa	300
gtgcggcgcc	aactgcacct	gcgacccctg	cacctgcaag	tgagacgacg	gcggcgccga	360
tgacgctgca	gggtctgcag	gcctgatg	ggtcggaagg	actctttatc	ttcttagcta	420
attaataaag	tctagctagt	atataatatt	ctagcagtg	cgtttgcgtg	gttttgycg	480
agtcagttag	acagtcagcc	gcgtgccatg	ggccat			

(2) INFORMATION FOR SEQ ID NO:4167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4167:

Met	Ser	Cys	Cys	Gly	Gly	Asn	Cys	Gly	Cys	Gly	Ala	Gly	Cys	Lys	Cys	
1			5						10					15		
Gly	Ser	Gly	Cys	Gly	Gly	Cys	Lys	Met	Tyr	Pro	Asp	Met	Ala	Glu	Gln	
			20					25					30			
Val	Thr	Thr	Thr	Gln	Thr	Val	Ile	Met	Gly	Val	Ala	Pro	Ser	Lys	Gly	
			35				40					45				
Gly	Phe	Glu	Ala	Ala	Ala	Gly	Ala	Glu	Asn	Gly	Gly	Cys	Lys	Cys	Gly	
			50				55					60				
Ala	Asn	Cys	Thr	Cys	Asp	Pro	Cys	Thr	Cys	Lys						
			65				70									

(2) INFORMATION FOR SEQ ID NO:4168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4168:

Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile
1 5 10 15
Met Gly Val Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala
20 25 30
Glu Asn Gly Gly Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys
35 40 45
Thr Cys Lys
50

(2) INFORMATION FOR SEQ ID NO:4169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1579759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4169:

Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile Met Gly Val Ala
1 5 10 15
Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala Glu Asn Gly Gly
20 25 30
Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:4170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1579776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4170:

atctgattct	gtgatcgaga	tcgaggccga	tcggccaggt	ttctgtgtgcg	tcgcgtctgc	60
tactgcatgg	cggtagctca	ccttcttctc	caactctctg	ccggaggtcaa	tggagctagc	120
aggaacagga	tgctcaattcc	agccatttct	tcgattcttc	agcttattca	cctcgacagc	180
ccggggagcgc	gcggggcagga	cttctacgat	gttagcctcg	tcgacggcct	caacgtgccg	240
gtgcgcgtgtg	cgccctcggg	cggcgggtggc	gactgtcgtc	ccgcggcgctg	cgccggcgac	300
gtgaacgcga	tgtgccccgc	ggacctccgc	gtcgtcgctc	cgtccggcag	cgccggcgctc	360
gtggcgctaca	agagcgcgtg	cagcgcctac	ggcagcgcg	gctactgctg	caccggccag	420
tacggcacgc	cgagg					

(2) INFORMATION FOR SEQ ID NO:4171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1579777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4171:

Met Ala Val Ala His Leu Leu Leu Gln Leu Ser Ala Gly Val Asn Gly
1 5 10 15
Ala Ser Arg Asn Arg Met Leu Ile Pro Ala Ile Leu Ser Ile Leu Gln

[illegible]

(2) INFORMATION FOR SEQ ID NO:4174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4174:

actccaagtc	caagccacct	ctcagctctc	accagctagc	tctactctcg	cggcgcttcc	60
cctcgccgtt	cgtgcacat	gattgacatt	ggccaaccc	aaccgcgcag	ctagatagat	120
ctacgtcgac	cggcggcgcc	gagggacgct	cgctcgctcg	tgcctcgaca	tggcgaaatg	180
cagcagcaag	atccggtaca	tctgtgtgct	gcggcagacg	ctgcggcggt	ggcggtccc	240
cgcgccggt	cgcgsgggg	tcccggcggg	ccacgtggcg	gtgtgcgtgg	gcggcgcggc	300
gcggcggtt	gtgtgcggg	cggcgcacct	gaaccacccc	gtgttcggg	agctgtcccg	360
gcaggcgga	gaggagtag	ggttcccgct	gggggcctcg	gcgggcccc	tcgcgctccc	420
ctgcgacga	ggcctcttc	agcacgtcct	cgccacacct	tctctcccg		

(2) INFORMATION FOR SEQ ID NO:4175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4175:

Met	Ala	Lys	Cys	Ser	Ser	Lys	Ile	Arg	Tyr	Ile	Val	Trp	Leu	Arg	Gln
1		5						10					15		
Thr	Leu	Arg	Arg	Trp	Arg	Ser	Arg	Ala	Ala	Ala	Arg	Xaa	Ala	Val	Pro
		20						25					30		
Ala	Gly	His	Val	Ala	Val	Cys	Val	Gly	Gly	Ala	Ala	Arg	Arg	Phe	Val
		35						40					45		
Val	Arg	Ala	Ala	His	Leu	Asn	His	Pro	Val	Phe	Arg	Glu	Leu	Leu	Arg
		50				55				60					
Gln	Ala	Glu	Glu	Glu	Tyr	Gly	Phe	Pro	Ser	Gly	Ala	Cys	Ala	Gly	Pro
		65			70				75				80		
Ile	Ala	Leu	Pro	Cys	Asp	Glu	Gly	Leu	Phe	Glu	His	Val	Leu	Gly	His
				85				90					95		
Leu	Ser	Ser	Pro												
			100												

(2) INFORMATION FOR SEQ ID NO:4176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4176:

Met	Gln	Gln	Gln	Asp	Pro	Val	His	Arg	Val	Ala	Ala	Ala	Asp	Ala	Ala
1				5				10					15		
Ala	Val	Ala	Val	Pro	Arg	Gly	Gly	Ser	Xaa	Gly	Gly	Pro	Gly	Gly	Pro

Ala	Trp	Ser	Gln	Phe	Val	Ala	Asp	Gly	Val	Phe	Phe	Ala	Glu	Leu	Asn
1			5						10					15	
Glu	Met	Leu	Thr	Arg	Glu	Leu	Ala	Glu	Asp	Gly	Tyr	Ser	Gly	Val	Glu
			20					25					30		
Val	Arg	Val	Thr	Pro	Met	Arg	Thr	Glu	Ile	Ile	Ile	Arg	Ala	Thr	Arg
			35				40					45			
Thr	Gln	Asn	Val	Leu	Gly	Gly	Leu	Gly	Arg	Arg	Ile	Arg	Glu	Leu	Thr
	50					55					60				
Ser	Val	Val	Gln	Lys	Arg	Phe	Asn	Phe	Pro	Glu	Gly	Gly	Val	Glu	Leu
65				70						75				80	
Tyr	Ala	Glu	Lys	Val	Asn	Asn	Arg	Gly	Leu	Cys	Ala	Ile	Ala	Gln	Ala
			85					90						95	
Glu	Ser	Leu	Arg	Tyr	Lys	Leu	Leu	Gly	Gly	Leu	Ala	Val	Arg	Arg	Ala
			100					105				110			
Cys	Tyr	Gly	Val	Leu	Arg	Phe	Val	Met	Glu	Ser	Gly	Ala	Lys	Gly	Cys
		115				120					125				
Glu	Val	Ile	Val	Ser	Gly	Lys	Leu	Arg	Ala	Gln	Arg	Ala	Lys	Ser	Met
	130					135				140					

Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His
145 150 155

(2) INFORMATION FOR SEQ ID NO:4179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1579803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4179:

Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val
1 5 10 15
Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr
20 25 30
Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser
35 40 45
Val Val Gln Lys Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr
50 55 60
Ala Glu Lys Val Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu
65 70 75 80
Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys
85 90 95
Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu
100 105 110
Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys
115 120 125
Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His
130 135

(2) INFORMATION FOR SEQ ID NO:4180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1579804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4180:

Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu
1 5 10 15
Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Val Val Gln Lys
20 25 30
Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr Ala Glu Lys Val
35 40 45
Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
50 55 60
Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu
65 70 75 80
Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser
85 90 95
Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys Phe Lys Asp Gly
100 105 110
Tyr Met Ile Ser Ser Gly His
115

(2) INFORMATION FOR SEQ ID NO:4181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..529
(D) OTHER INFORMATION: / Ceres Seq. ID 1579820
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4181:
aggagagagac cctttccatc caagctagcc aaaccctagc caccgtcggg tccaatctgc 60
caacatctcg tccgctgggt ggtggctcgg cctcgggggc atggcctcgt ccgcctacgc 120
ttgggacgccc gcggaggagg cggacatcga cgctccgca tcgcaggagg agctcaatcgt 180
ccgcgcccgc ttcattcccc gtgacaatga ggaggagggg gaggggggagg gggaggggga 240
ggaggaggag gaggaggagg tcgaggtgtt cagcacgccc cctctcacgc atcaggaccc 300
gcagagtcgg ggggaagaag tcatcgccat gtgctccatc cccctcaccc agcctgaccc 360
cacgcctcct cccgctcccg ctcctcccc tcctcggac agtaagagtc gccgtccgga 420
gcgggtcaaa ttgaagccgc ggaagaaggt ctgcaagagg aaagagtgtc tgcaatgagg 480
aaggtgagaa gagccaaaca agatcaggtc tccgactccg aagccgcag
(2) INFORMATION FOR SEQ ID NO:4182:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1579821
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4182:
Gly Glu Thr Leu Ser Ile Gln Ala Ser Gln Thr Leu Ala Thr Val Gly
1 5 10 15
Ser Asn Leu Pro Thr Ser Arg Pro Leu Val Gly Gly Ser Ala Ser Ala
20 25 30
Ala Trp Pro Arg Pro Pro Thr Leu Gly Thr Pro Arg Arg Arg Arg Thr
35 40 45
Ser Thr Pro Pro His Arg Arg Arg Ser Ser Ser Ser Ala Pro Ala Ser
50 55 60
Ser Pro Val Thr Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Gly Arg
65 70 75 80
Arg Arg Arg Arg Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg
85 90 95
Ile Arg Thr Arg Arg Val Arg Gly Lys Ser Ser Pro Cys Ala Pro
100 105 110
Ser Pro Ser Pro Ser Leu Thr Pro Arg Leu Leu Pro Leu Xaa Leu Pro
115 120 125
Pro Leu Pro Arg Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn
130 135 140
(2) INFORMATION FOR SEQ ID NO:4183:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1579822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4183:

```
Met Ala Ser Ser Ala Tyr Ala Trp Asp Ala Ala Glu Glu Ala Asp Ile
1      5      10      15
Asp Ala Ser Ala Ser Gln Glu Glu Leu Ile Val Arg Ala Arg Phe Ile
20      25      30
Ser Arg Asp Asn Glu Glu Glu Gly Glu Gly Glu Gly Glu Glu
35      40      45
Glu Glu Glu Glu Glu Val Glu Val Phe Ser Thr Pro Pro Leu Thr His
50      55      60
Gln Asp Pro Gln Ser Pro Gly Glu Glu Val Ile Ala Met Cys Ser Ile
65      70      75      80
Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Ala Xaa Ala Pro Ser
85      90      95
Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg Val Lys Leu Lys
100      105      110
Pro Arg Lys Lys Val Cys Lys Arg Lys Glu Cys Leu Gln
115      120      125
```

(2) INFORMATION FOR SEQ ID NO:4184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4184:

```
Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Gly Arg Arg Arg Arg
1      5      10      15
Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg Ile Arg Thr Arg
20      25      30
Arg Val Arg Gly Lys Lys Ser Ser Pro Cys Ala Pro Ser Pro Ser Pro
35      40      45
Ser Leu Thr Pro Arg Leu Leu Pro Leu Xaa Leu Pro Leu Pro Arg
50      55      60
Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn
65      70      75
```

(2) INFORMATION FOR SEQ ID NO:4185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4185:

```
aaggtccaga agcccagaac cagacgagca cggacggatc tcccccaacg cgcgtgcgtc 60
cgcaactagc gtctcgccgc ggcgccttct tccgaccccc ccgacgcggc aaggagcccc 120
cgcccatgag ggtccaccgc gcccccggga agcgacccat cgccgtgcaa cgctgcgctt 180
ccgcgcgggc gggcgcgctc ggcgggaaga agctgcggcg cgtgcggcac atattcgaca 240
aggtgctgga gctcccgctc gccgcccagc cggacgtgtc cgtcgaggag gacgcggcgg 300
cgctgcgggt cgctgcggcc gccacgagat tctccctcgc gggcgccgcg gcgcacggcg 360
tcgagatcca cccagggtgc accaagggtc tcgtccgcgg cctctcctcc tectccctcg 420
ggcgcgatgg cgaacgac
```

(2) INFORMATION FOR SEQ ID NO:4186:

(i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1579829
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4186:
Arg Ser Arg Ser Pro Glu Pro Asp Glu His Gly Arg Ile Ser Pro Asn
1 5 10 15
Ala Arg Ala Ser Ala Thr Ser Val Cys Arg Arg Arg Leu Leu Pro His
20 25 30
Pro Pro Thr Arg Gln Gly Ala Pro Arg His Glu Gly Pro Pro Gly Pro
35 40 45
Ala Glu Ala His His Arg Arg Ala Thr Leu Arg Leu Arg Gly Gly Gly
50 55 60
Arg Ala Arg Arg Glu Glu Ala Ala Pro Pro Ala Ala His Ile Arg Gln
65 70 75 80
Gly Ala Gly Ala Pro Val Arg Gly Arg Arg Gly Arg Val Arg Arg Gly
85 90 95
Gly Arg Gly Gly Ala Val Arg Arg Arg Arg Arg Val Leu Pro
100 105 110
Arg Gly Arg Pro Arg Ala Arg Arg Arg Asp Pro Pro Arg Gly His Gln
115 120 125
Gly Arg Arg Pro Arg Pro Leu Leu Leu Leu Pro Arg Arg Arg Trp Arg
130 135 140
Arg
145
(2) INFORMATION FOR SEQ ID NO:4187:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1579830
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4187:
Gly Pro Glu Ala Gln Asn Gln Thr Ser Thr Asp Gly Ser Pro Pro Thr
1 5 10 15
Arg Val Arg Pro Gln Leu Ala Ser Ala Ala Gly Ala Phe Phe Arg Thr
20 25 30
Pro Arg Arg Gly Lys Glu Pro Pro Ala Met Arg Val His Pro Ala Pro
35 40 45
Arg Lys Arg Thr Ile Ala Val Gln Arg Cys Ala Ser Ala Ala Ala Gly
50 55 60
Ala Leu Gly Gly Lys Lys Leu Arg Arg Leu Pro His Ile Phe Asp Lys
65 70 75 80
Val Leu Glu Leu Pro Phe Ala Ala Asp Ala Asp Val Ser Val Glu Glu
85 90 95
Asp Ala Ala Ala Leu Arg Phe Val Ala Ala Ala Asp Glu Phe Ser Leu
100 105 110
Ala Gly Ala Arg Ala His Ala Val Glu Ile His Pro Gly Val Thr Lys
115 120 125
Val Val Val Arg Gly Leu Ser Ser Ser Ser Leu Gly Gly Asp Gly Asp
130 135 140
Asp

145

(2) INFORMATION FOR SEQ ID NO:4188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4188:

Met Arg Val His Pro Ala Pro Arg Lys Arg Thr Ile Ala Val Gln Arg
1 5 10 15
Cys Ala Ser Ala Ala Ala Gly Ala Leu Gly Gly Lys Lys Leu Arg Arg
20 25 30
Leu Pro His Ile Phe Asp Lys Val Leu Glu Leu Pro Phe Ala Ala Asp
35 40 45
Ala Asp Val Ser Val Glu Glu Asp Ala Ala Ala Leu Arg Phe Val Ala
50 55 60
Ala Ala Asp Glu Phe Ser Leu Ala Gly Ala Arg Ala His Ala Val Glu
65 70 75 80
Ile His Pro Gly Val Thr Lys Val Val Val Arg Gly Leu Ser Ser Ser
85 90 95
Ser Leu Gly Gly Asp Gly Asp Asp
100

(2) INFORMATION FOR SEQ ID NO:4189:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..425

(D) OTHER INFORMATION: / Ceres Seq. ID 1579836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4189:

attcctcttc cagctccaagc tatttccacc gcacattgtc cacgtctgcc attggcccat 60
tgccggttcc tctcgtcaag cctagctcc aaccaaccgc ttcccatggg agccatagca 120
gttgcaagcc ttctactcct cgctggggta atctggcgtg cgcgggcgat gttcggcgcg 180
gaggccgcgc gcacgacggt gttcacgctg cacaacaact gcacccacac ggtctggccg 240
gccacactgt ccgggaacag cgcggcgccc gtcggggcgc ggggcttcga gctgtcgccc 300
ggcgccacgc tctcgttccc ggcgcggcgc ggctggctcg gccgctgtg ggcgcgcacg 360
ggctgcgtcg cgtcgtcgtc gtccccgcgc ggccgcctct cgtgcgcacg ggcgactgca 420
gcggc

(2) INFORMATION FOR SEQ ID NO:4190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1579837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4190:

Ile Pro Leu Pro Ala Pro Ala Ile Ser Thr Ala His Cys Pro Arg Leu
1 5 10 15

Pro Leu Ala His Cys Arg Phe Leu Ser Ser Ser Pro Ser Ser Asn Gln
20 25 30
Pro Val Ser Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Leu Ala
35 40 45
Gly Val Ile Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly
50 55 60
Thr Thr Val Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro
65 70 75 80
Ala Thr Leu Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Gly Phe
85 90 95
Glu Leu Ser Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp
100 105 110
Ser Gly Arg Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser
115 120 125
Pro Ala Gly Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:4191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4191:

Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Ala Gly Val Ile
1 5 10 15
Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val
20 25 30
Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu
35 40 45
Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Phe Glu Leu Ser
50 55 60
Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg
65 70 75 80
Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser Pro Ala Gly
85 90 95
Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala
100 105

(2) INFORMATION FOR SEQ ID NO:4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4192:

Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val Phe Thr Leu His Asn
1 5 10 15
Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu Ser Gly Asn Ser Ala
20 25 30
Ala Ala Val Gly Gly Gly Gly Phe Glu Leu Ser Pro Gly Ala Thr Val
35 40 45
Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg Leu Trp Ala Arg Thr

50 55 60
Gly Cys Val Ala Ser Ser Ser Pro Ala Gly Arg Leu Ser Cys Ala
65 70 75 80
Arg Ala Thr Ala Ala

(2) INFORMATION FOR SEQ ID NO:4193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1579865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4193:

aacaaatagt	agccatggcg	atgatggcgt	tggctattgg	gtccgatcag	atatctactc	60
aagctaggag	ggacagtatc	attagtggac	tgaacaacct	tccaagcaat	gtcagcgaag	120
tctccaagct	agatgctgga	atgaaggagc	tgcctctctc	gctgatcgac	tcagagtcgc	180
tcctcggtgt	cggaagggtt	tacaactacg	ccaccgcgct	ggaggcgccc	ctgaaggtca	240
aggagggtgc	gctgatgcac	agcgaaggca	tgctcgctgg	cgagatgaag	cacggaccgc	300
tggccctcgt	ggacgagaac	ctccccatca	ttgtcattgc	gactcgcgac	cggtgcttca	360
gcaagcagca	gtcgggtgatc	cagcagctcc	ctcgcgtag	ggggcg		

(2) INFORMATION FOR SEQ ID NO:4194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1579866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4194:

Gln	Ile	Val	Ala	Met	Ala	Met	Met	Ala	Leu	Ala	Ile	Gly	Ser	Asp	Gln
1		5							10					15	
Ile	Ser	Thr	Gln	Ala	Arg	Arg	Asp	Ser	Ile	Ile	Ser	Gly	Leu	Asn	Asn
		20					25						30		
Leu	Ser	Ser	Asn	Val	Ser	Glu	Val	Leu	Lys	Leu	Asp	Ala	Gly	Met	Lys
		35					40				45				
Glu	Leu	Ala	Ser	Ser	Leu	Ile	Asp	Ser	Glu	Ser	Leu	Leu	Val	Phe	Gly
		50				55					60				
Arg	Gly	Tyr	Asn	Tyr	Ala	Thr	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Val	Lys
		65				70			75				80		
Glu	Val	Ala	Leu	Met	His	Ser	Glu	Gly	Met	Leu	Ala	Gly	Glu	Met	Lys
		85						90					95		
His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Glu	Asn	Leu	Pro	Ile	Ile	Val	Ile
		100					105						110		
Ala	Thr	Arg	Asp	Ala	Cys	Phe	Ser	Lys	Gln	Gln	Ser	Val	Ile	Gln	Gln
		115					120						125		
Leu	Leu	Ser	Arg	Arg	Gly										
		130													

(2) INFORMATION FOR SEQ ID NO:4195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4195:

Met Ala Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln
1 5 10 15
Ala Arg Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn
20 25 30
Val Ser Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser
35 40 45
Ser Leu Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn
50 55 60
Tyr Ala Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu
65 70 75 80
Met His Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu
85 90 95
Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp
100 105 110
Ala Cys Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg
115 120 125
Arg Gly
130

(2) INFORMATION FOR SEQ ID NO:4196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4196:

Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln Ala Arg
1 5 10 15
Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn Val Ser
20 25 30
Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser Ser Leu
35 40 45
Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn Tyr Ala
50 55 60
Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu Met His
65 70 75 80
Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu Ala Leu
85 90 95
Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp Ala Cys
100 105 110
Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg Arg Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:4197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..489
(D) OTHER INFORMATION: / Ceres Seq. ID 1579873
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4197:
aaggccaggg atgacgaagg acaagagaag aaaaagccaa agaagaaaaa agatccgaat 60
gctccgaaac gagccatgac ccggttcgat tatttctcaa tggctgagcg aggaacatg 120
aagagcagca acccagattt gcctacgact gagatcgcaa agaagcttgg ggagatgtgg 180
caaaagatgt caggcgaaga gaacagcct tacatccagc aggccagggt cgacaagaaa 240
cgttatgaaa aagaatccgc tgtctatcgc ggtgaagcta cagtgcgatg ggattctggg 300
aacgagtcgt actagagatc caagctcttg ggctggcatg gtggcagcgg atgaagtct 360
agtgccatgt gtgctattgt tatgtcagca actgttgcca acaacattgc tgacagtaaa 420
gagagtttct ctgcagcgt acctctgcag gcaaaaagaa tgtaacgagt tagtctagt 480
attttgtgt

(2) INFORMATION FOR SEQ ID NO:4198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1579874
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4198:
Lys Ala Arg Asp Asp Glu Gly Gln Glu Lys Lys Lys Pro Lys Lys Lys
1 5 10 15
Lys Asp Pro Asn Ala Pro Lys Arg Ala Met Thr Pro Phe Met Tyr Phe
20 25 30
Ser Met Ala Glu Arg Gly Asn Met Lys Ser Ser Asn Pro Asp Leu Pro
35 40 45
Thr Thr Glu Ile Ala Lys Lys Leu Gly Glu Met Trp Gln Lys Met Ser
50 55 60
Gly Glu Glu Lys Gln Pro Tyr Ile Gln Gln Ala Val Asp Lys Lys
65 70 75 80
Arg Tyr Glu Lys Glu Ser Ala Val Tyr Arg Gly Glu Ala Thr Val Asp
85 90 95
Val Asp Ser Gly Asn Glu Ser Asp
100

(2) INFORMATION FOR SEQ ID NO:4199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1579875
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4199:
Met Thr Pro Phe Met Tyr Phe Ser Met Ala Glu Arg Gly Asn Met Lys
1 5 10 15
Ser Ser Asn Pro Asp Leu Pro Thr Thr Glu Ile Ala Lys Lys Leu Gly
20 25 30
Glu Met Trp Gln Lys Met Ser Gly Glu Glu Lys Gln Pro Tyr Ile Gln
35 40 45
Gln Ala Gln Val Asp Lys Lys Arg Tyr Glu Lys Glu Ser Ala Val Tyr
50 55 60
Arg Gly Glu Ala Thr Val Asp Val Asp Ser Gly Asn Glu Ser Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO:4200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1579876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4200:

Met	Lys	Lys	Asn	Pro	Leu	Ser	Ile	Ala	Val	Lys	Leu	Gln	Ser	Met	Trp	
1			5						10					15		
Ile	Leu	Gly	Thr	Ser	Leu	Thr	Arg	Asp	Pro	Ser	Ser	Trp	Ala	Gly	Met	
			20					25						30		
Val	Ala	Arg	Asp	Glu	Ser	Leu	Val	Pro	Cys	Val	Leu	Leu	Leu	Cys	Gln	
			35					40						45		
Gln	Leu	Leu	Pro	Thr	Thr	Leu	Leu	Thr	Val	Lys	Arg	Val	Ser	Leu	Ala	
			50				55					60				
Ala	Tyr	Leu	Cys	Arg	Ala	Lys	Glu	Cys	Thr	Ser	Val	Val				
65				70					75							

(2) INFORMATION FOR SEQ ID NO:4201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..356
(D) OTHER INFORMATION: / Ceres Seq. ID 1579877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4201:

attattagga	agaacactgt	tttgtctccg	gcccgctcga	gcccaccatgc	cgtagcgcgcc	60
accctgcggg	cgcacccggc	cccgccagcg	cgttcgagcg	cgacgcgcgc	cgccacctgc	120
cgcgctacgc	tccggccatt	ccgtccccct	caccattctg	cgcgctccac	cgacgcagcc	180
gcggggatgc	gacccgcctc	ctctctctcc	cgcttctcgg	ccacaacatc	tccgtctcgc	240
tgccgacctg	aacaacgagg	cacactccat	tgttgcccat	gcttgatctc	ctcactctgc	300
tgcaagtctg	ccgtggaagg	gaggccagtg	cggggaacaac	ccagactcgc	agcgcc	

(2) INFORMATION FOR SEQ ID NO:4202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1579878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4202:

Ile	Ile	Arg	Lys	Asn	Thr	Val	Leu	Ser	Pro	Ala	Arg	Arg	Ser	Pro	Thr	
1			5					10					15			
Ala	Val	Arg	Ala	Thr	Leu	Pro	Ala	His	Pro	Ala	Pro	Pro	Ala	Arg	Ser	
			20					25					30			
Arg	Pro	Thr	Arg	Ala	Ala	Thr	Cys	Arg	Val	Thr	Leu	Arg	Pro	Phe	Leu	
			35				40						45			
Pro	Pro	His	His	Ser	Ala	Ala	Ser	Thr	Ala	Ala	Ala	Ala	Ala	Met	Arg	
			50				55					60				
Pro	Ala	Ser	Ser	Ser	Ser	Arg	Phe	Ser	Ala	Thr	Thr	Ser	Pro	Ser	Arg	

(2) INFORMATION FOR SEO ID NO:4203:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4203:
```

Leu	Leu	Gly	Arg	5	Thr	Leu	Phe	Cys	Leu	Arg	10	Pro	Val	Ala	Ala	15	Pro	Leu
Pro	Cys	Ala	Pro	20	Pro	Cys	Arg	Arg	Thr	Arg	25	Pro	Arg	Gln	Arg	30	Val	Arg
Gly	Arg	Arg	Ala	35	Pro	Pro	Pro	Ala	Ala	Ser	40	Arg	Ser	Gly	His	45	Ser	Cys
Pro	Leu	Thr	Ile	50	Leu	Pro	Pro	Pro	Pro	Gln	55	Gln	Pro	Arg	Arg	60	Cys	Asp
Pro	His	Pro	Pro	65	Pro	Pro	Ala	Ser	Arg	Pro	70	Gln	His	Leu	Arg	75	Leu	Ala
Ala	Asp	Leu	Asn	85	Asn	Glu	Ala	His	Ser	Ile	90	Val	Gly	His	Ala	80		

(2) INFORMATION FOR SEQ ID NO:4204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..476
(D) OTHER INFORMATION: / Ceres Seq. ID 1579904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4204:

taattgtctat	tgtctgcaag	aactttccctg	agtcgctgata	taaaagcccta	gtcgacacctg	120
gcggttctga	cgctcataatt	gtgtgttccga	accagaatgt	gcgaagctga	gtccaaattct	160
tagaatgccc	atgtctctaaa	gatcttggaaa	gggtgatgatg	tggacttaat	gatcatgtct	180
aggaagaacac	cgggatcttc	gtgtgcgacg	cttgtcaact	tggttaaatgt	tgtcgtgctt	240
aaggctgcga	tggatgtgtgc	aaaagctgtc	acaaatggat	atcttgagta	tgcgaaggac	300
caaatcatga	tgggttagtg	gcggaaagtc	cgagttatct	ctgacgaat	caggaaagat	360
acagcatacc	atgagggaag	gcatacggct	gtgtcgaatc	acacagaagg	agctcacacct	420
gtccacacac	ctccatcatc	acgtcggaaa	atgcgcctag	aaatgtgtgac	ccaact	

(2) INFORMATION FOR SEQ ID NO:4205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide
(B) LOCATION: 1..114
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(D) OTHER INFORMATION: / Ceres Seq. ID 1579905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4205:

Met	Ser	Lys	Ile	Leu	Lys	Gly	Asp	Asp	Val	Asp	Leu	Met	Ile	Ile	Ala	
1				5							10				15	
Arg	Gly	Thr	Pro	Gly	Phe	Ser	Gly	Ala	Asp	Leu	Ala	Asn	Leu	Val	Asn	
			20					25						30		
Val	Ala	Ala	Leu	Lys	Ala	Ala	Met	Asp	Gly	Ala	Lys	Ala	Val	Thr	Met	
			35					40					45			
Asp	Asp	Leu	Glu	Tyr	Ala	Lys	Asp	Arg	Ile	Met	Met	Gly	Ser	Glu	Arg	
			50				55					60				
Lys	Ser	Ala	Val	Ile	Ser	Asp	Glu	Cys	Arg	Lys	Leu	Thr	Ala	Tyr	His	
			65			70				75				80		
Glu	Gly	Gly	His	Ala	Leu	Val	Ala	Ile	His	Thr	Glu	Gly	Ala	His	Pro	
				85					90					95		
Val	His	Lys	Ala	Thr	Ile	Val	Pro	Arg	Gly	Met	Ala	Leu	Gly	Met	Val	
			100					105						110		
Ala	Gln															

(2) INFORMATION FOR SEQ ID NO:4206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1579906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4206:

Met	Ile	Ile	Ala	Arg	Gly	Thr	Pro	Gly	Phe	Ser	Gly	Ala	Asp	Leu	Ala	
1				5					10					15		
Asn	Leu	Val	Asn	Val	Ala	Ala	Leu	Lys	Ala	Ala	Met	Asp	Gly	Ala	Lys	
			20					25					30			
Ala	Val	Thr	Met	Asp	Asp	Leu	Glu	Tyr	Ala	Lys	Asp	Arg	Ile	Met	Met	
			35				40					45				
Gly	Ser	Glu	Arg	Lys	Ser	Ala	Val	Ile	Ser	Asp	Glu	Cys	Arg	Lys	Leu	
			50			55					60					
Thr	Ala	Tyr	His	Glu	Gly	Gly	His	Ala	Leu	Val	Ala	Ile	His	Thr	Glu	
			65			70				75				80		
Gly	Ala	His	Pro	Val	His	Lys	Ala	Thr	Ile	Val	Pro	Arg	Gly	Met	Ala	
				85					90					95		
Leu	Gly	Met	Val	Ala	Gln											
			100													

(2) INFORMATION FOR SEQ ID NO:4207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1579907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4207:

Met	Asp	Gly	Ala	Lys	Ala	Val	Thr	Met	Asp	Asp	Leu	Glu	Tyr	Ala	Lys	
1				5					10					15		
Asp	Arg	Ile	Met	Met	Gly	Ser	Glu	Arg	Lys	Ser	Ala	Val	Ile	Ser	Asp	
			20					25					30			
Glu	Cys	Arg	Lys	Leu	Thr	Ala	Tyr	His	Glu	Gly	Gly	His	Ala	Leu	Val	

35 40 45
Ala Ile His Thr Glu Gly Ala His Pro Val His Lys Ala Thr Ile Val
50 55 60
Pro Arg Gly Met Ala Leu Gly Met Val Ala Gln
65 70 75

(2) INFORMATION FOR SEQ ID NO:4208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4208:

aaacgcgatt	cccccttttt	tctttatatt	cttcgtcttc	ttcgtctcga	ctcgcgcgcc	60
agtcacctca	aatcccttcg	atccaatctc	caaacycctag	gcaatcccaac	atcaaaagtat	120
tagctgcgcc	cttcgtcaaa	ccgcgcgcgc	gcgcgcctagg	cccacgcgcg	cgcgccgcgg	180
aaggcggaag	tgacgcgcga	cctggcgggtg	gacggcgagg	gcacgcgcac	gctcaaccgc	240
actgtgtctg	agcgccctcga	cccgcccggtt	gaggatatct	tcattcacgc	ggctcacgtc	300
acgctgtacg	actttgacac	cgatgtcaac	cagtggaagac	ggaaggacgt	ggaggggctc	360
ctcttcgtcg	tcaagaggaa	tgctcaacct	agattccagt	tcattggtcat	gaaccgcagg	420
aatacagata	atctagtgtg					

(2) INFORMATION FOR SEQ ID NO:4209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4209:

Thr	Asp	Phe	Pro	Leu	Phe	Ser	Leu	Phe	Ser	Ser	Ser	Ser	Ser	Arg
1			5					10					15	
Leu	Ala	Ala	Gln	Ser	Pro	Gln	Ile	Pro	Ser	Ile	Gln	Ser	Pro	Asn
			20				25					30		Xaa
Arg	Gln	Ser	Asn	Ile	Lys	Val	Leu	Ala	Ala	Pro	Phe	Val	Lys	Pro
		35					40				45			Arg
Arg	Arg	Gly	His	Gly	Pro	Arg	Arg	Arg	Arg	Glu	Gly	Glu	Gly	Asp
		50				55				60				
Ala	Glu	Pro	Gly	Gly	Gly	Arg	Arg	Gly	His	Ala	His	Ala	Gln	Pro
		65				70				75			80	
Cys	Ala	Ala	Ala	Pro	Arg	Pro	Gly	Arg						
			85											

(2) INFORMATION FOR SEQ ID NO:4210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4210:

(2) INFORMATION FOR SEQ ID NO:4211:

(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1579922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4211:

(2) INFORMATION FOR SEQ ID NO:4212:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..16

(D) OTHER INFORMATION: / Ceres Seq. ID 1579923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4212:

Lys	Ala	Leu	Cys	Leu	Cys	Ala	Ser	Ala	Arg	Glu	Arg	Glu	Ser	Glu	Arg
1				5					10					15	
Glu	Arg	Glu	Gly	Gly	Asp	Leu	Ala	Glu	Glu	Arg	Ser	Lys	Gln	Gly	Gly
			20					25					30		
Lys	Glu	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Cys	Arg	Lys	Gly	Asn	Met	Leu
			35				40					45			
Pro	Pro	His	Leu	Thr	Glu	Asn	Gly	Ala	Val	Met	Ile	Gln	Phe	Gly	His
			50				55				60				
Gln	Met	Pro	Asp	Tyr	Asp	Ser	Pro	Ala	Thr	Gln	Ser	Thr	Ser	Glu	Thr
65				70						75				80	
Ser	His	Gln	Glu	Ala	Ser	Gly	Met	Ser	Glu	Gly	Ser	Leu	Asn	Glu	His
				85				90						95	
Asn	Asn	Asp	His	Ser	Gly	Asn	Leu	Asp	Gly	Tyr	Ser	Lys	Ser	Asp	Glu
			100					105					110		
Asn	Lys	Met	Met	Ser	Ala	Leu	Ser	Leu	Gly	Asn	Pro	Glu	Thr	Ala	Tyr
			115				120					125			

Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile Ser Tyr
130 135 140
Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Tyr Gly
145 150 155 160
Pro His Ala Ile Met
165

(2) INFORMATION FOR SEQ ID NO:4213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1579924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4213:

Met Leu Pro Pro His Leu Thr Glu Asn Gly Ala Val Met Ile Gln Phe
1 5 10 15
Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr Gln Ser Thr Ser
20 25 30
Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn
35 40 45
Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser
50 55 60
Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr
65 70 75 80
Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile
85 90 95
Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala
100 105 110
Tyr Gly Pro His Ala Ile Met
115

(2) INFORMATION FOR SEQ ID NO:4214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1579925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4214:

Met Ile Gln Phe Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr
1 5 10 15
Gln Ser Thr Ser Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu
20 25 30
Gly Ser Leu Asn Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly
35 40 45
Tyr Ser Lys Ser Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly
50 55 60
Asn Pro Glu Thr Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln
65 70 75 80
Ser Phe Ala Ile Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala
85 90 95
Val Ala Ala Ala Tyr Gly Pro His Ala Ile Met
100 105

(2) INFORMATION FOR SEQ ID NO:4215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..436
(D) OTHER INFORMATION: / Ceres Seq. ID 1579926
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4215:
agcaggcggt tgggcgagtg agtgagtcag tgaggctggg atagcagcag cagtgccgcg 60
cactcaactt ctcttcttgc cgtgcggtgt gcgcgcgcgc gggaggcacc gcacggccgc 120
aagcaatgcc gcgcgcgcag aggaacgcgc gcagcagagg gctcaaggcg gaggacttcg 180
tcgactcggt gctcaacttc ggcgcgcgag agggagatgg ggaagaggag aagcaggagg 240
cgcgcgcggc cggccagccg gcgcgcggagt tcaagtccaa gaacctggag gccgagcgga 300
agcgcgcggc caagctcaac cgcaacatcc tcgcgctcag gcccggtggt cogaacatca 360
ccaagatgag caaggagatcc accctctcgg acgctatcga cctcatcaag aagctccaga 420
accaggctct tgagct

(2) INFORMATION FOR SEQ ID NO:4216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..103
(D) OTHER INFORMATION: / Ceres Seq. ID 1579927
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4216:
Met Pro Arg Arg Gln Arg Thr Arg Ser Ser Glu Glu Lys Ala Glu
1 5 10 15
Asp Phe Val Asp Ser Val Leu Asn Phe Gly Gly Glu Glu Asp Gly
20 25 30
Glu Glu Glu Lys Gln Glu Ala Gly Gly Asp Gly Gln Pro Ala Ala Glu
35 40 45
Phe Lys Ser Lys Asn Leu Glu Ala Glu Arg Lys Arg Arg Gly Lys Leu
50 55 60
Asn Arg Asn Ile Leu Ala Leu Arg Ala Val Val Pro Asn Ile Thr Lys
65 70 75 80
Met Ser Lys Glu Ser Thr Leu Ser Asp Ala Ile Asp Leu Ile Lys Lys
85 90 95
Leu Gln Asn Gln Val Leu Glu
100

(2) INFORMATION FOR SEQ ID NO:4217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..278
(D) OTHER INFORMATION: / Ceres Seq. ID 1579931
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4217:
ctaataaaac gtgccccctcc gtcccaaccg tccgcgcgct cccctccctt cgcgtccgcg 60
aagaccctcc tcttcacccc actcacccag etccccctga cccagagaag acgcgcgcga 120
ccatgcggcc accgagaggg cgcgcgcgag gcgcgcggtt gccggaagtg gaggccgagg 180
cgcgcgcggt ggccggttcg gcgcgcgagg ccgtggtggc cggttcggcg gcgggttcgc 240

cgacgagggc cgcgccgcag aggttcgtcg aggtgtcg

(2) INFORMATION FOR SEQ ID NO:4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4218:

Leu	Ile	Asn	Arg	Ala	Pro	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Ser	Leu	Pro
1			5					10						15	
Phe	Arg	Ser	Ala	Lys	Thr	Leu	Leu	Leu	Thr	Pro	Leu	Thr	Gln	Leu	Pro
			20					25					30		
Ser	Ser	Pro	Glu	Ala	Pro	Arg	Ala	Pro	Cys	Gly	His	Arg	Glu	Gly	Ala
			35				40					45			
Ala	Ala	Ala	Ala	Val	Arg	Arg	Arg	Trp	Arg	Pro	Arg	Arg	Arg	Arg	Trp
			50				55				60				
Pro	Val	Arg	Arg	Arg	Arg	Pro	Trp	Trp	Pro	Val	Arg	Arg	Arg	Val	Pro
65					70					75				80	
Arg	Arg	Gly	Pro	Ala	Arg	Arg	Gly	Ser	Ser	Arg	Cys				
					85					90					

(2) INFORMATION FOR SEQ ID NO:4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4219:

Asn	Lys	Pro	Cys	Pro	Ser	Val	Pro	Thr	Val	Arg	Arg	Leu	Pro	Pro	Phe
1			5					10					15		
Pro	Leu	Arg	Gln	Asp	Pro	Pro	Pro	His	Pro	Thr	His	Pro	Ala	Pro	Leu
			20					25				30			
Glu	Pro	Arg	Ser	Thr	Ala	Arg	Thr	Met	Arg	Pro	Pro	Arg	Gly	Arg	Gly
			35				40					45			
Gly	Gly	Gly	Gly	Ser	Ala	Glu	Val	Glu	Ala	Glu	Ala	Ala	Ala	Val	Ala
			50				55				60				
Gly	Ser	Ala	Ala	Glu	Ala	Val	Val	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Ala
65					70					75				80	
Thr	Arg	Ala	Arg	Pro	Gln	Arg	Phe	Val	Glu	Val	Ser				
					85					90					

(2) INFORMATION FOR SEQ ID NO:4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4220:

Met Arg Pro Pro Arg Gly Arg Gly Gly Gly Gly Ser Ala Glu Val
1 5 10 15
Glu Ala Glu Ala Ala Val Ala Gly Ser Ala Ala Glu Ala Val Val
20 25 30
Ala Gly Ser Ala Ala Gly Ser Ala Thr Arg Ala Arg Pro Gln Arg Phe
35 40 45
Val Glu Val Ser
50

(2) INFORMATION FOR SEQ ID NO:4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4221:

aaaacgctga	tccgagcaac	gaagcccgca	gccatgccga	cggcgacggc	cacggcagct	60
cctcgccaacg	cggcgctctt	cctgcccctg	ctgctgtccc	tgctcggcct	ccacgccaacg	120
tccgcgcggc	ccgcgcgcgc	gggcgtcgcc	gtggacggc	agctcacgtc	caccaagccg	180
tcccggctcc	ccaagaagcc	cagcgtgaag	ccgcccggcc	ccggcgccgc	gagcccgacc	240
ttcccggctc	tccgcatccc	cgggatgggc	gggttcggca	tcccgggatg	gggcgcgggc	300
gggtggggcg	cgcgctacgg	cgggcccgcc	ggcgggtacg	cccgcggcgg	cgtggtggcg	360
cccaccgtga	cgtgctccga	gaaggggccc	tgctacagga	agaaggtcac	ctgcccacaa	420
aagtgcctct	cctcgtacag	cggcgcggca	aggggtacg			

(2) INFORMATION FOR SEQ ID NO:4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4222:

Lys	Thr	Leu	Ile	Gly	Ala	Thr	Lys	Pro	Ala	Ala	Met	Pro	Thr	Ala	Thr
1		5						10					15		
Ala	Thr	Ala	Ala	Pro	Arg	His	Ala	Ala	Leu	Phe	Leu	Pro	Leu	Leu	Leu
		20						25					30		
Leu	Leu	Leu	Gly	Leu	His	Ala	Thr	Ser	Ala	Ala	Ala	Ala	Arg	Ala	Gly
		35						40					45		
Val	Ala	Val	Asp	Ala	Glu	Leu	Thr	Ser	Thr	Lys	Pro	Ser	Pro	Val	Pro
		50						55					60		
Lys	Lys	Pro	Ser	Val	Lys	Pro	Pro	Gly	Pro	Gly	Ala	Ala	Ser	Pro	Thr
		65						70					75		80
Phe	Pro	Gly	Phe	Gly	Ile	Pro	Gly	Met	Gly	Gly	Phe	Gly	Ile	Pro	Gly
Met	Gly	Ala	Gly	Gly	Trp	Gly	Gly	Gly	Tyr	Gly	Gly	Pro	Ala	Gly	Gly
Tyr	Ala	Arg	Gly	Gly	Val	Val	Ala	Pro	Thr	Val	Thr	Cys	Ser	Glu	Lys
Gly	Pro	Cys	Tyr	Arg	Lys	Lys	Val	Thr	Cys	Pro	Lys	Lys	Cys	Phe	Ser
Ser	Tyr	Ser	Gly	Ala	Ala	Arg	Gly	Thr							
145															

(2) INFORMATION FOR SEQ ID NO:4223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1579955
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4223:
Asn Ala Asp Arg Ser Asn Glu Ala Arg Ser His Ala Asp Gly Asp Gly
1 5 10 15
His Gly Ser Ser Pro Arg Gly Ala Val Pro Ala Pro Ala Ala Ala
20 25 30
Pro Ala Arg Pro Pro Arg His Val Arg Arg Arg Arg Ala Arg Gly Arg
35 40 45
Arg Arg Gly Arg Arg Ala His Val His Gln Ala Val Pro Gly Pro Glu
50 55 60
Glu Ala Gln Arg Glu Ala Ala Arg Pro Arg Arg Glu Pro Asp Leu
65 70 75 80
Pro Gly Leu Arg His Pro Arg Asp Gly Arg Val Arg His Pro Arg Asp
85 90 95
Gly Arg Arg Arg Val Gly Arg Arg Leu Arg Arg Ala Arg Arg Val
100 105 110
Arg Pro Arg Arg Arg Gly Gly Ala His Arg Asp Val Leu Arg Glu Gly
115 120 125
Ala Leu Leu Gln Glu Glu Gly His Leu Pro Gln Glu Val Leu Leu Leu
130 135 140
Val Gln Arg Arg Gly Lys Gly Tyr
145 150
(2) INFORMATION FOR SEQ ID NO:4224:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1579956
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4224:
Met Pro Thr Ala Thr Ala Thr Ala Ala Pro Arg His Ala Ala Leu Phe
1 5 10 15
Leu Pro Leu Leu Leu Leu Leu Leu Gly Leu His Ala Thr Ser Ala Ala
20 25 30
Ala Ala Arg Ala Gly Val Ala Val Asp Ala Glu Leu Thr Ser Thr Lys
35 40 45
Pro Ser Pro Val Pro Lys Lys Pro Ser Val Lys Pro Pro Gly Pro Gly
50 55 60
Ala Ala Ser Pro Thr Phe Pro Gly Phe Gly Ile Pro Gly Met Gly Gly
65 70 75 80
Phe Gly Ile Pro Gly Met Gly Ala Gly Gly Trp Gly Gly Tyr Gly
85 90 95
Gly Pro Ala Gly Gly Tyr Ala Arg Gly Gly Val Val Ala Pro Thr Val
100 105 110
Thr Cys Ser Glu Lys Gly Pro Cys Tyr Arg Lys Lys Val Thr Cys Pro
115 120 125
Lys Lys Cys Phe Ser Ser Tyr Ser Gly Ala Ala Arg Gly Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:4225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..524
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4225:

tttttagcacc	acctctcatg	actaynacat	ttcttttcggg	aaagtagaaa	aaaatctatt	60
accocatgagg	ccatgatact	ttccacttgg	acgaagcgaa	attgttaatt	octcccttcc	120
agtatatagc	tcgctcgctc	acactcggag	ctcgtaacaa	agtcacact	catcacatga	180
gcttgcttgt	gactgccagc	tttgcccaat	gttcacgcc	catggaagag	cgggcaactgt	240
tcocgggtgtc	cgattccagc	accacctgca	gcagctctgg	ctgtaccggc	cccaactccc	300
ctgtctcgtc	gtcgcagtat	ttggacgaca	ccagcgacgg	cgccggcagc	tcgagcagcc	360
ggaagcggcc	gcgcggggag	ctgaagcatc	caacgtaccg	cggcgtgcgc	atgcgtgcgt	420
ggggcaagt	ggtgtccgag	atccgggagc	cccgcaagaa	gtcgcgcgac	tggctgggca	480
ccttcgacac	tcgccmaga	tgccgcgcgc	cgcgcatgac	gtcg		

(2) INFORMATION FOR SEQ ID NO:4226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4226:

Met	Ser	Leu	Leu	Val	Thr	Ala	Ser	Phe	Ala	Gln	Cys	Ser	Ser	Pro	Met
1				5						10				15	
Glu	Glu	Arg	Ala	Leu	Phe	Pro	Val	Ser	Asp	Ser	Ser	Thr	Thr	Cys	Ser
			20					25					30		
Ser	Ser	Gly	Cys	Thr	Gly	Pro	Asn	Ser	Pro	Val	Ser	Ser	Ser	Gln	Tyr
			35				40					45			
Leu	Asp	Asp	Thr	Ser	Asp	Gly	Ala	Gly	Ser	Ser	Ser	Ser	Arg	Lys	Arg
	50					55					60				
Pro	Arg	Arg	Glu	Leu	Lys	His	Pro	Thr	Tyr	Arg	Gly	Val	Arg	Met	Arg
	65				70					75				80	
Ala	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser
				85					90						
Arg	Ile	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Pro	Xaa	Arg	Trp	Pro	Arg	Ala
			100				105						110		
Arg	Met	Thr	Ser												
															115

(2) INFORMATION FOR SEQ ID NO:4227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4227:

```

Met Glu Glu Arg Ala Leu Phe Pro Val Ser Asp Ser Ser Thr Thr Cys
1          5          10          15
Ser Ser Ser Gly Cys Thr Gly Pro Asn Ser Pro Val Ser Ser Ser Gln
          20          25          30
Tyr Leu Asp Asp Thr Ser Asp Gly Ala Gly Ser Ser Ser Arg Lys
          35          40          45
Arg Pro Arg Arg Glu Leu Lys His Pro Thr Tyr Arg Gly Val Arg Met
          50          55          60
Arg Ala Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys
65          70          75          80
Ser Arg Ile Trp Leu Gly Thr Phe Asp Thr Pro Xaa Arg Trp Pro Arg
          85          90          95
Ala Arg Met Thr Ser
          100

```

(2) INFORMATION FOR SEQ ID NO:4228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4228:

```

acttcacccc tctcaatctc gtcctacact ctctccacc ttcacttcac ctgctctctc 60
tggtctcgag ctagctcaca tcagggggag gaagaggaac cagcacctgc ctgcacatgt 120
cgctcctccat ggtgtccaaag aacgcggccg cgccggccgg gtacggcgac ggcgaaaggca 180
gcgtgctcga ggcgcggccg gtgacgagct gcctgtacct gcgccccggg gcggggggcgc 240
tggaacaggga cgcgctgctg cgccgcacat gccaccggag gcgccacgac cgctccaccg 300
acacgctgcg ctccatggtg caggcgccgc cgcggtcggc tgagccggac ggcattggaag 360
gcgcagaacg gcacctcccg tggccgctcg acgacgcctt ctcgccgcct tagcttttgt 420
aataatagaat tagtctcttg tgcagattaa gsaaatgcac atggaacatg gtccagttcg 480
cctctctcttg tgtagactgt gaataacaga tgc

```

(2) INFORMATION FOR SEQ ID NO:4229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4229:

```

Leu His Pro Ser Gln Ser Arg Ser Ser Leu Ser Pro Thr Phe Thr Ser
1          5          10          15
Pro Ala Leu Ser Val Leu Glu Leu Ala His Ile Arg Gly Arg Lys Arg
          20          25          30
Asn Gln His Leu Pro Arg His Val Val Leu His Gly Val Gln Glu Arg
          35          40          45
Ala Ala Ala Gly Arg Val Arg Arg Arg Arg Gln Arg Arg Arg Gly
          50          55          60
Arg Ala Gly Asp Glu Leu Pro Val Pro Ala Pro Arg Gly Gly Ala
65          70          75          80
Gly Gln Gly Arg Arg Ala Ala Pro His Pro Pro Pro Glu Ala Pro Arg
          85          90          95
Pro Pro Pro Arg His Ala Ala Leu His Gly Ala Gly Ala Ala Val
          100          105          110

```

Gly

(2) INFORMATION FOR SEQ ID NO:4230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4230:

Met	Ser	Ser	Ser	Met	Val	Ser	Lys	Asn	Ala	Pro	Pro	Pro	Ala	Gly	Tyr
1				5					10					15	
Gly	Asp	Gly	Glu	Gly	Ser	Val	Val	Glu	Ala	Ala	Pro	Val	Thr	Ser	Cys
			20					25					30		
Leu	Tyr	Leu	Arg	Pro	Gly	Ala	Gly	Ala	Leu	Asp	Arg	Asp	Ala	Val	Leu
			35				40						45		
Arg	Arg	Ile	Arg	His	Arg	Arg	Arg	His	Asp	Arg	Leu	His	Asp	Thr	Leu
			50				55				60				
Arg	Ser	Met	Val	Gln	Ala	Pro	Pro	Arg	Ser	Ala	Glu	Pro	Asp	Gly	Met
				70						75				80	
Asp	Gly	Ala	Glu	Arg	His	Leu	Pro	Trp	Pro	Leu	Asp	Asp	Ala	Phe	Ser
				85					90					95	
Ala	Pro														

(2) INFORMATION FOR SEQ ID NO:4231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4231:

Met	Val	Ser	Lys	Asn	Ala	Pro	Pro	Pro	Ala	Gly	Tyr	Gly	Asp	Gly	Glu
1				5					10					15	
Gly	Ser	Val	Val	Glu	Ala	Ala	Pro	Val	Thr	Ser	Cys	Leu	Tyr	Leu	Arg
				20				25					30		
Pro	Gly	Ala	Gly	Ala	Leu	Asp	Arg	Asp	Ala	Val	Leu	Arg	Arg	Ile	Arg
				35				40					45		
His	Arg	Arg	Arg	His	Asp	Arg	Leu	His	Asp	Thr	Leu	Arg	Ser	Met	Val
				50			55				60				
Gln	Ala	Pro	Pro	Arg	Ser	Ala	Glu	Pro	Asp	Gly	Met	Asp	Gly	Ala	Glu
				65			70			75				80	
Arg	His	Leu	Pro	Trp	Pro	Leu	Asp	Asp	Ala	Phe	Ser	Ala	Pro		
				85				90							

(2) INFORMATION FOR SEQ ID NO:4232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1579979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4232:

ctctccacgc	ccgcgcacgc	ccgctccgcc	actcccacct	tctactcacc	gccgccaccg	60
ctccggtccg	cccggtgcga	gcgcacgcga	ccaagccccc	ccgcgcctcc	ctcgtctctg	120
tccgcgcctc	cagctcggac	ctctccgcagc	agcagctcaa	ctctcccggtg	ctccggttca	180
ccctcgggat	tccgggggtg	gacgaatcgt	acctcccccg	gtggataggc	ctcgggttcc	240
gcgcgctcgt	cgtgctcaac	caacctctct	ctgcgtcccc	gacgcccgcg	cagctcaggt	300
ccgaggctgt	ggggctgtgc	ctggcccggt	tctcggcgac	gctgcggttc	ctggggaggt	360
tccttgaggg	cgctgatgct	gccagccgag	tgccgttgcc	cgaggggagc	atccaagtat	420
tgcctatgtc	tgagaacctg	tcagctgtgc	agaaggagga	catggcggtg	gcgtcgtacg	480

(2) INFORMATION FOR SEQ ID NO:4233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1579980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4233:

Ser	Pro	Arg	Pro	Arg	Thr	Ala	Ala	Pro	Pro	Leu	Pro	Pro	Ser	Thr	His
1			5						10					15	
Arg	Arg	His	Arg	Ser	Ala	Pro	Pro	Val	Arg	Ser	Ala	Ser	Asp	Gln	Ala
			20					25					30		
Pro	Pro	Pro	Leu	Pro	Arg	Pro	Arg	Pro	Arg	Leu	Gln	Leu	Gly	Pro	Ser
			35				40					45			
Ala	Ala	Ala	Ala	Gln	Pro	Leu	Arg	Ala	Pro	Leu	His	Pro	Arg	Asp	Ser
			50				55				60				
Gly	Ala	Gly	Arg	Ile	Val	Pro	Pro	Pro	Val	Asp	Arg	Pro	Arg	Phe	Arg
			65				70			75				80	
Arg	Ala	Arg	Arg	Ala	Gln	Pro	Pro	Pro	Leu	Cys	Val	Pro	Asp	Ala	Arg
							85			90				95	
Ala	Ala	Gln	Val	Arg	Gly	Cys	Gly	Ala	Val	Pro	Gly	Arg	Val	Leu	Gly
			100					105					110		
Asp	Ala	Ala	Val	Pro	Gly	Glu	Val	Pro							
			115				120								

(2) INFORMATION FOR SEQ ID NO:4234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1579981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4234:

Leu	His	Ala	Arg	Ala	Pro	Pro	Leu	Arg	His	Ser	His	Leu	Leu	Leu	Thr
1				5					10					15	
Ala	Ala	Thr	Ala	Arg	Leu	Arg	Pro	Cys	Ala	Ala	Pro	Ala	Thr	Lys	Pro
				20				25					30		
Arg	Arg	Arg	Ser	Leu	Val	Leu	Val	Arg	Ala	Ser	Ser	Ser	Asp	Pro	Pro
				35			40					45			
Gln	Gln	Gln	Leu	Asn	Leu	Ser	Val	Leu	Arg	Phe	Thr	Leu	Gly	Ile	Pro
				50			55			60					
Gly	Leu	Asp	Glu	Ser	Tyr	Leu	Pro	Arg	Trp	Ile	Gly	Leu	Gly	Phe	Gly

65	70	75	80
Ala Leu Val Val Leu Asn His Leu Leu Ser Ala Ser Pro Thr Pro Ala			
	85	90	95
Gln Leu Arg Ser Glu Ala Val Gly Leu Cys Leu Ala Ala Phe Ser Ala			
	100	105	110
Thr Leu Pro Phe Leu Gly Arg Phe Leu Glu Gly Ala Asp Ala Ala Ser			
	115	120	125
Arg Val Pro Leu Pro Glu Gly Ser Ile Gln Val Phe Val Met Ser Glu			
	130	135	140
Asn Leu Ser Ala Val Gln Lys Glu Asp Met Ala Trp Ala Ser Tyr			
	145	150	155

(2) INFORMATION FOR SEQ ID NO:4235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4235:

cgaggagtta tggagttaat gttgtagttg caatcaacaa atttgcatca gatactgagg	60
cagaaatgaa ggcagtgca acgtgcagcta tggctgtctg tgccttttgac gctgtttgct	120
gcacacacca tgcccatggt ggtaaaggag cggttgagct tggacttgct gttcaacgag	180
catgcgaag ccaggcgagaa cctctgaagt ttttgatcc cttggaatct agcataaagg	240
agaagattga gtcaattgct aagttctatg gtgctagtgg cgttgaatat tccgagcagg	300
ctgagaagca gattgagatg tacaccaagc aagggttctc cagcctcccc atttgcatgg	360
cgaagaccga gtactcgttc tcacatgtcc cgtccatgaa gggcgccccg accggttttg	420
ttctgcgat aagagacgtg agggccagca tcggcgtctg gttcatctac ccgctcgtgg	480

gc

(2) INFORMATION FOR SEQ ID NO:4236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4236:

Arg Ser Tyr Gly Val Asn Val Val Val Ala Ile Asn Lys Phe Ala Ser	
1	5
Asp Thr Glu Ala Glu Met Lys Ala Val His Ser Ala Ala Met Ala Ala	
	20
Gly Ala Phe Asp Ala Val Val Cys Thr His His Ala His Gly Gly Lys	
	35
Gly Ala Val Glu Leu Gly Leu Ala Val Gln Arg Ala Cys Glu Ser Gln	
	50
Ala Glu Pro Leu Lys Phe Leu Tyr Pro Leu Glu Ser Ser Ile Lys Glu	
	65
Lys Ile Glu Ser Ile Ala Lys Phe Tyr Gly Ala Ser Gly Val Glu Tyr	
	85
Ser Glu Gln Ala Glu Lys Gln Ile Glu Met Tyr Thr Lys Gln Gly Phe	
	100
Ser Ser Leu Pro Ile Cys Met Ala Lys Thr Gln Tyr Ser Phe Ser His	
	115
Val Pro Ser Met Lys Gly Ala Pro Thr Gly Phe Val Leu Pro Ile Arg	

(2) INFORMATION FOR SEO ID NO:4237:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1579988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4237:

Met	Lys	Ala	Val	His	Ser	Ala	Ala	Met	Ala	Ala	Gly	Ala	Phe	Asp	Ala
1				5					10					15	
Val	Val	Cys	Thr	His	His	Ala	His	Gly	Gly	Lys	Gly	Ala	Val	Glu	Leu
			20					25					30		
Gly	Leu	Ala	Val	Gln	Arg	Ala	Cys	Glu	Ser	Gln	Ala	Glu	Pro	Leu	Lys
		35					40					45			
Phe	Leu	Tyr	Pro	Leu	Glu	Ser	Ser	Ile	Lys	Glu	Lys	Ile	Glu	Ser	Ile
	50					55					60				
Ala	Lys	Phe	Tyr	Gly	Ala	Ser	Gly	Val	Glu	Tyr	Ser	Glu	Gln	Ala	Glu
65				70						75				80	
Lys	Gln	Ile	Glu	Met	Tyr	Thr	Lys	Gln	Gly	Phe	Ser	Ser	Leu	Pro	Ile
				85					90					95	
Cys	Met	Ala	Lys	Thr	Gln	Tyr	Ser	Phe	Ser	His	Val	Pro	Ser	Met	Lys
			100					105					110		
Gly	Ala	Pro	Thr	Gly	Phe	Val	Leu	Pro	Ile	Arg	Asp	Val	Arg	Ala	Ser
		115					120					125			
Ile	Gly	Ala	Gly	Phe	Ile	Tyr	Pro	Leu	Val	Gly					
	130					135									

(2) INFORMATION FOR SEQ ID NO:4238:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1579989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4238:

Met	Ala	Ala	Gly	Ala	Phe	Asp	Ala	Val	Val	Cys	Thr	His	His	Ala	His
1				5					10					15	
Gly	Gly	Lys	Gly	Ala	Val	Glu	Leu	Gly	Leu	Ala	Val	Gln	Arg	Ala	Cys
			20					25					30		
Glu	Ser	Gln	Ala	Glu	Pro	Leu	Lys	Phe	Leu	Tyr	Pro	Leu	Glu	Ser	Ser
		35				40						45			
Ile	Lys	Glu	Lys	Ile	Glu	Ser	Ile	Ala	Lys	Phe	Tyr	Gly	Ala	Ser	Gly
	50					55				60					
Val	Glu	Tyr	Ser	Glu	Gln	Ala	Glu	Lys	Gln	Ile	Glu	Met	Tyr	Thr	Lys
65				70					75						80
Gln	Gly	Phe	Ser	Ser	Leu	Pro	Ile	Cys	Met	Ala	Lys	Thr	Gln	Tyr	Ser
				85				90					95		
Phe	Ser	His	Val	Pro	Ser	Met	Lys	Gly	Ala	Pro	Thr	Gly	Phe	Val	Leu
			100					105					110		

Pro Ile Arg Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr Pro
115 120 125
Leu Val Gly
130

(2) INFORMATION FOR SEQ ID NO:4239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..433
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4239:

acaatttgat	tttgaccggt	cgccctgcctg	gcgcgcctct	agtcgtaatc	cgcccccgcc	60
gcctccccct	ctcggccctt	ctccgctccg	cgccggcgcc	atgtcggtga	cgctgcacac	120
gaacctgggc	gacatcaagt	gcgaggtgtt	ctgcgaccag	gtgccgcgca	cgccggagaa	180
cttcctggcg	ctctgcggca	gcggctacta	cgacggcacc	gtgttccacc	gcaacatcaa	240
gggcttcatg	gtccaggggc	gcgacccac	cgccaccggc	aaggcggggt	gttccatctg	300
ggcgcgcaag	ttcggcgacg	agttgagggg	gtcgctcaag	cacaacgcgc	gggggatcat	360
gtcgatggcc	aacagcgggc	ccaacaccaa	cgcgagccag	ttcttcacaa	cctacgcgaa	420
gcagccgcac	ctc					

(2) INFORMATION FOR SEQ ID NO:4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4240:

Gl n	P he	A sp	P he	A sp	P ro	S er	P ro	A la	T rp	P ro	P ro	S er	A rg	A sn	
1				5					10					15	
P ro	A la	P ro	P ro	P ro	P ro	P ro	L eu	A rg	P ro	S er	P ro	L eu	A rg	A la	G ly
				20				25					30		
A la	M et	S er	V al	T hr	L eu	H is	T hr	A sn	L eu	G ly	A sp	I le	L ys	C ys	G lu
				35			40					45			
V al	P he	C ys	A sp	G ln	V al	P ro	A rg	T hr	A la	G lu	A sn	P he	L eu	A la	L eu
				50			55				60				
C ys	G ly	S er	G ly	T yr	T yr	A sp	G ly	T hr	V al	P he	H is	A rg	A sn	I le	L ys
				65			70				75			80	
G ly	P he	M et	V al	G ln	G ly	G ly	A sp	P ro	T hr	G ly	T hr	G ly	L ys	G ly	G ly
				85				90						95	
S er	S er	I le	T rp	G ly	A la	L ys	P he	A la	A sp	G lu	L eu	A rg	G lu	S er	L eu
				100				105					110		
L ys	H is	A sn	A la	A rg	G ly	I le	M et	S er	M et	A la	A sn	S er	G ly	P ro	A sn
				115			120						125		
T hr	A sn	G ly	S er	G ln	P he	P he	I le	T hr	T yr	A la	L ys	G ln	P ro	H is	L eu
				130			135						140		

(2) INFORMATION FOR SEQ ID NO:4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1579996
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4241:
Met Ser Val Thr Leu His Thr Asn Leu Gly Asp Ile Lys Cys Glu Val
1 5 10 15
Phe Cys Asp Gln Val Pro Arg Thr Ala Glu Asn Phe Leu Ala Leu Cys
 20 25 30
Gly Ser Gly Tyr Asp Gly Thr Val Phe His Arg Asn Ile Lys Gly
 35 40 45
Phe Met Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Lys Gly Gly Ser
 50 55 60
Ser Ile Trp Gly Ala Lys Phe Ala Asp Glu Leu Arg Glu Ser Leu Lys
65 70 75 80
His Asn Ala Arg Gly Ile Met Ser Met Ala Asn Ser Gly Pro Asn Thr
 85 90 95
Asn Gly Ser Gln Phe Phe Ile Thr Tyr Ala Lys Gln Pro His Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:4242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..291
 (D) OTHER INFORMATION: / Ceres Seq. ID 1580028
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4242:
acctggccgc caccttcctt ctacctgtc cccctgttc cctgaccgag cagcgcccag 60
gcaaccgcgt agcacccgct gacctgtacc gccaggagcc cgaccgcgc aagccccacc 120
gccaggagcg cagcgcgccg accgaccccg aagccgcccg cgtccctgca cagcagcgcg 180
caccgaggac cgacgcccagg actcgaccgc gaccaggct accgtcgcca cgtcgcgcca 240
ggccgagccc tgcattccgc ccgagcgacc gcgcccaggaa cccgacaccg g

(2) INFORMATION FOR SEQ ID NO:4243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..96
 (D) OTHER INFORMATION: / Ceres Seq. ID 1580029
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4243:
Leu Ala Ala Thr Phe Leu Leu Pro Arg Pro Pro Ala Ser Leu Thr Glu
1 5 10 15
Gln Arg Pro Gly Asn Arg Ile Ala Pro Arg Asp Pro Asp Arg Gln Glu
 20 25 30
Pro Asp Arg Pro Lys Pro His Arg Gln Asp Ala Ser Arg Ala Thr Arg
 35 40 45
Pro Glu Ala Ala Arg Val Pro Ala His Asp Ala Pro Pro Arg Thr Asp
 50 55 60
Ala Arg Thr Arg Pro Arg Pro Arg Leu Pro Ser Pro Arg Arg Ala Arg
65 70 75 80
Pro Ser Pro Ala Ser Ala Pro Ser Asp Arg Ala Arg Asn Pro Thr Pro

85

90

95

(2) INFORMATION FOR SEQ ID NO:4244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4244:

attctctccc	ttcgccatga	cgccgcccgc	gcgcctccg	tgccctgcct	gcctcctcac	60
ctctctctct	ctcgccgcgc	cgccgcccgc	accgcccgc	gccatctgcg	tcccgcgcaa	120
tcccgggtgc	cacagcaagc	caggagcgcc	ggcgaagccc	gcgccaccga	aactaaagcc	180
cttcacgccc	cgccgcccgc	cgccgcccga	gccgacgcgc	atggccccgc	gcgccgacat	240
cgtcgggagc	ctgtgacctga	agaccgacta	ccccgacctg	tgcatgtcgc	ccatcgcgaa	300

(2) INFORMATION FOR SEQ ID NO:4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4245:

Ile	Ser	Ser	Leu	Arg	His	Asp	Ala	Ala	Ala	Ala	Ser	Val	Pro	Arg	
1			5						10			15			
Leu	Pro	Pro	His	Pro	Pro	Pro	Pro	Arg	Arg	Gly	Gly	Xaa	Thr	Gly	
			20					25				30			
Arg	Arg	His	Leu	Arg	Pro	Ala	Gln	Ser	Arg	Trp	Pro	Gln	Gln	Ala	Arg
			35				40				45				
Ser	Ala	Gly	Gln	Ala	Arg	Ala	Thr	Glu	Thr	Lys	Ala	Pro	His	Ala	Arg
			50			55				60					
Gly	Ala	Gly	Ala	Ala	Glu	Ala	Asp	Ala	Asp	Gly	Pro	Gly	Arg	Arg	His
			65			70			75					80	
Arg	Ala	Glu	Pro	Val	Pro	Glu	Asp	Arg	Leu	Pro	Arg	Pro	Val	His	Val
				85				90					95		
Gly	His	Arg	Glu												
			100												

(2) INFORMATION FOR SEQ ID NO:4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4246:

Phe	Leu	Pro	Phe	Ala	Met	Thr	Pro	Pro	Pro	Pro	Cys	Leu	Ala	
1				5				10				15		

Cys Leu Leu Thr Leu Leu Leu Leu Ala Ala Ala Ala Ala Xaa Pro Ala
20 25 30
Gly Ala Ile Cys Val Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly
35 40 45
Ala Pro Ala Lys Pro Ala Pro Lys Leu Lys Pro Leu Thr Pro Ala
50 55 60
Ala Pro Ala Pro Pro Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile
65 70 75 80
Val Arg Ser Leu Cys Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser
85 90 95
Ala Ile Ala Lys
100

(2) INFORMATION FOR SEQ ID NO:4247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4247:

Met Thr Pro Pro Pro Pro Pro Cys Leu Ala Cys Leu Leu Thr Leu
1 5 10 15
Leu Leu Leu Ala Ala Ala Ala Xaa Pro Ala Gly Ala Ile Cys Val
20 25 30
Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly Ala Pro Ala Lys Pro
35 40 45
Ala Pro Pro Lys Leu Lys Pro Leu Thr Pro Ala Ala Pro Ala Pro Pro
50 55 60
Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile Val Arg Ser Leu Cys
65 70 75 80
Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser Ala Ile Ala Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO:4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4248:

cgcgccctcct ctcgcccctcg ctcgcccgcgc gccgcccgcgc cgccgcacatca agcaccgcgcc 60
ccgcccgcgc ctagggtaga caccaatccg ccgcccattggg gcgtatgcac agccgcggga 120
agggtatctc atcgtcgggc ctcgctgtaca agaggacgcc tctcccttg tcaagatcct 180
cgcatctc aaggcccatg ggctggcacc agaaatcccc gaggacctgt acttccctat 240
caagaaggcg gtggcgataa ggaagcacct tgagagggaac aggaaggaca aagactctaa 300
attcaggctc attctgttgg agagcaggat ccaccgcctt gcccgctact acaagcgcac 360
aaagaagcctt ccaccacct ggaagtatga gtaaccaca gcgagcactc tgggtgg

(2) INFORMATION FOR SEQ ID NO:4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1580052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4249:

Arg Ala Ser Ser Arg Pro Arg Ser Ala Ala Ala Pro His
1 5 10 15
Gln Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro
20 25 30
Trp Gly Val Cys Thr Ala Ala Gly Arg Val Ser His Arg Arg Arg Cys
35 40 45
Arg Thr Arg Gly Arg Leu Leu Pro Cys Gln Asp Pro Pro His Pro Gln
50 55 60
Gly Pro Trp Ala Gly Thr Arg Asn Pro Arg Gly Pro Val Leu Pro His
65 70 75 80
Gln Glu Gly Gly Gly Asp Lys Glu Ala Pro
85 90

(2) INFORMATION FOR SEQ ID NO:4250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1580053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4250:

Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu
1 5 10 15
Pro Tyr Lys Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser
20 25 30
Arg Pro Met Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser
35 40 45
Ser Arg Arg Arg Trp Arg
50

(2) INFORMATION FOR SEQ ID NO:4251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1580054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4251:

Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys
1 5 10 15
Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser Arg Pro Met
20 25 30
Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser Ser Arg Arg
35 40 45
Arg Trp Arg
50

(2) INFORMATION FOR SEQ ID NO:4252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..290
(D) OTHER INFORMATION: / Ceres Seq. ID 1580058
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4252:
atatatatgat tatagagagg caaacaacc tcgcccactc caacacgtga ccccccgcg 60
cgcgctctcc cgcacgccc ccactctctc accgccaccg cggagatggc cgctgtctcc 120
caactcgccg cgcgggtgg ctcttccctc gccgcgcgcg cagtgtgtcg ttccccggcg 180
cattctcag cgcgcgcgcg ctctgcgcgc ctccggtcga cgctgcgttt ctccgagcgc 240
ggcctgtcgg ttaagggaag caggcgact ttccgtggg tcgccgcgcg

(2) INFORMATION FOR SEQ ID NO:4253:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..96
(D) OTHER INFORMATION: / Ceres Seq. ID 1580059
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4253:
Tyr Ile Asp Tyr Arg Glu Ala Asn Lys Pro Arg Pro Leu Gln His Val
1 5 10 15
Thr Pro Arg Gly Ala Pro Pro Pro His Ala Pro Thr Leu Ser Pro Pro
20 25 30
Pro Pro Arg Trp Pro Pro Ala Pro Thr Ser Pro Pro Arg Val Ala Leu
35 40 45
Pro Leu Pro Pro Pro Gln Trp Phe Val Pro Arg Arg Ile Pro Gln Pro
50 55 60
Pro Pro Pro Ser Arg Ala Ser Gly Arg Arg Cys Val Ser Arg Ala Pro
65 70 75 80
Ala Cys Arg Leu Arg Glu Ala Gly Arg Leu Ser Arg Gly Ser Pro Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:4254:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..61
(D) OTHER INFORMATION: / Ceres Seq. ID 1580060
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4254:
Met Ala Ala Cys Ser His Leu Ala Ala Ala Gly Gly Ser Ser Pro Ala
1 5 10 15
Ala Ala Ala Val Val Arg Ser Pro Ala His Ser Ser Ala Ala Ala Ala
20 25 30
Phe Ala Arg Leu Arg Ser Thr Leu Arg Phe Ser Ser Ala Gly Leu Ser
35 40 45
Val Lys Gly Ser Arg Ala Thr Phe Pro Trp Val Ala Ala
50 55 60
(2) INFORMATION FOR SEQ ID NO:4255:

```
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..107
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(D) OTHER INFORMATION: / Ceres Seq. ID 1580063
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4257:
Met Glu Ser Pro Pro Asp Gln Ala Ala Ala Ala Arg Gln Asp
1 5 10 15
Lys Glu Gln Arg Asp Tyr Arg Leu Ile Ala Lys Ala Val Asp Glu Ala
20 25 30
Tyr Arg Ala Val Glu Cys Asp Gly Gly Tyr Pro Phe Gly Ala Val
35 40 45
Val Val His Gly Gly Gly Asp Glu Val Val Ser Ser Ser His Asn
50 55 60
Ser Val Arg Lys Asp Ala Asp Pro Ser Ala His Ala Glu Val Thr Ala
65 70 75 80
Ile Arg Gln Ala Cys Lys Lys Leu Gly Lys Thr Ser Leu Ala Gly Cys
85 90 95
Glu Ile Tyr Thr Ser Cys Glu Pro Cys Arg Cys
100 105

(2) INFORMATION FOR SEQ ID NO:4258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1580068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4258:

tcacgacgtg cgccctctggg acotggacgc cgarggggtc ggcacgtgct gctcgcctac 60
gcggargcgc tkcggcaact cggggarac cctgcggtgc agtatgttca ggtgtttaag 120
aaccatgggg catctgtgtg agcttcgatg gcgcattcac acagccaaat gttgggaact 180
ccctttgtcc ctccctctgt tacaactcgg cttaactgca tgaaggagat ttttgacaga 240
tc

(2) INFORMATION FOR SEQ ID NO:4259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1580069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4259:

Ser Arg Arg Ala Pro Leu Gly Pro Gly Arg Arg Xaa Gly Arg Asp Val
1 5 10 15
Leu Leu Ala Tyr Ala Xaa Arg Xaa Arg Gln Leu Gly Xaa His Pro Ala
20 25 30
Val Gln Tyr Val Gln Val Phe Lys Asn His Gly Ala Ser Ala Gly Ala
35 40 45
Ser Met Ala His Ser His Ser Gln Met Leu Gly Thr Pro Phe Val Pro
50 55 60
Pro Ser Val Thr Thr Arg Leu Asn Cys Met Lys Glu Ile Phe Asp Arg
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1580070
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4260:
His Asp Val Arg Leu Trp Asp Leu Asp Ala Xaa Gly Val Ala Thr Cys
1 5 10 15
Cys Ser Pro Thr Arg Xaa Ala Xaa Gly Asn Ser Gly Xaa Thr Leu Arg
20 25 30
Cys Ser Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu
35 40 45
Arg Trp Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu
50 55 60
Pro Leu Leu Gln Leu Gly Leu Thr Ala
65 70

(2) INFORMATION FOR SEQ ID NO:4261:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: / Ceres Seq. ID 1580071
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4261:
Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu Arg Trp
1 5 10 15
Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu Pro Leu
20 25 30
Leu Gln Leu Gly Leu Thr Ala
35

(2) INFORMATION FOR SEQ ID NO:4262:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..407
(D) OTHER INFORMATION: / Ceres Seq. ID 1580072
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4262:
aaaatatata cagaacagca tcaactcttc gactgcgccca gtaacgtatt gccccgcgtg 60
tgcggttaatc tggcagtgct ggcgcagcac aagttcggga tcaactacgg gcagatcgcg 120
aacgacacctc cggagccggc gcaggtggcg acgtctctgc agtcgatggg cgtgaacaag 180
gtgaagctgt acgacgcgga cccccgggtg ctgacggcgt tcgccaaacac gggcgctcggc 240
ttcaccatcg ccgtggggcaa cgaggacctg caggcgatgg cggccagccc ggacgcggcg 300
cgccggttggg tggcgccgcaa cgtgcagccc tacgtccgg ccacgcgcat caccctgcgtc 360
accgtcggca acgaggtcct gtcgggcaac gacacggcgg cgatggc

(2) INFORMATION FOR SEQ ID NO:4263:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1580073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4263:

Lys	Ile	Tyr	Thr	Glu	Gln	His	Gln	Leu	Phe	Asp	Cys	Ala	Ser	Asn	Val	
1				5				10						15		
Leu	Pro	Arg	Val	Cys	Val	Asn	Leu	Ala	Val	Ser	Ala	Gln	His	Lys	Phe	
			20					25					30			
Gly	Ile	Asn	Tyr	Gly	Gln	Ile	Ala	Asn	Asp	Leu	Pro	Glu	Pro	Ala	Gln	
		35					40					45				
Val	Ala	Thr	Leu	Leu	Gln	Ser	Met	Gly	Val	Asn	Lys	Val	Lys	Leu	Tyr	
	50					55					60					
Asp	Ala	Asp	Pro	Arg	Val	Leu	Thr	Ala	Phe	Ala	Asn	Thr	Gly	Val	Gly	
	65				70				75					80		
Phe	Thr	Ile	Ala	Val	Gly	Asn	Glu	Asp	Leu	Gln	Ala	Met	Ala	Ala	Ser	
			85					90						95		
Pro	Asp	Ala	Ala	Arg	Arg	Trp	Val	Ala	Ala	Asn	Val	Gln	Pro	Tyr	Val	
			100					105						110		
Pro	Ala	Thr	Arg	Ile	Thr	Cys	Val	Thr	Val	Gly	Asn	Glu	Val	Leu	Ser	
		115				120							125			
Gly	Asn	Asp	Thr	Ala	Ala	Met										
	130					135										

(2) INFORMATION FOR SEQ ID NO:4264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1580074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4264:

Met	Gly	Val	Asn	Lys	Val	Lys	Leu	Tyr	Asp	Ala	Asp	Pro	Arg	Val	Leu	
1				5				10						15		
Thr	Ala	Phe	Ala	Asn	Thr	Gly	Val	Gly	Phe	Thr	Ile	Ala	Val	Gly	Asn	
			20					25					30			
Glu	Asp	Leu	Gln	Ala	Met	Ala	Ala	Ser	Pro	Asp	Ala	Ala	Arg	Arg	Trp	
		35				40						45				
Val	Ala	Ala	Asn	Val	Gln	Pro	Tyr	Val	Pro	Ala	Thr	Arg	Ile	Thr	Cys	
	50					55					60					
Val	Thr	Val	Gly	Asn	Glu	Val	Leu	Ser	Gly	Asn	Asp	Thr	Ala	Ala	Met	
	65				70				75					80		

(2) INFORMATION FOR SEQ ID NO:4265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 466 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1580088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4265:

acctatccgc cgctctccaa tcactctgcc cccaaactcc caccgccgag catccccacg

```
ccaccacacc tcgtcgcgtc gcgtcgtcac cggcgtgaag atggctcgggc caggcctcta 120
caccgagatc ggcaagaaga ccagggatct gctgtacaag gactaccaga ctgaccacaa 180
gttcacccctc actaccctaca cctccaatgg cgtcgtgtga actgcttcta gcacaaagaa 240
agctgacctg atcctctggcg agatccaatc acagataaag aacaagaaca tgaccataga 300
tgtgaaagca aactcggagt caaatatcat tacgacaatt actgttgatg agattgcaac 360
accagggctg aagaccatct taagctttgc tgttctgatg cagagatctg gaaaaggttg 420
agctccmgtg tttgcatgat tatgctggag ttaattgcaag catcgg
```

(2) INFORMATION FOR SEQ ID NO:4266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1580089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4266:

```
Pro Ile Arg Arg Leu Pro Ile Ile Leu Pro Pro Asn Ser His Pro Ala
1      5      10      15
Ala Ser Pro Arg His His Thr Ser Ser Arg Arg Val Val Thr Gly Val
20      25      30
Lys Met Val Gly Pro Gly Leu Tyr Thr Glu Ile Gly Lys Lys Thr Arg
35      40      45
Asp Leu Leu Tyr Lys Asp Tyr Gln Thr Asp His Lys Phe Thr Leu Thr
50      55      60
Thr Tyr Thr Ser Asn Gly Val Ala Val Thr Ala Ser Ser Thr Lys Lys
65      70      75      80
Ala Asp Leu Ile Leu Gly Glu Ile Gln Ser Gln Ile Lys Asn Lys Asn
85      90      95
Met Thr Ile Asp Val Lys Ala Asn Ser Glu Ser Asn Ile Ile Thr Thr
100      105      110
Ile Thr Val Asp Glu Ile Ala Thr Pro Gly Leu Lys Thr Ile Leu Ser
115      120      125
Phe Ala Val Pro Asp Gln Arg Ser Gly Lys Gly
130      135
```

(2) INFORMATION FOR SEQ ID NO:4267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1580090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4267:

```
Met Val Gly Pro Gly Leu Tyr Thr Glu Ile Gly Lys Thr Arg Asp
1      5      10      15
Leu Leu Tyr Lys Asp Tyr Gln Thr Asp His Lys Phe Thr Leu Thr Thr
20      25      30
Tyr Thr Ser Asn Gly Val Ala Val Thr Ala Ser Ser Thr Lys Lys Ala
35      40      45
Asp Leu Ile Leu Gly Glu Ile Gln Ser Gln Ile Lys Asn Lys Asn Met
50      55      60
Thr Ile Asp Val Lys Ala Asn Ser Glu Ser Asn Ile Ile Thr Thr Ile
65      70      75      80
Thr Val Asp Glu Ile Ala Thr Pro Gly Leu Lys Thr Ile Leu Ser Phe
85      90      95
```

Ala Val Pro Asp Gln Arg Ser Gly Lys Gly
100 105

(2) INFORMATION FOR SEQ ID NO:4268:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..488
(D) OTHER INFORMATION: / Ceres Seq. ID 1580112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4268:

acaagcacaa	agagaggccc	cgaccgcgat	ggatcgtcag	cgacagaccg	accgtgacac	60
agccaacaac	taacacgcac	gcgcgcgcga	gagaaagaga	gctgcccggg	agagagagag	120
agaggaaatc	aaacgaaggg	gacgacgtac	ggagacggca	tgcccgatca	ccaccaccac	180
caccaccacg	ggcatccgcc	ggacggggccc	ggcggcgccg	gggaccagct	ggagtgtaac	240
aaggagcagg	accggctgct	gcccacgcgc	aacgtcggcc	gcacatgaa	gcagatccctg	300
ccgcccacag	ccaagatctc	caaggaggccc	aaggagacga	tcaggagtg	cgtgtccgag	360
ttcatcagct	tcgtcacggg	cgaggcctcc	gacaagtgcc	acaaggagaa	gcgcaagacc	420
gtcaacggcg	acgacgtctg	ctgcgccttc	ggcgcgctcg	gcttcgacga	ctacgtcgac	480
cccatgcg						

(2) INFORMATION FOR SEQ ID NO:4269:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1580113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4269:

Lys	His	Lys	Glu	Arg	Pro	Arg	Pro	Arg	Trp	Ile	Val	Ser	Asp	Arg	Pro
1			5						10				15		
Thr	Val	Thr	Gln	Pro	Thr	Thr	Asn	Thr	His	Ala	Arg	Glu	Arg	Glu	Arg
			20				25					30			
Glu	Leu	Pro	Gly	Arg	Glu	Arg	Glu	Arg	Lys	Ser	Asn	Glu	Gly	Asp	Asp
			35				40				45				
Val	Arg	Arg	Arg	His	Gly	Arg	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Ala
			50				55				60				
Ser	Ala	Gly	Arg	Ala	Arg	Arg	Gly	Gly	Pro	Ala	Gly	Gly	Asn	Gln	
65							70			75			80		
Gly	Ala	Gly	Pro	Ala	Ala	Ala	His	Arg	Gln	Arg	Arg	Pro	His	His	Glu
							85			90			95		
Ala	Asp	Pro	Ala	Ala	Gln	Arg	Gln	Asp	Leu	Gln	Gly	Gly	Gln	Gly	Asp
							100			105			110		
Asp	Ala	Gly	Val	Arg	Val	Arg	Val	His	Gln	Leu	Arg	His	Gly	Arg	Gly
							115			120			125		
Leu	Arg	Gln	Val	Pro	Gln	Gly	Glu	Ala	Gln	Asp	Arg	Gln	Arg	Arg	Arg
							130			135			140		
Arg	Leu	Leu	Arg	Leu	Arg	Ala	Arg	Leu	Arg	Arg	Leu	Arg	Arg	Pro	
145							150			155				160	
His	Ala														

(2) INFORMATION FOR SEQ ID NO:4270:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1580114
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4270:
Met Ala Asp His His His His His His His Gly His Pro Pro Asp Gly
1 5 10 15
Pro Gly Gly Ala Gly Asp Gln Leu Glu Val Ile Lys Glu Gln Asp Arg
20 25 30
Leu Leu Pro Ile Ala Asn Val Gly Arg Ile Met Lys Gln Ile Leu Pro
35 40 45
Pro Asn Ala Lys Ile Ser Lys Glu Ala Lys Glu Thr Met Gln Glu Cys
50 55 60
Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys
65 70 75 80
His Lys Glu Lys Arg Lys Thr Val Asn Gly Asp Asp Val Cys Cys Ala
85 90 95
Phe Gly Ala Leu Gly Phe Asp Asp Tyr Val Asp Pro Met
100 105

(2) INFORMATION FOR SEQ ID NO:4271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1580115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4271:

gacaagcaga gtcgcgccgg ccgaaccgcc acctcccttt ggcgcctcact catcagtcatt 60
ggcgctcgctg ccgcctggag ctccggcgctg gtcggtgacc ctgagcctaa ggcaaccgtgg 120
cgggctggag atccgtgccc cgccggagaa cttgctccca ggggtggggcc cgccgggggga 180
cgccatgtcc ctccgtctcc gctcccgccg ctgcctctct ctctccgtca catccaattg 240
cgccgctgct ccgcggcgca ccacacagcc cgcccgccgc ccgcgcggca cgagggctcgt 300
ccgcttctcg cggagcaggt gggcgccgct gccgcgggca cctccatttg gaggcgcaag 360
aaacagcccc cgccgcgcgc cgccgtgccc ccggaactgcc gggaccacgc gactegaacg 420
ctggcgccgc ctgtc

(2) INFORMATION FOR SEQ ID NO:4272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1580116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4272:

Asp Lys Gln Ser Arg Gly Gly Arg Thr Ala Thr Ser Leu Cys Ala Ser
1 5 10 15
Leu Ile Ser His Gly Val Ala Ala Ala Trp Thr Ser Gly Val Val Gly
20 25 30
Asp Pro Glu Pro Lys Ala Pro Trp Arg Ala Gly Asp Pro Cys Arg Arg
35 40 45
Gly Glu Leu Ala Pro Arg Val Gly Pro Arg Arg Gly Ala His Val Pro

(2) INFORMATION FOR SEQ ID NO:4273:

(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..144
(D) OTHER INFORMATION: / Ceres Seq. ID 1580117

Thr	Ser	Arg	Val	Ala	Ala	Ala	Glu	Pro	Pro	Pro	Phe	Ala	Pro	His
1			5					10					15	
Ser	Ser	Val	Met	Ala	Ser	Leu	Pro	Pro	Gly	Pro	Pro	Ala	Trp	Ser
1			20					25				30		Val
Thr	Leu	Ser	Leu	Arg	His	Arg	Gly	Gly	Leu	Glu	Ile	Arg	Ala	Ala
		35					40					45		
Glu	Asn	Leu	Leu	Pro	Gly	Trp	Gly	Arg	Gly	Gly	Glu	Arg	Met	Ser
	50					55					60			Leu
Leu	Leu	Arg	Leu	Arg	Arg	Cys	Leu	Leu	Ser	Val	Thr	Ser	Asn	Cys
65					70				75					80
Gly	Gly	Arg	Pro	Ala	Ala	Thr	Thr	Gln	Pro	Gly	Pro	Pro	Arg	Gly
				85				90					95	
Ser	Arg	Val	Val	Arg	Phe	Leu	Arg	Ser	Arg	Trp	Ala	Arg	Leu	Pro
			100					105				110		Arg
Ala	Pro	Pro	Phe	Gly	Gly	Ala	Arg	Asn	Ser	Pro	Arg	Arg	Ala	Pro
		115					120					125		Pro
Cys	Arg	Arg	Thr	Ala	Gly	Thr	Ser	Gly	Val	Glu	Arg	Trp	Arg	Gly
	130					135					140			Leu

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1580118

Met	Ala	Ser	Leu	Pro	Pro	Gly	Pro	Pro	Ala	Trp	Ser	Val	Thr	Leu	Ser
1				5					10					15	
Leu	Arg	His	Arg	Gly	Gly	Leu	Glu	Ile	Arg	Ala	Ala	Ala	Glu	Asn	Leu
			20					25					30		

Leu Pro Gly Trp Gly Arg Gly Gly Glu Arg Met Ser Leu Leu Leu Arg
35 40 45
Leu Arg Arg Cys Leu Leu Leu Ser Val Thr Ser Asn Cys Gly Gly Arg
50 55 60
Pro Ala Ala Thr Thr Gln Pro Gly Pro Pro Pro Arg Gly Ser Arg Val
65 70 75 80
Val Arg Phe Leu Arg Ser Arg Trp Ala Arg Leu Pro Arg Ala Pro Pro
85 90 95
Phe Gly Gly Ala Arg Asn Ser Pro Arg Arg Ala Pro Pro Cys Arg Arg
100 105 110
Thr Ala Gly Thr Ser Gly Val Glu Arg Trp Arg Gly Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:4275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4275:

aaggagcgcc	tgatagtcta	cgattacatg	cogaacctga	gcatacactc	tcagctccat	60
gggcagcacg	cggcggaagt	caacctcagc	tgggagagga	ggatgaggat	cgtgtggac	120
tcgcggaag	ggatcgcccta	cctgcaccac	agcgcgacgc	cgcacatcat	ccacagagac	180
gtgaaggcga	gcaacgtgct	cctggacgccc	gacttcagg	cgcgggtcgc	cgacttcggc	240
ttcgccaaac	tggtcccgga	cggcgcgacg	cacgtcacca	caagggtaaa	ggcacgctgg	300
ggtaacctgc	gccggagtag	cgatgctcgc	ggaaggcctc	cgagagctgc	gacgtcttca	360
gcttcggggt	cacgtcgtc					

(2) INFORMATION FOR SEQ ID NO:4276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4276:

Lys Glu Arg Leu Ile Val Tyr Asp Tyr Met Pro Asn Leu Ser Ile His
1 5 10 15
Ser Gln Leu His Gly Gln His Ala Ala Glu Cys Asn Leu Ser Trp Glu
20 25 30
Arg Arg Met Arg Ile Ala Val Asp Ser Ala Glu Gly Ile Ala Tyr Leu
35 40 45
His His Ser Ala Thr Pro His Ile Ile His Arg Asp Val Lys Ala Ser
50 55 60
Asn Val Leu Leu Asp Ala Asp Phe Gln Ala Arg Val Ala Asp Phe Gly
65 70 75 80
Phe Ala Lys Leu Val Pro Asp Gly Ala Thr His Val Thr Thr Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1580121
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4277:

Gly Ala Pro Asp Ser Leu Arg Leu His Ala Glu Pro Glu His Thr Leu
1 5 10 15
Ser Ala Pro Trp Ala Ala Arg Gly Gly Val Gln Pro Gln Leu Gly Glu
 20 25 30
Glu Asp Glu Asp Arg Cys Gly Leu Arg Gly Arg Asp Arg Leu Pro Ala
 35 40 45
Pro Gln Arg Asp Ala Ala His His Pro Gln Arg Arg Glu Gly Glu Gln
50 55 60
Arg Ala Pro Gly Arg Arg Leu Pro Gly Ala Gly Arg Arg Leu Arg Leu
65 70 75 80
Arg Gln Ala Gly Pro Gly Arg Arg Asp Ala Arg His His Lys Val Lys
 85 90 95
Gly Thr Leu Gly Tyr Leu Ala Pro Glu Tyr Ala Met Leu Gly Lys Ala
 100 105 110
Ser Glu Ser Cys Asp Val Phe Ser Phe Gly Val Thr Leu
 115 120 125

(2) INFORMATION FOR SEQ ID NO:4278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..86
 (D) OTHER INFORMATION: / Ceres Seq. ID 1580122
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4278:

Met Pro Asn Leu Ser Ile His Ser Gln Leu His Gly Gln His Ala Ala
1 5 10 15
Glu Cys Asn Leu Ser Trp Glu Arg Arg Met Arg Ile Ala Val Asp Ser
 20 25 30
Ala Glu Gly Ile Ala Tyr Leu His His Ser Ala Thr Pro His Ile Ile
 35 40 45
His Arg Asp Val Lys Ala Ser Asn Val Leu Leu Asp Ala Asp Phe Gln
50 55 60
Ala Arg Val Ala Asp Phe Gly Phe Ala Lys Leu Val Pro Asp Gly Ala
65 70 75 80
Thr His Val Thr Thr Arg
 85

(2) INFORMATION FOR SEQ ID NO:4279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..405
 (D) OTHER INFORMATION: / Ceres Seq. ID 1580127
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4279:

aatgcagagg tcgctgtgac ggcacaggaa gcagcagcag agcaggccag gaacaagaac 60
agcaatgaac tcgcgcgcgg gcgacgacgg cggcggcagc ggcacagcgt tattcgggtc 120
gggcggcatc cgcgggttcg gctacggcgt cggcgtgtcc atcggcatcc tctcgggtgc 180

caccaccatc gcgcctgcga tctacttctg caccgcgcacc tccatgcccc tgctccgcgc 240
cgccgcagcg ccgcgcgcgc agggcgcgga cgccggcgcg gccatcgacg aggccacgct 300
cgaggcggtc ccgcgcgttg cctacgcgga gccaggaag gcggcgcgga accaggcggtg 360
ctgctgcccc gtctgcctcg agtgctacgg cgacggcgac gtggt

(2) INFORMATION FOR SEQ ID NO:4280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1580128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4280:

Asn Ala Glu Val Ala Leu Thr Ala Gln Glu Ala Ala Glu Gln Ala
1 5 10 15
Arg Asn Lys Asn Ser Asn Glu Leu Ala Ala Gly Arg Arg Arg Arg Arg
20 25 30
Gln Arg Ala Arg Leu Ile Arg Val Gly Arg His Pro Arg Val Arg Leu
35 40 45
Arg Arg Arg Arg Val His Arg His Pro Pro Gly Gly His His His Arg
50 55 60
Ala Arg His Leu Leu Leu His Ala His Leu His Ala Arg Val Arg Arg
65 70 75 80
Arg Ala Ser Ala Ala Ala Gly Arg Arg Arg Ala Gly His Arg
85 90 95
Arg Gly His Ala Arg Gly Val Pro Gly Gly Gly Leu Arg Gly Gly
100 105 110
Glu Gly Gly Gly Glu Pro Gly Val Leu Leu Pro Arg Leu Pro Arg Val
115 120 125
Leu Arg Arg Arg Arg Arg Gly
130 135

(2) INFORMATION FOR SEQ ID NO:4281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1580129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4281:

Met Asn Ser Pro Pro Gly Asp Asp Gly Gly Gly Ser Ala His Gly Leu
1 5 10 15
Phe Gly Ser Gly Gly Ile Arg Gly Phe Gly Tyr Gly Val Gly Val Ser
20 25 30
Ile Gly Ile Leu Leu Val Ala Thr Thr Ile Ala Leu Ala Ile Tyr Phe
35 40 45
Cys Thr Arg Thr Ser Met Pro Val Ser Ala Ala Ala Pro Ala Pro Pro
50 55 60
Arg Gln Gly Gly Asp Ala Gly Arg Gly Ile Asp Glu Ala Thr Leu Glu
65 70 75 80
Ala Phe Pro Ala Val Ala Tyr Ala Glu Ala Arg Lys Ala Ala Ala Asn
85 90 95
Gln Ala Cys Cys Cys Pro Val Cys Leu Glu Cys Tyr Gly Asp Gly Asp
100 105 110
Val